









/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Pac I; Site 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5', AACTGGAAGATTAAATAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

Query Match 0.6%; Score 17.6; DB 1; Length 28;  
Best Local Similarity 83.3%; Pred. No. 2.5e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2804  
Db 1 AAATAAAATAAATAAATAA 24

RESULT 2253  
BQ583967/c

LOCUS BQ583967 29 bp mRNA linear EST 06-DEC-2002

DEFINITION S013297-024-004-B01-T7 MP1Z-ADIS-024-inflorescence Beta vulgaris

ACCESSION BQ583967

VERSION BQ583967.1 GI:26113544

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189

PUBMED 12472698

COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 29 Std Error: 0.00  
Plate: 4 row: B column: 01  
Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES  
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/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:182728"  
/db\_xref="taxon:161934"  
/clone="024-004-B01"  
/tissue\_type="inflorescence"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-inflorescence"  
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
SP6-Sali-CCACCGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match

0.6%; Score 17.6; DB 1; Length 29;

Query Match 0.6%; Score 17.6; DB 1; Length 29;  
Best Local Similarity 83.3%; Pred. No. 2.6e+03;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2804  
Db 29 AAAAAAAACAAAAA 6

RESULT 2254  
AZ492630/c

LOCUS AZ492630 29 bp DNA linear GSS 05-OCT-2000

DEFINITION 1M0326B22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0326B22 R, genomic survey sequence.

ACCESSION AZ492630

VERSION AZ492630.1 GI:10665537

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 29)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0326 row: B column: 22  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 29.

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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0326B22"  
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.6; DB 1; Length 29;



Thu Jun 10 13:10:24 2004

Best Local Similarity 83.3%; Pred. No. 2.6e+03; Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;		30 bp mRNA linear EST 18-AUG-2003	
LOCUS	CF331804	NACL--08-B04.b1 Rice callus plasmid cDNA library (NACL) Oryza	
DEFINITION		sativa cDNA clone NACL--08-B04, mRNA sequence.	
ACCESSION	CF331804		
VERSION	CF331804.1	GI:33811833	
KEYWORDS	EST.		
SOURCE	Oryza sativa		
ORGANISM	Oryza sativa		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.		
REFERENCE	1 (bases 1 to 30)		
AUTHORS	Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.		
TITLE	Large-scale Sequencing Analysis of Rice ESTs		
JOURNAL	Unpublished (2003)		
COMMENT	Contact: Nahm B.H.		
	Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University		
	Yongin, Kyeonggi, Korea		
	Tel: 82 31 330 6193		
	Fax: 82 31 321 6355		
	Email: bhnaem@gbio.com, bhnaem@bio.myongji.ac.kr.		
FEATURES	Location/Qualifiers		
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	/clone="NACL--08-B04"		
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	/dev_stage="proliferated callus on 2N6 media for 30 days"		
	/lab_host="E.coli DH10B"		
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	/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."		
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Best Local Similarity 83.3%; Pred. No. 2.6e+03;		VS Dictyostelium discoideum cDNA clone VSH136 5', mRNA	
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;			
QY	2779	AGATTGAAAAA	2802
Db	24	AGAAAGAGAGAAAAA	1
RESULT 2257		sequence.	
AU266959/c		AU266959	
LOCUS	AU266959	VS Dictyostelium discoideum	
DEFINITION		sequence.	
ACCESSION	AU266959		
VERSION	AU266959.1	GI:20525757	
KEYWORDS	EST.		
SOURCE	Dictyostelium discoideum		
ORGANISM	Dictyostelium discoideum		
	Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.		
REFERENCE	1 (bases 1 to 33)		
AUTHORS	Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M., Takeuchi, I., Kohara, Y. and Tanaka, Y.		
TITLE	Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum		
JOURNAL	Unpublished (2002)		
COMMENT	Contact: Hideko Urushihara		
	Institute of Biological Sciences		
	University of Tsukuba		
	1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan		
	Tel: 81-298-53-4664		
	Fax: 81-298-53-6614		
	Email: hideko@biol.tsukuba.ac.jp.		
FEATURES	Location/Qualifiers		
source	1..33		

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Best Local Similarity 83.3%; Pred. No. 2.6e+03; Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;		29 bp mRNA linear EST 06-DEC-2002	
LOCUS	BQ586486	E012391-024-012-J22-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone	
DEFINITION		024-012-J22 5-PRIME, mRNA sequence.	
ACCESSION	BQ586486		
VERSION	BQ586486.1	GI:26116068	
KEYWORDS	EST.		
SOURCE	Beta vulgaris		
ORGANISM	Beta vulgaris		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.		
REFERENCE	1 (bases 1 to 29)		
AUTHORS	Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M., Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H. and Radelof, U.		
TITLE	Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes		
JOURNAL	Plant J. 32 (5), 845-857 (2002)		
MEDLINE	22362189		
PUBMED	12472698		
COMMENT	Contact: Weisshaar B		
	ADIS DNA core facility at MP1Z		
	Max-Planck-Institute for Plant Breeding Research		
	Carl-von-Linne Weg 10, 50829 Koeln, Germany		
	Fax: 00492215062851		
	Email: weisshaar@mpiz-koeln.mpg.de		
	Insert Length: 29 Std Error: 0.00		
	Plate: 12 row: J column: 22		
	Seq primer: SP6; CATACGATTTAGTGACACTATAG.		
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	/db_xref="taxon:161934"		
	/clone="024-012-J22"		
	/tissue_type="leaf"		
	/lab_host="EMDH10B"		
	/clone_lib="MP1Z-ADIS-024-leaf"		
	/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:		
	SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"		
Query Match 0.6%; Score 17.6; DB 1; Length 29;		0.6%; Score 17.6; DB 1; Length 29;	
Best Local Similarity 83.3%; Pred. No. 2.6e+03;		Pred. No. 2.6e+03;	
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;			
QY	2779	AGATTGAAAAA	2802
Db	6	AGAGACCAAAAAA	29
RESULT 2256			
CF331804/c			



inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2783 TTGAAAAA 2801  
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Db 1 TTA 19

RESULT 2260  
AW248747 19 bp mRNA linear EST 07-JAN-2000  
LOCUS 2821119.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821119 3',  
DEFINITION mRNA sequence.  
ACCESSION AW248747  
VERSION AW248747.1 GI:6591740  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2821119.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 7 contiguous  
PHRED high quality bases following vector sequence. Very Low  
Quality Sequence: Trace file contained 19 contiguous distinct peaks  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LLCMS row: P column: 16  
High quality sequence stop: 7.

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/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match

0.6%; Score 17.4; DB 1; Length 19;

Best Local Similarity 94.7%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTT 2184  
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Db 1 TTTT 19

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LOCUS 2821119.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821119 3',  
DEFINITION mRNA sequence.  
ACCESSION AW248747  
VERSION AW248747.1 GI:6591740  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2821119.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 7 contiguous  
PHRED high quality bases following vector sequence. Very Low  
Quality Sequence: Trace file contained 19 contiguous distinct peaks  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LLCMS row: P column: 16  
High quality sequence stop: 7.

FEATURES  
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/tissue\_type="small cell carcinoma"  
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/lab\_host="DH10B (phage-resistant)"  
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/note="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.6%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAA 2804  
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Db 19 AAAAAA 1



RESULT 2262  
CF291665  
LOCUS  
DEFINITION  
CF291665  
14ROOT--02-D01.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--02-D01, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 19)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

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FEATURES
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Query Match  
 Best Local Similarity 0.6%; Score 17.4; DB 1; Length 19;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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CF291665/c				
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DEFINITION	14ROOT--02-D01.g1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--02-D01, mRNA sequence.			
ACCESSION	CF291665			
VERSION	CF291665.1	GI:33660698		
KEYWORDS	EST.			
SOURCE	Oryza sativa			
ORGANISM	Oryza sativa			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.			
AUTHORS	1 (bases 1 to 19) Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.			
TITLE	Large-scale Sequencing Analysis of Rice ESTs			
JOURNAL	Unpublished (2003)			
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355			

```

Email: bhnaheggbio.com, bhnahe@bio.myongji.ac.kr.
FEATURES
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      /organism="Oryza sativa"
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      /tissue_type="root"
      /dev_stage="14 days after germination"
      /lab_host="E.coli DH10B"
      /clone_lib="Rice root plasmid cDNA library (14ROOT)"
      /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
      with oligoribonucleotides and then used as templates for
      RT-PCR."

Query Match      0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2784 TCAAAAAAAAAAAAAAAAAAAAAA 2802
Db 19 TCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 2264
CF291899
LOCUS
DEFINITION
  CF291899 19 bp mRNA linear EST 14-AUG-2003
  sativa cDNA clone 14ROOT--02-I08, mRNA sequence.
ACCESSION
  CF291899
VERSION
  CF291899.1 GI:33660932
KEYWORDS
  EST.
SOURCE
  Oryza sativa
  Oryza sativa
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 19)
  Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
  Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Gyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
REFERENCE
  AUTHORS
  TITLE
  JOURNAL
  COMMENT

```

```

Email: bhnaahm@ggbio.com, bhnaahm@bio.myongji.ac.kr.
FEATURES
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      /mol_type="mRNA"
      /cultivar="Nackdong"
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      /dev_stage="14 days after germination"
      /lab_host="E.coli DH10B"
      /clone_lib="Rice root plasmid cDNA library (14ROOT)"
      /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.6%;   Score 17.4;   DB 1;   Length 19;
Best Local Similarity 94.7%;   Pred. No. 1.1e+03;
Matches 18;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy      2166  TTTTTTTTTTTTTTTTTTTT 2184
          | | | | | | | | | | | | | | | |
Db      1    TGT TTT TTT TTT TTT TTT TTT 19

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Query Match      0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 1.1e+03;
Matches 18: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT	2267
CF292072/c	
LOCUS	CF292072
DEFINITION	14ROOT--02-M03.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--02-M03, mRNA sequence.
ACCESSION	CF292072
VERSION	CF292072.1
KEYWORDS	EST.
SOURCE	Oryza sativa
ORGANISM	Oryza sativa
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 19)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

Fax: 82 31 321 6355  
E-mail: [bhnahm@ccbio.com](mailto:bhnahm@ccbio.com)  
[bhnahm@bio.pyongji.ac.kr](mailto:bhnahm@bio.pyongji.ac.kr)

FEATURES	Location/Qualifiers
----------	---------------------

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location, genome, and source
1. .19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--02-M03"
/tissue_type="root"
/age="14 days after germination"

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/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match 0.6%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
 |||||  
 19 AAAAAAAAAAAAAAAAAA 1  
 pb

Young, Kyeonggi, N  
Tel: 82 31 330 6193

RESULT 2268  
CF292144

LOCUS  
DEFINITION  
CF292144 19 bp mRNA linear EST 14-AUG-2003  
14ROOT--02-N17.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--02-N17, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
EST.  
CF292144.1 GI:33661177

ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 19)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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location/Qualifiers
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/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match	0.6%;	Score 17.4;	DB 1;	Length 19;
Best Local Similarity	94.7%;	Pred. NO. 1.1e+03;		
Matches 18; Conservative	0;	Mismatches 1.	Indels	0.

Qy	2166	TTTTTTTTTTTTTTTTTTTT	2184
Dd	1	TGTTTTTTTTTTTTTTTTTTTT	19

RESULT	2269				
CF292144/c					
LOCUS	CF292144	19 bp	mRNA	linear	EST 14-AUG-2003
DEFINITION	14ROOT--02-N17.b1	Rice root	plasmid	CDNA library	(14ROOT) Oryza
	sativa	CDNA clone	14ROOT--02-N17,	mRNA sequence.	
ACCESSION	CF292144				
VERSION	CF292144.1	GI:33661177			

REFERENCE	Emmalotcolueae; Oryzeae; Oryza.
AUTHORS	1 (bases 1 to 19) Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: [bhnam@ggbio.com](mailto:bhnam@ggbio.com), [bhnam@bio.myongji.ac.kr](mailto:bhnam@bio.myongji.ac.kr).  
Location/Qualifiers  
1. 19

## FEATURES

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1. .19
/organism="Oryza sativa"
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/tissue_type="root"
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/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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Query Match 0.6%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2804  
||| ||| ||| ||| ||| ||| |||  
Db 19 AAAAAAAAAAAAAACA 1

RESULT 2270  
CF309636/c

LOCUS CF309636 19 bp mRNA linear EST 15-AUG-2003  
DEFINITION ABF--03-008.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) *Oryza sativa* cDNA clone ABF--03-008, mRNA sequence.  
ACCESSION CF309636  
VERSION CF309636.1 GI:33681397  
KEYWORDS EST.  
SOURCE *Oryza sativa*  
ORGANISM *Oryza sativa*  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; *Oryza*.  
1 (bases 1 to 19)  
REFERENCE Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
CONTACT: Nahm, B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: [bhnam@ggbio.com](mailto:bhnam@ggbio.com), [bhnam@bio.myongji.ac.kr](mailto:bhnam@bio.myongji.ac.kr).  
Location/Qualifiers

FEATURES	SOURCE
1. <b>High Accuracy:</b> The model achieves a high accuracy rate, indicating its effectiveness in predicting the target variable.	Model Performance Metrics
2. <b>Robustness:</b> The model demonstrates robustness against various input variations and noise, ensuring reliable predictions.	Model Performance Metrics
3. <b>Scalability:</b> The model is designed to handle large-scale data efficiently, making it suitable for big data applications.	Model Performance Metrics
4. <b>Interpretability:</b> The model's predictions are interpretable, allowing users to understand the underlying factors influencing the results.	Model Performance Metrics
5. <b>Real-time Processing:</b> The model is optimized for real-time data processing, enabling immediate insights and decision-making.	Model Performance Metrics
6. <b>Customizable:</b> The model can be tailored to specific use cases and requirements, providing flexibility in its application.	Model Performance Metrics
7. <b>Integration:</b> The model seamlessly integrates with existing systems and workflows, facilitating easy adoption.	Model Performance Metrics
8. <b>Security:</b> The model adheres to strict security protocols, ensuring that data and predictions are protected from unauthorized access.	Model Performance Metrics
9. <b>Compliance:</b> The model is designed to comply with relevant industry regulations and standards, ensuring legal and ethical use.	Model Performance Metrics
10. <b>Support:</b> Comprehensive support and documentation are provided to assist users in maximizing the model's potential.	Model Performance Metrics

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1. .19
/organism="Oryza sativa"
/mol_type="mRNA"
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/db_xref="taxon:4530"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

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Query Match	0.6%	Score 17.4;	DB 1;	Length 19;
Best Local Similarity	94.7%;	Pred. NO. 1.1e+03;		
Matches 18; Conservative		0; Mismatches 1;	Indels 0;	Gaps 0;



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QY      2782 ATTGAAAAA 2800
Db      19 ATTCAAAAA 1

RESULT 2271
CF310688      19 bp mRNA linear EST 15-AUG-2003
LOCUS      ABF--05-H18.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION      library (ABF) Oryza sativa cDNA clone ABF--05-H18, mRNA sequence.
ACCESSION      CF310688
VERSION      CF310688.1 GI:33682449
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES      source
            /organism="Oryza sativa"
            /mol_type="mRNA"
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            /db_xref="taxon:4530"
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            /lab_host="E.coli DH10B"
            /clone_lib="ABF3-overexpressing transgenic rice plasmid
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            /note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
            for 2hrs. Oligo-capped mRNA was reverse transcribed and
            then used for PCR. mRNA was prepared from ABA-responsive
            element binding transcription factor 3 overexpression
            line."

Query Match      0.6%; Score 17.4; DB 1; Length 19;
Best Local Similarity      94.7%; Pred. No. 1.1e+03;
Matches      18; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      2166 TTTT 2184
Db      19 TGT 1

RESULT 2273
CF329136      19 bp mRNA linear EST 18-AUG-2003
LOCUS      NACL--04-F15.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION      sativa cDNA clone NACL--04-F15, mRNA sequence.
ACCESSION      CF329136
VERSION      CF329136.1 GI:33806509
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 19)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES      source
            /organism="Oryza sativa"
            /mol_type="mRNA"
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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES      source
            /organism="Oryza sativa"
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            /db_xref="taxon:4530"
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            /clone_lib="Rice callus plasmid cDNA library (NACL)"
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 2274  
CF329136/c  
LOCUS  
DEFINITION  
NACL--04-F15.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--04-F15, mRNA sequence.  
CF329136  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 19)

AUTHORS  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE  
Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL  
COMMENT  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES  
source  
Location/Qualifiers  
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/organism="Oryza sativa"  
/mol\_type="mRNA"  
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Query Match 0.6%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA AAAAAA 2804  
Db 19 AAAG AAAAAA AAAAAA AAAAAA 1

RESULT 2275  
CF329137/c  
LOCUS  
DEFINITION  
NACL--04-F15.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--04-F15, mRNA sequence.  
CF329137  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 19)

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 19)

AUTHORS  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE  
Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL  
COMMENT  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES  
source  
Location/Qualifiers  
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/organism="Oryza sativa"  
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Query Match 0.6%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2174 TTTT TTTT TTTT TTTT TTTT TTTT 2192  
Db 19 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 2276  
CF334610  
LOCUS  
DEFINITION  
JMT--03-P13.b1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--03-P13, mRNA sequence.  
CF334610  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 19)

AUTHORS  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE  
Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL  
COMMENT  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES  
source  
Location/Qualifiers  
1..19  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="JMT--03-P13"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"





purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2803  
|||||||  
Db 1 GAAAAAAAAAAAAAAAAAAAAA 19

RESULT 2279  
AZ363907  
LOCUS  
DEFINITION  
AZ363907 19 bp DNA linear GSS 02-OCT-2000  
1M0109113R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0109113 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0109 row: I column: 13  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0109113"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to

TITLE  
JOURNAL  
COMMENT

FEATURES  
source  
High quality sequence stop: 19.  
Location/Qualifiers  
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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184  
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Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 2280  
AZ363907/c  
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DEFINITION  
AZ363907 19 bp DNA linear GSS 02-OCT-2000  
1M0109113R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0109113 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0109 row: I column: 13  
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musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to

TITLE  
JOURNAL  
COMMENT

FEATURES  
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High quality sequence stop: 19.  
Location/Qualifiers  
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/clone="UUGC1M0109113"  
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Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match          0.6%;   Score 17.4;   DB 1;   Length 19;
Best Local Similarity 94.7%;   Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 ph 19 AAAAAAAAAATAAAAAAAAA 1

RESULT	2281
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DEFINITION	AZ447251 19 bp DNA linear GSS 04-OCT-2000 IM0244JL19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0244JL19 F. genomic survey sequence.

ACCESSION	AZ447251	
VERSION	AZ447251.1	GI:10599050
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 19)	
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.	
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb	

JOURNAL  
COMMENT

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
 Insert Length: 1000 Std Error: 0.00  
 Plate: 0244 row: J column: 19  
 Seq primer: CGTTCGTAACACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.

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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

```

laboratory mouse DNA resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWPA2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match	0.6%;	Score 17.4;	DB 1;	Length 19;
Best Local Similarity	94.7%;	Pred. No. 1.1e+03;		
Matches 18;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

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||| ||| ||| ||| ||| ||| ||| ||| |||  
pb 1 TTTTTTTTTTTTTTTATAA 19

RESULT 2282

LOCUS	AZ513919	19 bp	DNA	linear	GSS 05-OCT-2000
DEFINITION	1M0360E13F	Mouse 10kb plasmid	UUGCLM library	Mus musculus genomic	
		clone	UUGCLM0360E13 F.	genomic survey sequence.	

ACCESSION AZ513919  
VERSION AZ513919.1  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
COMMENT

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Fax: 801.303.2774  
 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
 Insert Length: 10000    Std Error: 0.00  
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/note="Vector: PWD42nv;
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Laboratory Mouse DNA Res
(http://www.jax.org/resG
was hydrodynamically she
0.005 inch orifice at cc
was blunt end-repaired w
polynucleotide kinase. A
ligated to the blunt end
adapted DNA was purifi
10.5 kb range using prep
electrophoresis. Vector
of PWD42 (gi|4732114|gb
inducible derivative of
with adaptors complement
purified. The sheared, a
adapted vector DNA, an
chemically-competent E.
and selected for ampicil

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Query Match 0.6%; Score 17.4; DB 1; Length 19;  
 Best Local Similarity 94.7%; Pred. No. 1.1e+03;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTCTTTTCTTTTCTTTT 2184  
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 Db 1 TTTTCTTTTCTTTTCTTTT 19

RESULT 2283  
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LOCUS  
 DEFINITION  
 AZ513919 19 bp DNA linear GSS 05-OCT-2000  
 1M0360E13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0360E13 F, genomic survey sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS

TITLE

JOURNAL  
 COMMENT

Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0360 row: E column: 13  
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 Class: plasmid ends  
 High quality sequence stop: 19.

FEATURES  
 source

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Query Match 0.6%; Score 17.4; DB 1; Length 19;  
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 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
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 Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 2284  
 AZ645841

LOCUS  
 DEFINITION  
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 1M0511G04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0511G04 R, genomic survey sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS

TITLE

JOURNAL  
 COMMENT

Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
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 High quality sequence stop: 19.

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Query Match

0.6%; Score 17.4; DB 1; Length 19;





QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
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RESULT 2287  
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LOCUS  
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clone UUGC1M0520N17 F, genomic survey sequence.

ACCESSION  
VERSION AZ650252.1 GI:11784550  
KEYWORDS  
SOURCE Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE  
AUTHORS 1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
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Plate: 0520 row: N column: 17  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

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Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184  
Db 19 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 2288  
AZ654747

LOCUS  
DEFINITION 1M0529F08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0529F08 F, genomic survey sequence.

ACCESSION  
VERSION AZ654747.1 GI:11791893  
KEYWORDS  
SOURCE Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE  
AUTHORS 1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0529 row: F column: 08  
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Class: plasmid ends  
High quality sequence stop: 19.

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Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 19;  
Best Local Similarity 94.7%; Pred. No. 1.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2184

Db

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RESULT 2289

AZ654747/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

19 bp DNA linear GSS 14-DEC-2000

1M0529F08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0529F08 F, genomic survey sequence.

AZ654747

AZ654747

GI:11791893

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0529 row: F column: 08

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/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity

Matches

18; Conservative

0;

Mismatches

1;

Indels

0;

Gaps

0;

QY

2786

AAAAAAAAAAAAAAAAAAAA 2804

|||||

Db

19 AAAAAAAAAAAAAAAAAA 1

RESULT 2290

AZ786336

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

19 bp DNA linear GSS 16-FEB-2001

2M0031H17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0031H17 R, genomic survey sequence.

AZ786336

AZ786336

GI:12923992

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0031 row: H column: 17

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. .19

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/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0031H17"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity

Matches

18; Conservative

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Mismatches

1;

Indels

0;

Gaps

0;

QY

2157

TTTTCTCTTTTTTTTTTT 2175

|||||

Db

1 TTTTCTCTTTTTTTTTTT 19



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RESULT 2291
CF308984/c
LOCUS
DEFINITION
  ABF--03-A01.g1 ABF3-overexpressing transgenic rice plasmid cDNA
  library (ABF) Oryza sativa cDNA clone ABF--03-A01, mRNA sequence.
ACCESSION
  CF308984
VERSION
  CF308984.1 GI:33680745
KEYWORDS
  EST.
SOURCE
  Oryza sativa
  Oryza sativa
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
  1 (bases 1 to 20)
AUTHORS
  Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
  Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
JOURNAL
  Contact: Nahm B.H.
COMMENT
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
  source
  1..20
  /organism="Oryza sativa"
  /mol_type="mRNA"
  /cultivar="Nackdong"
  /db_xref="taxon:4530"
  /clone="ABF--03-A01"
  /tissue_type="leaf"
  /dev_stage="14 days after germination"
  /lab_host="E.coli DH10B"
  /clone_lib="ABF3-overexpressing transgenic rice plasmid
  cDNA library (ABF)"
  /note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
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  then used for PCR. mRNA was prepared from ABA-responsive
  element binding transcription factor 3 overexpression
  line."
  Query Match 0.6%; Score 17.4; DB 1; Length 20;
  Best Local Similarity 94.7%; Pred. No. 1.3e+03;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
  |||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 2292
AZ375620
LOCUS
DEFINITION
  IM0129A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0129A08 F, genomic survey sequence.
ACCESSION
  AZ375620
VERSION
  AZ375620.1 GI:10489320
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
  Mus musculus
ORGANISM
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
  1 (bases 1 to 20)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Query Match 0.6%; Score 17.4; DB 1; Length 20;
  Best Local Similarity 94.7%; Pred. No. 1.3e+03;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
  |||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 2293
AZ486787/c
LOCUS
DEFINITION
  IM0315D23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0315D23 F, genomic survey sequence.
ACCESSION
  AZ486787
VERSION
  AZ486787.1 GI:10653904
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
  Mus musculus
ORGANISM
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 20)
AUTHORS
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Query Match 0.6%; Score 17.4; DB 1; Length 20;
  Best Local Similarity 94.7%; Pred. No. 1.3e+03;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
  |||||
Db 1 AAAAAAAAAATAAAAAAAAAAA 19
```

JOURNAL  
COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0129 row: A column: 08  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

## FEATURES

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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0129A08"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match

Best Local Similarity 94.7%; Score 17.4; DB 1; Length 20;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804

|||||

Db 1 AAAAAAAAAATAAAAAAAAAAA 19

RESULT 2293

AZ486787/c

LOCUS

DEFINITION

IM0315D23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0315D23 F, genomic survey sequence.

ACCESSION

AZ486787

VERSION

AZ486787.1 GI:10653904

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0315 row: D column: 23  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0315D23"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.3e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
Db 20 AAAAAAAAAAAAAAAAAAACAA 2

RESULT 2294  
AZ579122 20 bp DNA linear GSS 13-DEC-2000  
LOCUS 1M0363G19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0363G19 F, genomic survey sequence.  
ACCESSION AZ579122  
VERSION AZ579122.1 GI:11693583  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0363 row: G column: 19  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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/db\_xref="taxon:10090"  
/clone="UUGC1M0363G19"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.3e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAAAAAAAAAAAAA 19

RESULT 2295  
AZ949997 20 bp DNA linear GSS 27-APR-2001  
LOCUS 2M0213D24R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
DEFINITION clone UUGC2M0213D24 R, genomic survey sequence.  
ACCESSION AZ949997  
VERSION AZ949997.1 GI:13821224  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center







/clone\_lib="Mouse 10kb plasmid UUGClm library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 20;  
Best Local Similarity 94.7%; Pred. No. 1.3e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAA..... 2803  
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Db 19 GAAAAA..... 1

RESULT 2301  
AL048772

LOCUS AL048772 21 bp mRNA linear EST 04-SEP-2003  
DEFINITION DKFZp566N143\_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone  
DKFZp566N143, mRNA sequence.

ACCESSION AL048772.1 GI:4727843  
VERSION AL048772  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 21)  
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.  
TITLE EST (Koehrer, et al.)  
JOURNAL Unpublished (1999)  
COMMENT Contact: MIPS  
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES  
source  
Location/Qualifiers  
1..21  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp566N143"  
/tissue\_type="kidney"  
/dev\_stage="fetal"  
/lab\_host="X1-2blue"  
/clone\_lib="566 (synonym: hfkd2)"  
/note="Vector: pAMP1; Site\_1: NotI; Site\_2: SalI"

Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2783 TTGAAAAA..... 2801  
|||  
Db 3 TTAAAAA..... 21

RESULT 2302  
BX548564/c

LOCUS BX548564 21 bp mRNA linear EST 10-OCT-2003

DEFINITION BX548564 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tsel01g03\_plc, mRNA sequence.

ACCESSION BX548564  
VERSION BX548564.1 GI:33298798  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 21)

AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N

Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix qlc are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source

Location/Qualifiers  
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/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAA..... 2804  
|||||||  
Db 21 AAAAAA..... 3

RESULT 2303  
CF296213/c

LOCUS CF296213 21 bp mRNA linear EST 14-AUG-2003

DEFINITION 30DGS--06-H19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa cDNA clone 30DGS--06-H19, mRNA sequence.

ACCESSION CF296213  
VERSION CF296213.1 GI:33665246  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 21)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers  
1. .21  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 21 AAAAAAAAAACAAAAAAA 3

RESULT 2304

AZ308846/c

LOCUS

DEFINITION AZ308846 21 bp DNA linear GSS 29-SEP-2000  
1M0012H15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0012H15 F, genomic survey sequence.

ACCESSION

VERSION AZ308846.1 GI:10349246

KEYWORDS

SOURCE GSS.

ORGANISM Mus musculus (house mouse)

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS 1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss  
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University of Utah  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0012 row: H column: 15  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.

FEATURES

source

Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 21 AAAAAAAAAACAAAAAAA 3

RESULT 2305

AZ317208/c

LOCUS

DEFINITION AZ317208 21 bp DNA linear GSS 29-SEP-2000  
1M0035J02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0035J02 R, genomic survey sequence.

ACCESSION

VERSION AZ317208.1 GI:10365804

KEYWORDS

SOURCE GSS.

ORGANISM Mus musculus (house mouse)

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS 1 (bases 1 to 21)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0035 row: J column: 02  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.

FEATURES

source

Location/Qualifiers  
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/mol\_type="genomic DNA"  
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/clone="UUGC1M0035J02"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson



Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
||||| |||||||||  
Db 21 AAAAAAGAAAAAAAAAAAAAA 3

RESULT 2306  
AZ486776/c  
LOCUS  
DEFINITION 21 bp DNA linear GSS 05-OCT-2000  
clone UUGC1M0315M10 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE  
AUTHORS  
1 (bases 1 to 21)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
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84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0315 row: M column: 10  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
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/clone="UUGC1M0315M10"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
||||| |||||||||  
Db 21 AAAAAATAAAAAAAAAAAAAAA 3

RESULT 2307  
AZ822825

LOCUS  
DEFINITION 21 bp DNA linear GSS 20-FEB-2001  
clone UUGC2M0096I20 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 21)

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
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84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0096 row: I column: 20  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
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/clone="UUGC2M0096I20"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAACAAAAAAAAA 19

RESULT 2308  
AZ853429  
LOCUS AZ853429 21 bp DNA linear GSS 21-FEB-2001  
DEFINITION 2M0156D09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0156D09 R, genomic survey sequence.

ACCESSION AZ853429 GI:13041543  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 21)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0156 row: D column: 09  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers

FEATURES  
source  
1. .21  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAACAAAAAAAAA 19

RESULT 2309  
AZ627840/c  
LOCUS AZ627840 21 bp DNA linear GSS 13-DEC-2000  
DEFINITION 1M0474B05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0474B05 F, genomic survey sequence.

ACCESSION AZ627840 GI:11750126  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 21)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0474 row: B column: 05  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers

FEATURES  
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1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0474B05"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 21 AAAAAAAAAAAAAAAAAA 3

RESULT 2310  
CF319625/c  
LOCUS  
DEFINITION  
HD--10-D06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--10-D06, mRNA sequence.  
ACCESSION  
CF319625  
VERSION  
CF319625.1 GI:33691386  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa  
ORGANISM  
Oryza sativa

REFERENCE  
AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE  
Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1. .21  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="HD--10-D06"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2169 TTTTTTTTTTTTTTTT 2187  
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Db 21 TTTTTTTTTTTTTTATA 3

RESULT 2311  
AZ341108/c

LOCUS  
DEFINITION  
1M0073014F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0073014 F, genomic survey sequence.  
ACCESSION  
AZ341108  
VERSION  
AZ341108.1 GI:10417030  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus

REFERENCE  
AUTHORS  
1 (bases 1 to 21)

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0073 row: 0 column: 14  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
1. .21

FEATURES  
source  
1. .21

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 21;  
Best Local Similarity 94.7%; Pred. No. 1.5e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2162 CTCCTTTTTTTTTTTT 2180  
|  
Db 19 CCCCCCTTTTTTTTTT 1



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RESULT 2312
TA303G05P
LOCUS          TA303G05P          22 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION     T. brucei sheared genomic DNA clone 303g05, forward sequence,
                genomic survey sequence.
ACCESSION      AL497383
VERSION        AL497383.1  GI:11865504
KEYWORDS
SOURCE
ORGANISM       Trypanosoma brucei
                Trypanosoma brucei
                Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                Trypanosoma.
REFERENCE      1 (bases 1 to 22)
AUTHORS        Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
                Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
                Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE          Direct Submission
JOURNAL
COMMENT        Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
                project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
                Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                nh1@sanger.ac.uk
                Constructed at the Institute for Genomic Research (TIGR),
                Rockville, MD. Genomic DNA isolated from a cloned population of
                Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
                to give a tight size distribution (
                4 kb). The v + i method used for the library construction is
                described in detail in Smith, H. and Venter, J.C. (Making small
                insert libraries for whole genome shotgun sequencing projects. In
                Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
                Barrell, Oxford University Press, 1999).
                Email: nelsayed@tigr.org
                Details of T. brucei sequencing at the Sanger Centre are available
                at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES       Location/Qualifiers
                source
                1..22
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                Query Match          0.6%;   Score 17.4;   DB 1;   Length 22;
                Best Local Similarity 94.7%;   Pred. No. 1.7e+03;
                Matches 18;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      2786  AAAAAAAAAAAAAAAAAAAAAA 2804
        |||||
Db      1  AAAAAAAAAAAAGAAAAA 19

RESULT 2313
CF318882/c
LOCUS          CF318882          22 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION     HD--09-C23.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
                library (HD) Oryza sativa cDNA clone HD--09-C23, mRNA sequence.
ACCESSION      CF318882
VERSION        CF318882.1  GI:33690643
KEYWORDS       EST.
SOURCE         Oryza sativa
ORGANISM       Oryza sativa
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 22)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
```

```

Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES       Location/Qualifiers
                source
                1..22
                /organism="Oryza sativa"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:4530"
                /clone="HD--09-C23"
                /tissue_type="callus"
                /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                /lab_host="E.coli DH10B"
                /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
                cDNA library (HD)"
                /note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
                treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                reverse transcribed and then used for PCR. mRNA was
                derived from rice Histone Deacetylase overexpression
                line."
                Query Match          0.6%;   Score 17.4;   DB 1;   Length 22;
                Best Local Similarity 94.7%;   Pred. No. 1.7e+03;
                Matches 18;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      2782  ATTGAAAAAAAAAAAAAAAAAA 2800
        |||||
Db      19  ATTCAAAAAAAAAAAAAAAAAA 1

RESULT 2314
AZ307896
LOCUS          AZ307896          22 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION     IM0010N18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                clone UUGC1M0010N18 F, genomic survey sequence.
ACCESSION      AZ307896
VERSION        AZ307896.1  GI:10347346
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 22)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
                University of Utah Genome Center
                University of Utah
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                84112, USA
                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: ddunn@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0010 row: N column: 18
                Seq primer: CGTGTAAACGACGCCAGT
                Class: plasmid ends
                High quality sequence stop: 22.
FEATURES       Location/Qualifiers
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                1..22
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                /strain="C57BL/6J"
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                /sex="Male"
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                /clone_lib="Mouse 10kb plasmid UUGC1M library"
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 22;  
Best Local Similarity 94.7%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2165 CTTTCTTTTCTTTTCTTTT 2183  
| | | | | | | | | | | | | | | | | | | | | |  
Db 4 CTTTGTCTTTTCTTTTCTTTT 22

RESULT 2315  
AZ317017 22 bp DNA linear GSS 29-SEP-2000  
LOCUS 1M0035P09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0035P09 F, genomic survey sequence.

ACCESSION AZ317017  
VERSION AZ317017.1 GI:10365400  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0035 row: P column: 09  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.

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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 22;  
Best Local Similarity 94.7%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2162 CTCCTTTTCTTTTCTTTT 2180  
| | | | | | | | | | | | | | | | | | | | | |  
Db 4 CCCCTTTTCTTTTCTTTT 22

RESULT 2316  
AZ486853/c

LOCUS 23 bp DNA linear GSS 05-OCT-2000  
DEFINITION 1M0315M14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0315M14 R, genomic survey sequence.

ACCESSION AZ486853  
VERSION AZ486853.1 GI:10654033  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0315 row: M column: 14  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 23.

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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson





was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 23;  
Best Local Similarity 94.7%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
||||||| |||||||  
Db 1 AAAAAAAAAAAAAAAAAA 19

RESULT 2319  
AZ627841/C  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AZ627841 23 bp DNA linear GSS 13-DEC-2000  
1M0474E01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0474E01 F, genomic survey sequence.

AZ627841  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 23)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0474 row: E column: 01  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 23.

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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 23;  
Best Local Similarity 94.7%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
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Db 23 AAAAAAAAAATAAAAAAAAA 5

RESULT 2320  
TA55C06P  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
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/mol\_type="genomic DNA"  
/strain="TREU927"  
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/clone="55c06"

TA55C06P 23 bp DNA linear GSS 13-DEC-2000  
T. brucei sheared genomic DNA clone 55c06, forward sequence,  
genomic survey sequence.

AL455778  
AL455778.1 GI:11856729  
GSS.  
Trypanosoma brucei  
Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.  
1 (bases 1 to 23)  
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,  
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,  
Melville,S.E., Rajandream,M.A. and Barrell,B.G.  
Direct Submission  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nhl@sanger.ac.uk  
Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (  
4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available  
at http://www.sanger.ac.uk/Projects/T\_brucei/.

Query Match 0.6%; Score 17.4; DB 1; Length 23;  
Best Local Similarity 94.7%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
||||||| |||||||  
Db 1 AAAAAAAAAATAAAAAAAAA 19







Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. .24  
/organism="Oryza sativa"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 17.4; DB 1; Length 24;  
Best Local Similarity 94.7%; Pred. No. 2.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2172 TTTTCTTTTCTTTTAACT 2190

Db 1 TTTTCTTTTCTTTTAAAT 19

RESULT 2327

CF327904/c

LOCUS

DEFINITION NACL--02-J06.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--02-J06, mRNA sequence.

ACCESSION CF327904

VERSION CF327904.1 GI:33804058

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 24)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1. .24  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
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/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 17.4; DB 1; Length 24;  
Best Local Similarity 94.7%; Pred. No. 2.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2782 ATTTAAAAAATAAAAAA 2800

Db 19 ATTTAAAAAATAAAAAA 1

RESULT 2328

TA155F12Q/c

LOCUS

DEFINITION

T. brucei sheared genomic DNA clone 155f12, reverse sequence, genomic survey sequence.

ACCESSION AL472698

VERSION AL472698.1 GI:11838089

KEYWORDS GSS.

SOURCE

ORGANISM

Trypanosoma brucei

Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

1 (bases 1 to 24)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE

JOURNAL

COMMENT

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available

at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

FEATURES

source

1. .24  
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Query Match 0.6%; Score 17.4; DB 1; Length 24;  
Best Local Similarity 94.7%; Pred. No. 2.1e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2162 CTCCTTTTCTTTTCTTTTCTTTT 2180

Db 19 CCCCTTTTCTTTTCTTTTCTTTT 1

RESULT 2329

TA388E06P

LOCUS

DEFINITION

T. brucei sheared genomic DNA clone 388e06, forward sequence, genomic survey sequence.

ACCESSION AL498782

VERSION AL498782.1 GI:11874504

KEYWORDS GSS.

SOURCE

ORGANISM

Trypanosoma brucei

Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 25)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE

JOURNAL

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999). Email: nelsayed@tigr.org Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T\_brucei/.

FEATURES source  
1. .25  
/organism="Trypanosoma brucei"  
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Best Local Similarity 94.7%; Pred. No. 2.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
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Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 2330  
AV737092  
LOCUS AV737092 25 bp mRNA linear EST 17-OCT-2000  
DEFINITION AV737092 CB Homo sapiens cDNA clone CBFIB11 5', mRNA sequence.  
ACCESSION AV737092  
VERSION AV737092.1 GI:10854673  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z., Chen,S., Mao,M. and Chen,Z.  
TITLE Homo sapiens CB library cDNA clones  
JOURNAL Unpublished (2000)  
COMMENT Contact: Zhu Chen  
Shanghai Institute of Hematology, Rui-Jin Hospital  
197 Rui-Jin II Road, Shanghai 200025, P. R. China  
Tel: 86-21-64740490  
Fax: 86-21-64743206  
Email: mbshi@ms.stn.sh.cn  
This clone is available at Shanghai Hematology Institute in Shanghai.  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.

FEATURES source  
1. .25  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CBFIB11"  
/tissue\_type="cord blood"  
/cell\_type="CD34+ hematopoietic stem/progenitor cell"  
/lab\_host="BM25.8"  
/clone\_lib="CB"  
/note="Vector: pBluescript; Site 1: EcoRI; The insert is cloned randomly with the EcoRI digestion"

Query Match 0.6%; Score 17.4; DB 1; Length 25;  
Best Local Similarity 94.7%; Pred. No. 2.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804

Db 6 AAAAAAAAAAAAAAAAAAAAA 24  
|||||

RESULT 2331  
AU012885/c  
LOCUS AU012885 25 bp mRNA linear EST 03-AUG-1998  
DEFINITION AU012885 Schizosaccharomyces pombe late log phase cDNA  
Schizosaccharomyces pombe cDNA clone spc07426, mRNA sequence.  
ACCESSION AU012885  
VERSION AU012885.1 GI:3357794  
KEYWORDS EST.  
SOURCE Schizosaccharomyces pombe (fission yeast)  
ORGANISM Schizosaccharomyces pombe  
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
Schizosaccharomycetales; Schizosaccharomycetaceae;  
Schizosaccharomyces.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Morimyo,M. and Mita,K.  
TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe  
JOURNAL Unpublished (1998)  
COMMENT Contact: Mitsuoki Morimyo  
Genome Research Group  
National Institute of Radiological Sciences  
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan  
Email: morimyo@nirs.go.jp.

FEATURES source  
1. .25  
/organism="Schizosaccharomyces pombe"  
/mol\_type="mRNA"  
/strain="972"  
/db\_xref="taxon:4896"  
/clone="spc07426"  
/sex="h minus"  
/clone\_lib="Schizosaccharomyces pombe late log phase cDNA"  
/note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

Query Match 0.6%; Score 17.4; DB 1; Length 25;  
Best Local Similarity 94.7%; Pred. No. 2.2e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2176 TTTTTTTTTTAACTTTGA 2194  
|||||  
Db 25 TTTTTTTTTTAGCTTTGA 7

RESULT 2332  
BX554728/c  
LOCUS BX554728 26 bp mRNA linear EST 10-OCT-2003  
DEFINITION BX554728 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse17b03\_plc, mRNA sequence.  
ACCESSION BX554728  
VERSION BX554728.1 GI:33436050  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942

PUBMED  
COMMENT  
14519198  
Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix qlc are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source  
Location/Qualifiers  
1. .26  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tsel17b03\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17.4; DB 1; Length 26;  
Best Local Similarity 94.7%; Pred. No. 2.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||  
Db 26 AAAAAAAAAAAAAAAAAACA 8

RESULT 2333  
BQ585188/c  
LOCUS  
DEFINITION  
S014222-024-001-E10-SP6 MP1Z-ADIS-024-inflorescence Beta vulgaris  
cDNA clone 024-001-E10 5-PRIME, mRNA sequence.

ACCESSION  
BQ585188.1 GI:26114770  
VERSION  
BQ585188.1  
KEYWORDS  
EST.  
SOURCE  
Beta vulgaris  
ORGANISM  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE  
AUTHORS  
1 (bases 1 to 26)  
Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL  
MEDLINE  
PUBMED  
Plant J. 32 (5), 845-857 (2002)

COMMENT  
Contact: Weissshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaar@mpiz-koeln.mpg.de  
Insert Length: 26 Std Error: 0.00  
Plate: 1 Row: E Column: 10  
Seq primer: SP6; CATACGATTGAGTGACACTATAG.

FEATURES  
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Location/Qualifiers  
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/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:181514"

/db\_xref="taxon:161934"  
/clone="024-001-E10"  
/tissue\_type="inflorescence"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-inflorescence"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
Project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 17.4; DB 1; Length 26;  
Best Local Similarity 94.7%; Pred. No. 2.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2783 TTGAAAAAAAAAAAAAAAAAAAAA 2801  
|||  
Db 26 TTAATAAAAAAAAAAAAAAAAAA 8

RESULT 2334  
TA319G03Q  
LOCUS  
DEFINITION  
T. brucei sheared genomic DNA clone 319g03, reverse sequence,  
genomic survey sequence.

ACCESSION  
AL492820  
VERSION  
AL492820.1 GI:11867590  
KEYWORDS  
GSS.  
SOURCE  
Trypanosoma brucei  
ORGANISM  
Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.  
1 (bases 1 to 26)  
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,  
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,  
Melville,S.E., Rajandream,M.A. and Barrell,B.G.

TITLE  
JOURNAL  
Direct Submission  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxtton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk

COMMENT  
Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (  
4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available  
at http://www.sanger.ac.uk/Projects/T\_brucei/.

FEATURES  
source  
Location/Qualifiers  
1. .26  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="319g03"

Query Match 0.6%; Score 17.4; DB 1; Length 26;  
Best Local Similarity 94.7%; Pred. No. 2.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2162 CTCCTTTTCTTTTCTTTTCTTTT 2180  
|  
Db 8 CCCCTTTTCTTTTCTTTTCTTTT 26



RESULT 2335  
BX568027  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
FEATURES  
source

BX568027 29 bp mRNA linear EST 14-OCT-2003  
BX568027 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tse91d12\_q1c, mRNA sequence.  
BX568027.1 GI:33434924  
EST.  
Glossina morsitans morsitans  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscidae; Glossinidae; Glossina.  
1 (bases 1 to 29)  
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,  
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
Genome Biol. 4 (10), R63 (2003)  
22881942  
14519198  
Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all p1c reads are from  
the 3' end.  
Location/Qualifiers  
1. .29  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse91d12\_q1c"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17.4; DB 1; Length 29;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 2336  
AU268044  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
FEATURES  
source

AU268044 31 bp mRNA linear EST 10-MAY-2002  
AU268044 VS Dictyostelium discoideum cDNA clone VSH836 5', mRNA  
sequence.  
AU268044  
AU268044.1 GI:20526842  
EST.  
Dictyostelium discoideum  
Dictyostelium discoideum  
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
1 (bases 1 to 31)  
Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M.,  
Takeuchi, I., Kohara, Y. and Tanaka, Y.  
Population analysis of cDNAs from unicellular and multicellular

Query Match 0.6%; Score 17.4; DB 1; Length 29;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 2337  
AZ579477  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

AZ579477 31 bp DNA linear GSS 13-DEC-2000  
IM0367A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0367A08 F, genomic survey sequence.  
AZ579477  
AZ579477.1 GI:11693906  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 31)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0367 row: A column: 08  
Seq primer: CGTTGTAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 31.  
Location/Qualifiers  
1. .31  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0367A08"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.

Query Match 0.6%; Score 17.4; DB 1; Length 31;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 2337  
AZ579477  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

AZ579477 31 bp DNA linear GSS 13-DEC-2000  
IM0367A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0367A08 F, genomic survey sequence.  
AZ579477  
AZ579477.1 GI:11693906  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 31)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0367 row: A column: 08  
Seq primer: CGTTGTAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 31.  
Location/Qualifiers  
1. .31  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0367A08"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.

JOURNAL  
COMMENT  
stages of Dictyostelium discoideum  
Unpublished (2002)  
Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: hideko@biol.tsukuba.ac.jp.  
Location/Qualifiers  
1. .31  
/organism="Dictyostelium discoideum"  
/mol\_type="mRNA"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="VSH836"  
/sex="mat A"  
/dev\_stage="vegetative"  
/clone\_lib="VS"  
Query Match 0.6%; Score 17.4; DB 1; Length 31;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAAAAAAAAAAAAAA 19

RESULT 2337  
AZ579477  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

AZ579477 31 bp DNA linear GSS 13-DEC-2000  
IM0367A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0367A08 F, genomic survey sequence.  
AZ579477  
AZ579477.1 GI:11693906  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 31)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0367 row: A column: 08  
Seq primer: CGTTGTAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 31.  
Location/Qualifiers  
1. .31  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0367A08"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.4; DB 1; Length 31;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2803  
|||||  
Db 3 GAAAAAAAAAAAAAAAAAGA 21

RESULT 2338  
AL941390/c 32 bp DNA linear GSS 24-OCT-2002  
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-257B04-014921,  
DEFINITION genomic survey sequence.  
ACCESSION AL941390  
VERSION AL941390.1 GI:24397988  
KEYWORDS GSS.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.  
and Weisshaar,B.  
A pipeline for automated high-throughput generation of FSTs  
(flanking sequence tags) from Arabidopsis thaliana T-DNA  
transformed lines  
Unpublished  
2 Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.  
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)  
for flanking sequence tag based reverse genetics

Unpublished  
3 (bases 1 to 32)  
Rosso,M., Li,Y., Strizhov,N. and Weisshaar,B.  
Direct Submission  
Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer  
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
This sequence is recovered from the left border of the T-DNA. It  
indicates an insertion close to or within gene At5g42900. The  
sequences are generated at the MPI for Plant Breeding Research in  
the context of the GABI-Kat project. GABI-Kat is part of the German  
Plant Genomics program designated 'GABI'. Information on line  
availability can be found at:  
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES  
source  
1. .32  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="GK-257B04-014921"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thaliana nuclear genome sequence were processed for submission. T-DNA derived sequences were removed"

Query Match 0.6%; Score 17.4; DB 1; Length 32;  
Best Local Similarity 94.7%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 32 AAAAAAAAAAAAAAAAAAGA 14

RESULT 2339  
TA369C05P 37 bp DNA linear GSS 15-DEC-2000  
LOCUS T. brucei sheared genomic DNA clone 369c05, forward sequence,  
DEFINITION genomic survey sequence.  
ACCESSION AL496346  
VERSION AL496346.1 GI:11872269  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.

REFERENCE 1 (bases 1 to 37)  
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,  
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,  
Melville,S.E., Rajandream,M.A. and Barrell,B.G.  
Direct Submission  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nhl@sanger.ac.uk  
Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (  
4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

FEATURES  
source  
1. .37  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="369c05"

Query Match 0.6%; Score 17.4; DB 1; Length 37;  
Best Local Similarity 94.7%; Pred. No. 2.4e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 2 AAAAAAAAAAGAAAAAAAAA 20

RESULT 2340  
CF642215 39 bp mRNA linear EST 02-OCT-2003  
LOCUS CF642215  
DEFINITION D49\_A04 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA





Insert Length: 10000 Std Error: 0.00  
Plate: 0286 row: I column: 12  
Seq primer: CACACAGGAACACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.

FEATURES

Location/Qualifiers  
1. .22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0286I12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17.2; DB 1; Length 22;  
Best Local Similarity 86.4%; Pred. No. 1.8e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2154 ATTTTTCCTCTTTT 2175  
Db 22 ATTTTTCCTCTTTT 1

RESULT 2343

CF311534/c  
LOCUS CF311534 23 bp mRNA linear EST 15-AUG-2003  
DEFINITION ABF--06-M14.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--06-M14, mRNA sequence.  
ACCESSION CF311534  
VERSION CF311534.1 GI:33683295  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers  
1. .23  
/organism="Oryza sativa"  
/mol\_type="mRNA"

/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="ABF--06-M14"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.6%; Score 17.2; DB 1; Length 23;  
Best Local Similarity 86.4%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2782 ATTGAAAAA 2803  
Db 22 AGTCACAAAAA 1

RESULT 2344

AU267617  
LOCUS AU267617 23 bp mRNA linear EST 10-MAY-2002  
DEFINITION AU267617 VS Dictyostelium discoideum cDNA clone VSH555 5', mRNA sequence.  
ACCESSION AU267617 GI:20526415  
VERSION AU267617.1  
KEYWORDS EST.  
SOURCE Dictyostelium discoideum  
ORGANISM Dictyostelium discoideum  
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriiki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.  
TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum  
JOURNAL Unpublished (2002)  
COMMENT Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: hideko@biol.tsukuba.ac.jp.

FEATURES

Location/Qualifiers  
1. .23  
/organism="Dictyostelium discoideum"  
/mol\_type="mRNA"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="VSH555"  
/sex="mat A"  
/dev\_stage="vegetative"  
/clone\_lib="VS"

Query Match 0.6%; Score 17.2; DB 1; Length 23;  
Best Local Similarity 86.4%; Pred. No. 2e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2777 TTAGAAATTGAAAAA 2798  
Db 2 TTAGAAATTGATAAAAAA 23

RESULT 2345

CF290998/c  
LOCUS CF290998 23 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--01-E03.g1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--01-E03, mRNA sequence.  
ACCESSION CF290998



DEFINITION NACL--02-007.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--02-007, mRNA sequence.  
ACCESSION CF328136  
VERSION CF328136.1 GI:33804522  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
FEATURES  
source  
1. .24  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="NACL--02-007"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."  
Query Match 0.6%; Score 17.2; DB 1; Length 24;  
Best Local Similarity 86.4%; Pred. No. 2.2e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2171 TTTTCTTTTCTTTTAACTTT 2192  
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Db 24 TTTTCTTTTCTTTTAACTCT 3  
RESULT 2349  
AZ349008  
LOCUS AZ349008 24 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0085013R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0085013 R, genomic survey sequence.  
ACCESSION AZ349008  
VERSION AZ349008.1 GI:10428245  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0085 row: 0 column: 13  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers  
FEATURES  
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1. .24  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0085013"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."  
Query Match 0.6%; Score 17.2; DB 1; Length 24;  
Best Local Similarity 86.4%; Pred. No. 2.2e+03;  
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2158 TTTTCTCTTTTCTTTTCTTTT 2179  
|||||  
Db 3 TTTGTTCTGTTTTTCTTTTCTTTT 24  
RESULT 2350  
AV740046  
LOCUS AV740046 25 bp mRNA linear EST 17-OCT-2000  
DEFINITION AV740046 CB Homo sapiens cDNA clone CBFANF04 5', mRNA sequence.  
ACCESSION AV740046  
VERSION AV740046.1 GI:10857627  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,  
Chen,S., Mao,M. and Chen,Z.  
TITLE Homo sapiens CB library cDNA clones  
JOURNAL Unpublished (2000)  
COMMENT Contact: Zhu Chen  
Shanghai Institute of Hematology, Rui-Jin Hospital  
197 Rui-Jin II Road, Shanghai 200025, P. R. China  
Tel: 86-21-64740490  
Fax: 86-21-64743206  
Email: mbshi@ms.stn.sh.cn  
This clone is available at Shanghai Hematology Institute in  
Shanghai.  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.  
Location/Qualifiers  
FEATURES  
source  
1. .25







/tissue\_type="storage root"  
/lab\_host="EMDH10B"  
/clone\_lib="MPIZ-ADIS-024-storage root"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAA 2802  
Db 1 AAAAAAAAAAAAAA 17  
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RESULT 2356  
BQ590687/c  
LOCUS  
DEFINITION  
BQ590687 17 bp mRNA linear EST 06-DEC-2002  
cDNA clone 024-018-B24-T7 MPIZ-ADIS-024-storage root Beta vulgaris  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 17)  
Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Weissshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaar@mpiz-koeln.mpg.de  
Insert Length: 17 Std Error: 0.00  
Plate: 18 row: B column: 24  
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Location/Qualifiers  
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/mol\_type="mRNA"  
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line)"  
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/db\_xref="taxon:161934"  
/clone="024-018-B24"  
/tissue\_type="storage root"  
/lab\_host="EMDH10B"  
/clone\_lib="MPIZ-ADIS-024-storage root"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet

FEATURES  
source  
1. .17  
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/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:189432"  
/db\_xref="taxon:161934"  
/clone="024-018-B24"  
/tissue\_type="storage root"  
/lab\_host="EMDH10B"  
/clone\_lib="MPIZ-ADIS-024-storage root"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"  
Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 17 TTTT TTTT TTTT TTTT TTTT 1  
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RESULT 2357  
BQ591177  
LOCUS  
DEFINITION  
BQ591177 17 bp mRNA linear EST 06-DEC-2002  
cDNA clone 024-017-B22-T7 MPIZ-ADIS-024-storage root Beta vulgaris  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 17)  
Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Weissshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaar@mpiz-koeln.mpg.de  
Insert Length: 17 Std Error: 0.00  
Plate: 17 row: B column: 22  
Seq primer: T7; GTAATACGACTCACTATAGGCG.  
Location/Qualifiers  
1. .17  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
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line)"  
/db\_xref="GABI:188948"  
/db\_xref="taxon:161934"  
/clone="024-017-B22"  
/tissue\_type="storage root"  
/lab\_host="EMDH10B"  
/clone\_lib="MPIZ-ADIS-024-storage root"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

FEATURES  
source  
1. .17  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:188948"  
/db\_xref="taxon:161934"  
/clone="024-017-B22"  
/tissue\_type="storage root"  
/lab\_host="EMDH10B"  
/clone\_lib="MPIZ-ADIS-024-storage root"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"  
Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
|||||







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/clone="7LEAF--02-A18"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.6%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT TTTT TTTT 2182
Db      1 TTTT TTTT TTTT TTTT TTTT TTTT 17

RESULT 2364
CF298589/c
LOCUS      CF298589      17 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION 7LEAF--02-A18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--02-A18, mRNA sequence.
ACCESSION  CF298589
VERSION     CF298589.1 GI:33670350
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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QY      2786 AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA 2802
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RESULT 2365
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LOCUS      CF302447      17 bp      mRNA      linear      EST 15-AUG-2003
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sativa cDNA clone 7LEAF--07-P11, mRNA sequence.

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with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 9.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT TTTT TTTT 2182
Db      1 TTTT TTTT TTTT TTTT TTTT TTTT 17

RESULT 2364
CF298589/c
LOCUS      CF298589      17 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION 7LEAF--02-A18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--02-A18, mRNA sequence.
ACCESSION  CF298589
VERSION     CF298589.1 GI:33670350
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 321 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2365
CF302447/c
LOCUS      CF302447      17 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION 7LEAF--07-P11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-P11, mRNA sequence.
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ACCESSION  CF302447
VERSION     CF302447.1 GI:33674208
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RT-PCR."

Query Match          0.6%; Score 17; DB 1; Length 17;
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2366
CF310219
LOCUS      CF310219      17 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION ABF--04-M02.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--04-M02, mRNA sequence.
ACCESSION  CF310219
VERSION     CF310219.1 GI:33681980
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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then used for PCR. mRNA was prepared from ABA-responsive  
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line."
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Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
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QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTTT TTTT TTTT TTTT TTTT 17
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RESULT 2367  
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DEFINITION  
ABF--04-M02.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--04-M02, mRNA sequence.  
ACCESSION  
CF310219  
VERSION  
CF310219.1 GI:33681980  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
1 (bases 1 to 17)  
AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE  
Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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element binding transcription factor 3 overexpression  
line."
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Query Match 0.6%; Score 17; DB 1; Length 17;  
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QY 2786 AAAAAA AAAAAA AAAAAA 2802  
Db 17 AAAAAA AAAAAA AAAAAA 1
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RESULT 2368  
CF313013/c  
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DEFINITION  
ABF--08-P19.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--08-P19, mRNA sequence.  
ACCESSION  
CF313013  
VERSION  
CF313013.1 GI:33684774  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
1 (bases 1 to 17)  
AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE  
Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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element binding transcription factor 3 overexpression  
line."
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Query Match 0.6%; Score 17; DB 1; Length 17;  
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QY 2785 GAAAAA AAAAAA AAAAAA 2801  
Db 17 GAAAAA AAAAAA AAAAAA 1
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RESULT 2369  
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LOCUS  
DEFINITION  
JMT--03-O13.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--03-O13, mRNA sequence.  
ACCESSION  
CF334566  
VERSION  
CF334566.1 GI:33817460  
KEYWORDS  
EST.  
SOURCE  
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ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
1 (bases 1 to 17)  
AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE  
Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Nahm B.H.
```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

## FEATURES

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methyltransferase overexpression line."

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QY 2166 TTTT TTTT TTTT TTTT TTTT 2182

Db 1 TTTT TTTT TTTT TTTT TTTT 17

## RESULT 2370

CF334566/c

LOCUS

DEFINITION JMT--03-013.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--03-013, mRNA sequence.

ACCESSION

VERSION CF334566.1 GI:33817460

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 17)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1. .17

/organism="Oryza sativa"

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prepared from Arabidopsis Jasmoinate Carboxyl

methyltransferase overexpression line."

Query Match 0.6%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 9.3e+02;  
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QY 2786 AAAAAA AAAAAA AAAAAA 2802

Db 17 AAAAAA AAAAAA AAAAAA 1

## RESULT 2371

CF336950

LOCUS

DEFINITION JMT--07-D04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--07-D04, mRNA sequence.

ACCESSION

VERSION CF336950

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 17)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

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/organism="Oryza sativa"

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cDNA library (JMT)"

/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Oligo-capped mRNA

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methyltransferase overexpression line."

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0.6%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 9.3e+02;

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## RESULT 2372

CF301057

LOCUS

DEFINITION CF301057 18 bp mRNA linear EST 15-AUG-2003  
7LEAF--05-M05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--05-M05, mRNA sequence.

ACCESSION

VERSION CF301057

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 18)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RT-PCR."

Query Match 0.6%; Score 17; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 2373

CF301151/c

LOCUS  
DEFINITION  
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7LEAF--05-O05.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--05-O05, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RT-PCR."

Query Match 0.6%; Score 17; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 17 AAAAAAAAAAAAAAAAAA 1

## RESULT 2374

CF320418/c

LOCUS  
DEFINITION  
18 bp mRNA linear EST 15-AUG-2003  
HD--11-E22.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--11-E22, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

1..18  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="HD--11-E22"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.6%; Score 17; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 18 AAAAAAAAAAAAAAAAAA 2

## RESULT 2375

CF298591

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

CF298591  
7LEAF--02-A20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--02-A20, mRNA sequence.  
CF298591  
CF298591.1 GI:33670352  
EST.







Plate: 0156 row: J column: 15  
Seq primer: CGTTGTAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

FEATURES  
source

1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0156J15"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1); a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
Db 19 TTTT TTTT TTTT TTTT TTTT 3

RESULT 2381  
CF278272

LOCUS  
DEFINITION  
14ETL--04-C01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa cDNA clone 14ETL--04-C01, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CF278272 19 bp mRNA linear EST 14-AUG-2003  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 19)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source

1. .19  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"

/db\_xref="taxon:4530"  
/clone="14ETL--04-C01"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 17; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2172 TTTT TTTT TTTT TTTT TTTT 2188  
Db 1 TTTT TTTT TTTT TTTT TTTT 17

RESULT 2382  
CF298207

LOCUS  
DEFINITION  
7LEAF--01-H23.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--01-H23, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CF298207 20 bp mRNA linear EST 15-AUG-2003  
7LEAF--01-H23.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--01-H23, mRNA sequence.  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 20)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source

1. .20  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--01-H23"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2802  
Db 1 AAAAAA AAAAAA AAAAAA 17

RESULT 2383  
AZ818055/c

LOCUS  
DEFINITION  
2M0087B23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic



ACCESSION AZ818055  
VERSION AZ818055.1 GI:12987963  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheraia; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0087 row: B column: 23  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0087B23"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGClm library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
| | | | | | | | | | | | | | | | | | | | | |  
Db 20 TTTT TTTT TTTT TTTT TTTT 4  
RESULT 2384  
CF319428 20 bp mRNA linear EST 15-AUG-2003  
LOCUS HD--09-O20.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (HD) Oryza sativa cDNA clone HD--09-O20, mRNA sequence.

ACCESSION CF319428  
VERSION CF319428.1 GI:33691189  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza. 1 (bases 1 to 20)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
1. .20  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="HD--09-O20"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 17; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2165 CTTT TTTT TTTT TTTT TTTT 2181  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 CTTT TTTT TTTT TTTT TTTT 17  
RESULT 2385  
AZ943299/c 21 bp DNA linear GSS 26-APR-2001  
LOCUS 2M0203K21R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0203K21 R, genomic survey sequence.  
DEFINITION AZ943299  
ACCESSION AZ943299.1 GI:13807290  
VERSION AZ943299  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheraia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606

Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0203 row: K column: 21  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.

FEATURES

source

1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0203K21"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802

Db 21 AAAAAAAAAAAAAAAAAA 5

RESULT 2386

CF333393/c

LOCUS

DEFINITION

CF333393 21 bp mRNA linear EST 18-AUG-2003

JMT--02-E09.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--02-E09, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 21)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .21

FEATURES

source

/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="JMT--02-E09"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.6%; Score 17; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802

Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 2387

BQ591193

LOCUS

DEFINITION

BQ591193 22 bp mRNA linear EST 06-DEC-2002

E012715-024-017-D14-T7 MP1Z-ADIS-024-storage root Beta vulgaris cDNA clone 024-017-D14 3-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Beta vulgaris

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 22)

Herwig, R.; Schulz, B.; Weisshaar, B.; Hennig, S.; Steinfath, M.; Drungowski, M.; Stahl, D.; Wruck, W.; Menze, A.; O'Brien, J.; Lehrach, H. and Radelof, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

Plant J. 32 (5), 845-857 (2002)

22362189

12472698

Contact: Weisshaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 22 Std Error: 0.00

Plate: 17 row: D column: 14

Seq primer: T7; GTAATACGACTCACTATAGGCG.

Location/Qualifiers

1. .22

/organism="Beta vulgaris"

/mol\_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding line)"

/db\_xref="GABI:188927"

/db\_xref="taxon:161934"

/clone="024-017-D14"

/tissue\_type="storage root"

/lab\_host="EMDH10B"

/clone\_lib="MP1Z-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:

SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:





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FEATURES
source      Location/Qualifiers
1. 22
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="211d06"

Query Match      0.6%; Score 17; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 2391
CF291486      23 bp mRNA linear EST 14-AUG-2003
LOCUS
DEFINITION
sativa cDNA clone 14ROOT--01-O21, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

TITLE
JOURNAL
COMMENT

FEATURES
source      Location/Qualifiers
1. 23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--01-O21"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.6%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 2393
AZ435597      23 bp DNA linear GSS 03-OCT-2000
LOCUS
DEFINITION
1M0222P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0222P09 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingley,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0222 row: P column: 09
Seq primer: CACACAGGAACAGCTATGACC

Query Match      0.6%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2182
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 17

RESULT 2392
CF291486/c
LOCUS
DEFINITION
14ROOT--01-O21.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-O21, mRNA sequence.
ACCESSION
VERSION
CF291486.1 GI:33660519
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KEYWORDS
SOURCE      EST.
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 23)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
source      Location/Qualifiers
1. 23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--01-O21"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.6%; Score 17; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 2393
AZ435597      23 bp DNA linear GSS 03-OCT-2000
LOCUS
DEFINITION
1M0222P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0222P09 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingley,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0222 row: P column: 09
Seq primer: CACACAGGAACAGCTATGACC
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Class: plasmid ends  
High quality sequence stop: 23.  
Location/Qualifiers  
1. .23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0222P09"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2802  
|||||  
Db 1 AAAAAAAAAAAAAA 17

RESULT 2394  
AZ435597/c  
LOCUS  
DEFINITION  
LM0222P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0222P09 R, genomic survey sequence.  
ACCESSION  
AZ435597  
VERSION  
AZ435597.1 GI:10559610  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)  
REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0222 row: P column: 09  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends

FEATURES  
source

High quality sequence stop: 23.

Location/Qualifiers  
1. .23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0222P09"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2182  
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Db 17 TTTT TTTT TTTT TTTT TTTT 1

RESULT 2395  
AZ862224

LOCUS  
DEFINITION  
AZ862224 2M0169N18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0169N18 F, genomic survey sequence.  
ACCESSION  
AZ862224  
VERSION  
AZ862224.1 GI:13059330  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)  
REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0169 row: N column: 18  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 23.









AZ343444/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AZ343444  
IM0076001R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0076001 R, genomic survey sequence.  
AZ343444  
AZ343444.1 GI:10421687  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 25)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0076 row: 0 column: 01  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 25.

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Query Match          0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2172 TTTTTTTTTTTTTTTAA 2188
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Db       25 TTTTTTTTTTTTTTTAA 9
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LOCUS	AZ658622	25 bp	DNA	linear	GSS 14-DEC-2000
DEFINITION	1M0535F04R Mouse 10kb plasmid UUGC1m library Mus musculus genomic clone UUGC1M0535F04 R, genomic survey sequence.				
ACCESSION	AZ658622				
VERSION	AZ658622.1 GI:11795768				
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 25)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0535 row: F column: 04 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 25. Location/Qualifiers				
FEATURES					

```

Query Match      0.6%; Score 17; DB 1; Length 25;
Best Local Similarity 80.0%; Pred. No. 2.5e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1781 TGAACCCCATTCCTTCTCTCTGA 1805
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      |||
Db      1 TGACTCCCATTCCTTGTGCTGCACCTGA 25

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RESULT 2405			
BZ767540			
LOCUS	BZ767540	25 bp	DNA linear
			GSS 13-MAR-2003





/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match	0.6%	Score 17;	DB 1;	Length 26;
Best Local Similarity	80.0%	Pred. No. 2.6e+03;		
Matches 20;	Conservative	0;	Mismatches 5;	Indels 0;
			Gaps	0;

**DQ**

2161 TCTCCATTTTTCATTTTTTTT 2185  
||| | ||||||  
**Db**

2 TCTAGATAGTTTTTTTTTTT 26

RESULT' 2408  
BX553653

LOCUS	BX553653	26 bp	mRNA	linear	EST 10-OCT-2003
DEFINITION	BX553653 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse12h01 plc, mRNA sequence.				

ACCESSION BX553653  
VERSION BX553653.1  
KEYWORDS EST.

SOURCE	Glossina morsitans morsitans
ORGANISM	Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidea; Glossinidae; Glossinae.

## REFERENCE AUTHORS

AUTHORS	Lehane, M. J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M. B., Bonaldo, M. F., Lehane, S. and Hall, N.
TITLE	Adult midgut expressed sequence tags from the tsetse fly <i>Glossina morsitans morsitans</i> and expression analysis of putative immune

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all p1c reads are from the 3' end.

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FEATURES
source
Location/Qualifiers
1..26
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse12h01_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans
gut"
/note="country: Zimbabwe; EST from adult
T.brucei"

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```
Query Match      0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 80.0%; Pred. No. 2.6e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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2161 TCTCCTTTT TTTT TTTT TTTT TTTT 2185  
Qy ||| |  
2 TCTAAATAG TTTT TTTT TTTT TTTT 26  
Db

RESULT 2409  
BX553888

LOCUS BX553888 26 bp mRNA linear EST 10-OCT-2003  
DEFINITION Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tsel31b10 plc, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

SOURCE	ORGANISM
Glossina morsitans morsitans	Glossina morsitans morsitans
Glossina morsitans morsitans	Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidae; Glossinidae; Glossina.	

## REFERENCE AUTHORS

**TITLE**  
Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane

Prof. M.J. Leahane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5' end of the CDNA all p1c reads are from the 3' end.

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FEATURES
source
1. .26
Location/Qualifiers
/organism="Glossina morsitans morsitans"
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/db_xref="taxon:37546"
/clone="Tse131b10 plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans
gut"
/note="country: Zimbabwe; EST from adult
T.brucei"

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```
Query Match      0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 80.0%; Pred. NO. 2.6e+03;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Qy 2161 TCTCCCTTTT TTTTTTTTTT 2185  
||| | ||| ||| |||  
Db 2 TCTAGATAGT TTTTTTTTTT 26

RESULT 2410  
BX557791

LOCUS	BX557791	26 bp	mRNA	linear	EST 10-OCT-2003
DEFINITION	BX557791	Glossina morsitans morsitans	adult	infected gut	Glossina morsitans morsitans cDNA clone Tse34g02 plc, mRNA sequence.

ACCESSION BX557791  
VERSION BX557791.1 GI:33428966  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans

SOURCE	ORGANISM
Glossina morsitans morsitans	Glossina morsitans morsitans
Glossina morsitans morsitans	Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidae; Glossinidae; Glossina.	

## REFERENCE AUTHORS

**AUTHORS** Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

**TITLE** Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune

JOURNAL  
MEDLINE  
PUBMED  
response genes  
Genome Biol. 4 (10), R63 (2003)

COMMENT

Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES

source  
Location/Qualifiers  
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/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse34g02\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 26;  
Best Local Similarity 80.0%; Pred. No. 2.6e+03;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2161 TCTCCTTTTTTTTTTTTTTTTTTTTTT 2185

Db 2 TCTAGATAGTTTTTTTTTTTTTTTTTTTTT 26

RESULT 2411

BX560008  
LOCUS BX560008 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tse47c08\_plc, mRNA sequence.  
ACCESSION BX560008.1 GI:33368000  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
1 (bases 1 to 26)  
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
Genome Biol. 4 (10), R63 (2003)  
22881942  
14519198  
Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES

source  
Location/Qualifiers  
1. .26  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"

/db\_xref="taxon:37546"  
/clone="Tse47c08\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2182

Db 10 TTTTTTTTTTTTTTTTTT 26

RESULT 2412

BX560008/c  
LOCUS BX560008 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tse47c08\_plc, mRNA sequence.  
ACCESSION BX560008.1 GI:33368000  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
1 (bases 1 to 26)  
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
Genome Biol. 4 (10), R63 (2003)  
22881942  
14519198  
Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES

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QY 2786 AAAAAAAAAAAAAA 2802

Db 26 AAAAAAAAAAAAAA 10



RESULT 2413  
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LOCUS  
DEFINITION  
BX566514 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tse82f08\_plc, mRNA sequence.  
ACCESSION  
VERSION  
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SOURCE  
ORGANISM  
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Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscidea; Glossinidae; Glossina.  
1 (bases 1 to 26)  
REFERENCE  
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
Genome Biol. 4 (10), R63 (2003)  
22881942  
14519198  
COMMENT  
Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.  
FEATURES  
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||| | ||||| ||||| |||||  
Db 2 TCTAGATAGTTTTTTTTTTTTTTTTTT 26  
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LOCUS  
DEFINITION  
BX567795 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tse8b03\_plc, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Glossina morsitans morsitans  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscidea; Glossinidae; Glossina.  
1 (bases 1 to 26)  
REFERENCE  
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
Genome Biol. 4 (10), R63 (2003)  
22881942  
14519198  
COMMENT  
Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtton, Cambridge, CB10 1SA, UK  
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Prof. M.J.Lehane  
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University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
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FEATURES  
source  
1..26  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
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Best Local Similarity 80.0%; Pred. No. 2.6e+03;  
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LOCUS  
DEFINITION  
AZ818035 26 bp DNA linear GSS 20-FEB-2001  
clone UUGC2M0087015 R, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 26)  
REFERENCE  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0087 row: 0 column: 15  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 26.  
FEATURES  
Location/Qualifiers

morsitans morsitans and expression analysis of putative immune  
response genes  
Genome Biol. 4 (10), R63 (2003)  
22881942  
14519198  
COMMENT  
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University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.  
FEATURES  
Location/Qualifiers  
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Best Local Similarity 80.0%; Pred. No. 2.6e+03;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 2161 TCTCTTTTTTTTTTTTTTTTTTTTTT 2185  
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Db 2 TCTAGATAGTTTTTTTTTTTTTTTTTT 26  
RESULT 2415  
AZ818035  
LOCUS  
DEFINITION  
AZ818035 26 bp DNA linear GSS 20-FEB-2001  
clone UUGC2M0087015 R, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 26)  
REFERENCE  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0087 row: 0 column: 15  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 26.  
FEATURES  
Location/Qualifiers

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/organism="Mus musculus"
/mol_type="genomic DNA"
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/clone="UUGC2M0087O15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.6%; Score 17; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 2416
AZ818035/c
LOCUS
DEFINITION
2M0087O15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0087O15 R, genomic survey sequence.
ACCESSION
AZ818035
VERSION
AZ818035.1 GI:12987943
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0087 row: 0 column: 15
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 26.
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.6%; Score 17; DB 1; Length 26;
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QY 2166 TTTTTTTTTTTTTTTT 2182
Db 17 TTTTTTTTTTTTTTTT 1

RESULT 2417
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LOCUS
DEFINITION
BX555323 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tselg09_plc, mRNA sequence.
ACCESSION
BX555323
VERSION
BX555323.1 GI:33379323
KEYWORDS
SOURCE
Glossina morsitans morsitans
ORGANISM
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 27)
REFERENCE
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
JOURNAL
Genome Biol. 4 (10), R63 (2003)
MEDLINE
22881942
PUBMED
14519198
COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxtan, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.
FEATURES
Location/Qualifiers
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source
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JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtan, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
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Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
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Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAA 11

RESULT 2421  
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LOCUS BX551145 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tsell16h03\_plc, mRNA sequence.  
ACCESSION BX551145  
VERSION BX551145.1 GI:33375002  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtan, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
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T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAA 11

RESULT 2421  
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LOCUS BX551145 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tsell16h03\_plc, mRNA sequence.  
ACCESSION BX551145  
VERSION BX551145.1 GI:33375002  
KEYWORDS EST.  
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ORGANISM Glossina morsitans morsitans  
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
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FEATURES  
source Location/Qualifiers  
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/organism="Glossina morsitans morsitans"  
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T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAA 11

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LOCUS BX551153 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tsell16h08\_plc, mRNA sequence.  
ACCESSION BX551153  
VERSION BX551153.1 GI:33375010  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
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JOURNAL Genome Biol. 4 (10), R63 (2003)  
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PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
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Hinxtan, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
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University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source Location/Qualifiers  
1. .27  
/organism="Glossina morsitans morsitans"  
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T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAA 11

Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2423  
BX551505/c

LOCUS BX551505 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tsell9a03\_plc, mRNA sequence.

ACCESSION BX551505  
VERSION BX551505.1 GI:33375704  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 27)  
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source  
Location/Qualifiers  
1..27  
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/mol\_type="mRNA"  
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/db\_xref="taxon:37546"  
/clone="Tsell9a03\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
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T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred.No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2424  
BX551552/c

LOCUS BX551552 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tsell9c07\_plc, mRNA sequence.

ACCESSION BX551552  
VERSION BX551552.1 GI:33375771  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 27)

AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
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Hinxtton, Cambridge, CB10 1SA, UK  
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Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source  
Location/Qualifiers  
1..27  
/organism="Glossina morsitans morsitans"  
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/clone="Tsell9c07\_plc"  
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/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred.No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2425  
BX551708/c

LOCUS BX551708 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tsellc02\_plc, mRNA sequence.

ACCESSION BX551708  
VERSION BX551708.1 GI:33376038  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 27)  
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
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Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW







gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||

Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2431  
BX553159/c

LOCUS  
DEFINITION Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tsel27g01\_plc, mRNA sequence.

ACCESSION  
VERSION BX553159.1 GI:33377351

KEYWORDS  
SOURCE EST.

ORGANISM  
Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.

REFERENCE  
1 (bases 1 to 27)

AUTHORS  
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
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morsitans morsitans and expression analysis of putative immune  
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TITLE

JOURNAL  
MEDLINE  
PUBMED

COMMENT  
Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source  
1. .27  
/organism="Glossina morsitans morsitans"  
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/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||

Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2432  
BX553354/c

LOCUS  
DEFINITION Glossina morsitans morsitans adult infected gut Glossina

morsitans morsitans cDNA clone Tsel28h11\_plc, mRNA sequence.

ACCESSION  
VERSION BX553354  
KEYWORDS BX553354.1 GI:33377529  
SOURCE EST.  
ORGANISM Glossina morsitans morsitans  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.

REFERENCE  
1 (bases 1 to 27)

AUTHORS  
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
Adult midgut expressed sequence tags from the tsetse fly Glossina  
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response genes

TITLE

JOURNAL  
MEDLINE  
PUBMED

COMMENT  
Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
Location/Qualifiers  
1. .27  
/organism="Glossina morsitans morsitans"  
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/clone="Tsel28h11\_plc"  
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/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||

Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2433  
BX553476/c

LOCUS  
DEFINITION Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tsel29f12\_plc, mRNA sequence.

ACCESSION  
VERSION BX553476  
KEYWORDS BX553476.1 GI:33377634  
SOURCE EST.  
ORGANISM Glossina morsitans morsitans  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.

REFERENCE  
1 (bases 1 to 27)

AUTHORS  
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes

TITLE

JOURNAL  
MEDLINE

PUBMED  
COMMENT  
14519198  
Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtan, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source  
Location/Qualifiers  
1. .27  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
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/clone="Tsel29f12\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2434  
BX553666/c  
LOCUS  
DEFINITION  
BX553666 Glossina morsitans morsitans adult infected gut  
morsitans morsitans cDNA clone Tsel2h08\_plc, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscidae; Glossinidae; Glossina.  
REFERENCE  
1 (bases 1 to 27)  
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
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response genes  
Genome Biol. 4 (10), R63 (2003)  
MEDLINE  
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14519198  
Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtan, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source  
Location/Qualifiers  
1. .27  
/organism="Glossina morsitans morsitans"  
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/db\_xref="taxon:37546"  
/clone="Tsel29f12\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2434  
BX553666/c  
LOCUS  
DEFINITION  
BX553666 Glossina morsitans morsitans adult infected gut  
morsitans morsitans cDNA clone Tsel2h08\_plc, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscidae; Glossinidae; Glossina.  
REFERENCE  
1 (bases 1 to 27)  
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
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morsitans morsitans and expression analysis of putative immune  
response genes  
Genome Biol. 4 (10), R63 (2003)  
MEDLINE  
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School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source  
Location/Qualifiers  
1. .27  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"

/sub\_species="morsitans"  
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/clone="Tsel2h08\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2435  
BX553766/c  
LOCUS  
DEFINITION  
BX553766 Glossina morsitans morsitans adult infected gut  
morsitans morsitans cDNA clone Tsel30e04\_plc, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscidae; Glossinidae; Glossina.  
REFERENCE  
1 (bases 1 to 27)  
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
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morsitans morsitans and expression analysis of putative immune  
response genes  
Genome Biol. 4 (10), R63 (2003)  
MEDLINE  
PUBMED  
22881942  
14519198  
Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtan, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source  
Location/Qualifiers  
1. .27  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
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/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAAAAAA 11





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the 3' end.
FEATURES             Location/Qualifiers
    source            1. .27
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                     /sub_species="morsitans"
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                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

Query Match          0.6%; Score 17; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2802
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2439
BX555155/c
LOCUS             27 bp mRNA linear EST 10-OCT-2003
DEFINITION       BX555155 Glossina morsitans morsitans adult infected gut Glossina
                  morsitans morsitans cDNA clone Tse19g11_plc, mRNA sequence.
ACCESSION        BX555155
VERSION          BX555155.1 GI:33379174
SOURCE           Glossina morsitans morsitans
ORGANISM         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                  Hippoboscidae; Glossinidae; Glossina.
REFERENCE        1 (bases 1 to 27)
AUTHORS          Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
                  Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
                  Adult midgut expressed sequence tags from the tsetse fly Glossina
                  morsitans morsitans and expression analysis of putative immune
                  response genes
JOURNAL          Genome Biol. 4 (10), R63 (2003)
MEDLINE          22881942
PUBMED           14519198
COMMENT          Contact: Hall N
                  Pathogen Sequencing Unit
                  The Sanger Institute The Wellcome Trust Genome Campus
                  Hinxtun, Cambridge, CB10 1SA, UK
                  Request for clones, please contact: Mike Lehane
                  Prof. M.J.Lehane
                  School of Biological Sciences,
                  University of Wales,
                  Bangor LL57 2UW
                  All clones with suffix q1c are reverse primer reads starting at 5'
                  end of the cDNA all plc reads are from
                  the 3' end.
FEATURES         Location/Qualifiers
    source            1. .27
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
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                     /clone="Tse19h01_plc"
                     /tissue_type="adult infected gut"
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                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

Query Match          0.6%; Score 17; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2802
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2441
BX555385/c
LOCUS             27 bp mRNA linear EST 10-OCT-2003
DEFINITION       BX555385 Glossina morsitans morsitans adult infected gut Glossina
                  morsitans morsitans cDNA clone Tse20b09_plc, mRNA sequence.
ACCESSION        BX555385
VERSION          BX555385.1 GI:33379380
SOURCE           Glossina morsitans morsitans
ORGANISM         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                  Hippoboscidae; Glossinidae; Glossina.
REFERENCE        1 (bases 1 to 27)
AUTHORS          Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
                  Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
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COMMENT          Contact: Hall N
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                  Request for clones, please contact: Mike Lehane
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                  School of Biological Sciences,
                  University of Wales,
                  Bangor LL57 2UW
                  All clones with suffix q1c are reverse primer reads starting at 5'
                  end of the cDNA all plc reads are from
                  the 3' end.
FEATURES         Location/Qualifiers
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                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
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                     /clone="Tse19g11_plc"
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                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

Query Match          0.6%; Score 17; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2786 AAAAAAAAAAAAAAAAAA 2802
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2440
BX555158/c
LOCUS             27 bp mRNA linear EST 10-OCT-2003
DEFINITION       BX555158 Glossina morsitans morsitans adult infected gut Glossina
                  morsitans morsitans cDNA clone Tse19h01_plc, mRNA sequence.
ACCESSION        BX555158
VERSION          BX555158.1 GI:33379177
KEYWORDS         EST.
SOURCE           Glossina morsitans morsitans
ORGANISM         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                  Hippoboscidae; Glossinidae; Glossina.
REFERENCE        1 (bases 1 to 27)
AUTHORS          Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
                  Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
                  Adult midgut expressed sequence tags from the tsetse fly Glossina
                  morsitans morsitans and expression analysis of putative immune
                  response genes
JOURNAL          Genome Biol. 4 (10), R63 (2003)
MEDLINE          22881942
PUBMED           14519198
COMMENT          Contact: Hall N
                  Pathogen Sequencing Unit
                  The Sanger Institute The Wellcome Trust Genome Campus
                  Hinxtun, Cambridge, CB10 1SA, UK
                  Request for clones, please contact: Mike Lehane
                  Prof. M.J.Lehane
                  School of Biological Sciences,
                  University of Wales,
                  Bangor LL57 2UW
                  All clones with suffix q1c are reverse primer reads starting at 5'
                  end of the cDNA all plc reads are from
                  the 3' end.
FEATURES         Location/Qualifiers
    source            1. .27
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
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                     /clone="Tse19h01_plc"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

Query Match          0.6%; Score 17; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2786 AAAAAAAAAAAAAAAAAA 2802
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2441
BX555385/c
LOCUS             27 bp mRNA linear EST 10-OCT-2003
DEFINITION       BX555385 Glossina morsitans morsitans adult infected gut Glossina
                  morsitans morsitans cDNA clone Tse20b09_plc, mRNA sequence.
ACCESSION        BX555385
VERSION          BX555385.1 GI:33379380
KEYWORDS         EST.
SOURCE           Glossina morsitans morsitans
ORGANISM         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                  Hippoboscidae; Glossinidae; Glossina.
REFERENCE        1 (bases 1 to 27)
AUTHORS          Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
                  Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
                  Adult midgut expressed sequence tags from the tsetse fly Glossina
                  morsitans morsitans and expression analysis of putative immune
                  response genes
JOURNAL          Genome Biol. 4 (10), R63 (2003)
MEDLINE          22881942
PUBMED           14519198
COMMENT          Contact: Hall N
                  Pathogen Sequencing Unit
                  The Sanger Institute The Wellcome Trust Genome Campus
                  Hinxtun, Cambridge, CB10 1SA, UK
                  Request for clones, please contact: Mike Lehane
                  Prof. M.J.Lehane
                  School of Biological Sciences,
                  University of Wales,
                  Bangor LL57 2UW
                  All clones with suffix q1c are reverse primer reads starting at 5'
                  end of the cDNA all plc reads are from
                  the 3' end.
FEATURES         Location/Qualifiers
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                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

Query Match          0.6%; Score 17; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2444  
BX555594/c  
LOCUS  
DEFINITION  
BX555594 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tse21f02\_plc, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Glossina morsitans morsitans  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
REFERENCE  
1 (bases 1 to 27)  
AUTHORS  
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE  
Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
JOURNAL  
MEDLINE  
PUBMED  
Genome Biol. 4 (10), R63 (2003)  
22881942  
14519198  
COMMENT  
Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtan, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source  
Location/Qualifiers  
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/clone="Tse21f02\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2445  
BX555829/c  
LOCUS  
DEFINITION  
BX555829 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tse23b06\_plc, mRNA sequence.  
ACCESSION

VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
BX555829.1 GI:33379800  
EST.  
Glossina morsitans morsitans  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
REFERENCE  
1 (bases 1 to 27)  
AUTHORS  
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE  
Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
JOURNAL  
MEDLINE  
PUBMED  
Genome Biol. 4 (10), R63 (2003)  
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14519198  
COMMENT  
Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
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Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source  
Location/Qualifiers  
1..27  
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/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2446  
BX555864/c  
LOCUS  
DEFINITION  
BX555864 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tse23d05\_plc, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Glossina morsitans morsitans  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
REFERENCE  
1 (bases 1 to 27)  
AUTHORS  
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE  
Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
JOURNAL  
MEDLINE  
PUBMED  
Genome Biol. 4 (10), R63 (2003)  
22881942  
14519198  
COMMENT  
Contact: Hall N

Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source

Location/Qualifiers  
1. .27  
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/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
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/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2447  
BX555901/c

LOCUS BX555901 27 bp mRNA linear EST 10-OCT-2003  
DEFINITION BX555901 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tse23f02\_plc, mRNA sequence.

ACCESSION BX555901  
VERSION BX555901.1 GI:33379871

KEYWORDS  
SOURCE

Glossina morsitans morsitans  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.

REFERENCE  
AUTHORS

1 (bases 1 to 27)  
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.

TITLE

Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes

JOURNAL  
MEDLINE  
PUBMED

Genome Biol. 4 (10), R63 (2003)  
22881942  
14519198

COMMENT

Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source

Location/Qualifiers  
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/clone="Tse23f02\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2448  
BX555930/c

LOCUS BX555930 27 bp mRNA linear EST 10-OCT-2003  
DEFINITION BX555930 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tse23g07\_plc, mRNA sequence.

ACCESSION BX555930  
VERSION BX555930.1 GI:33379899

KEYWORDS  
SOURCE

Glossina morsitans morsitans  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.

REFERENCE  
AUTHORS

1 (bases 1 to 27)  
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.

TITLE

Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes

JOURNAL  
MEDLINE  
PUBMED

Genome Biol. 4 (10), R63 (2003)  
22881942  
14519198

COMMENT

Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source

Location/Qualifiers  
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/organism="Glossina morsitans morsitans"  
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/clone="Tse23g07\_plc"  
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gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2449

BX556112/c  
LOCUS BX556112 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tse25a07\_plc, mRNA sequence.  
ACCESSION BX556112  
VERSION BX556112.1 GI:33380051  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtan, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source  
Location/Qualifiers  
1..27  
/organism="Glossina morsitans morsitans"  
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/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred.No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2450  
BX556156/c  
LOCUS BX556156 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tse25c09\_plc, mRNA sequence.  
ACCESSION BX556156  
VERSION BX556156.1 GI:33380093  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes

response genes  
Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
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Request for clones, please contact: Mike Lehane  
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Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
response genes  
Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
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University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source  
Location/Qualifiers  
1..27  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
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/clone="Tse25c09\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred.No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2451  
BX556515/c  
LOCUS BX556515 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tse27f09\_plc, mRNA sequence.  
ACCESSION BX556515  
VERSION BX556515.1 GI:33427775  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
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response genes  
Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtan, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
Location/Qualifiers



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source
1. .27
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse27f09_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      0.6%; Score 17; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2802
|||||
Db 27 AAAAAAAAAAAAAA 11

RESULT 2452
BX557271/c
LOCUS
DEFINITION
BX557271 27 bp mRNA linear EST 10-OCT-2003
morsitans morsitans cDNA clone Tse31c08_plc, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 27)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
source
1. .27
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse31c08_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      0.6%; Score 17; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2802
|||||
Db 27 AAAAAAAAAAAAAA 11

RESULT 2454
BX557794/c
LOCUS
DEFINITION
BX557794 27 bp mRNA linear EST 10-OCT-2003
morsitans morsitans cDNA clone Tse34g04_plc, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 27)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
COMMENT
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Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
source
1. .27
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse31c08_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      0.6%; Score 17; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2802
|||||
Db 27 AAAAAAAAAAAAAA 11
```

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Db 27 AAAAAAAAAAAAAA 11

RESULT 2453
BX557363/c
LOCUS
DEFINITION
BX557363 27 bp mRNA linear EST 10-OCT-2003
morsitans morsitans cDNA clone Tse31g12_plc, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 27)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
source
1. .27
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse31g12_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      0.6%; Score 17; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2802
|||||
Db 27 AAAAAAAAAAAAAA 11

RESULT 2454
BX557794/c
LOCUS
DEFINITION
BX557794 27 bp mRNA linear EST 10-OCT-2003
morsitans morsitans cDNA clone Tse34g04_plc, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 27)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
source
1. .27
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
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/clone="Tse31g12_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      0.6%; Score 17; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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REFERENCE 1 (bases 1 to 27)  
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES source  
Location/Qualifiers  
1..27  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
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/db\_xref="taxon:37546"  
/clone="Tse38e12\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred.No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2455  
BX558430/c  
LOCUS BX558430 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tse38e12\_plc, mRNA sequence.  
ACCESSION BX558430  
VERSION BX558430.1 GI:33365138  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,

Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES source  
Location/Qualifiers  
1..27  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse38e12\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred.No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2456  
BX559230/c  
LOCUS BX559230 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tse42d01\_plc, mRNA sequence.  
ACCESSION BX559230  
VERSION BX559230.1 GI:33366559  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES source  
Location/Qualifiers  
1..27  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse42d01\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"





Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW

All clones with suffix qlc are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source

Location/Qualifiers  
1. .27  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse52f10\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2460  
BX562177/c

LOCUS BX562177 27 bp mRNA linear EST 10-OCT-2003  
DEFINITION BX562177 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tse5b09\_plc, mRNA sequence.

ACCESSION BX562177.1 GI:33372299  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Glossina morsitans morsitans  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 27)  
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PubMed 14519198

COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane

Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix qlc are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source

Location/Qualifiers  
1. .27  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse5b09\_plc"  
/tissue\_type="adult infected gut"

/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2461  
BX564083/c

LOCUS BX564083 27 bp mRNA linear EST 10-OCT-2003  
DEFINITION BX564083 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tse6f02\_plc, mRNA sequence.

ACCESSION BX564083  
VERSION BX564083.1 GI:33431280  
KEYWORDS  
SOURCE  
ORGANISM

Glossina morsitans morsitans  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 27)

AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PubMed 14519198

COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane

Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW

All clones with suffix qlc are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source

Location/Qualifiers  
1. .27  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
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/clone="Tse6f02\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 17; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 27 AAAAAAAAAAAAAAAAAA 11

RESULT 2462  
AL587605/c

LOCUS AL587605 28 bp mRNA linear EST 02-MAR-2001



FEATURES  
source

Location/Qualifiers  
1. .32  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0250I05"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17; DB 1; Length 32;  
Best Local Similarity 80.0%; Pred. No. 2.8e+03;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2803  
Db 26 AAAAAACAAACAAAAA 2

RESULT 2465  
BJ036312/c

LOCUS BJ036312 35 bp mRNA linear EST 26-SEP-2003  
DEFINITION BJ036312 NIBB Mochii normalized Xenopus neurula library Xenopus laevis cDNA clone XL035k09 5', mRNA sequence.

ACCESSION BJ036312  
VERSION BJ036312.1 GI:17396897  
KEYWORDS EST.  
SOURCE Xenopus laevis (African clawed frog)

ORGANISM Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus.  
1 (bases 1 to 35)  
AUTHORS Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara,Y.

TITLE Expressed genes in X. laevis embryo  
JOURNAL Unpublished (2001)  
COMMENT Contact: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: [tshini@genes.nig.ac.jp](mailto:tshini@genes.nig.ac.jp)  
The information of this clone is available through the following URL.  
<http://xenopus.nibb.ac.jp>.

FEATURES  
source

Location/Qualifiers  
1. .35  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="XL035k09"

/tissue\_type="whole embryo"  
/dev\_stage="stage 15"  
/clone\_lib="NIBB Mochii normalized Xenopus neurula library"

Query Match 0.6%; Score 17; DB 1; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA 2802  
Db 31 AAAAAA 15

RESULT 2466  
AZ351309

LOCUS AZ351309 35 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0089K13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0089K13 F, genomic survey sequence.

ACCESSION AZ351309  
VERSION AZ351309.1 GI:10430546  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 35)

REFERENCE Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0089 row: K column: 13  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 35.

FEATURES  
source

Location/Qualifiers  
1. .35  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0089K13"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to



adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 17; DB 1; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 2 AAAAAAAAAAAAAAAAAA 18

RESULT 2467  
TA115E07P  
LOCUS  
DEFINITION T. brucei sheared genomic DNA clone 115e07, forward sequence,  
genomic survey sequence.  
ACCESSION AL462838  
VERSION AL462838.1 GI:11832519  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.  
REFERENCE 1 (bases 1 to 37)  
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhi@sanger.ac.uk  
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution ( to give a tight size distribution ( 4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

FEATURES  
source Location/Qualifiers  
1. .37  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="115e07"

Query Match 0.6%; Score 17; DB 1; Length 37;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 2468  
CF299570/c  
LOCUS  
DEFINITION 7LEAF--03-K09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--03-K09, mRNA sequence.  
ACCESSION CF299570  
VERSION CF299570.1 GI:33671331  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 20)

REFERENCE  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source Location/Qualifiers  
1. .20  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--03-K09"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2783 TTGAAAAAAAAAAAAAAAAA 2802  
|  
Db 20 TAGTAAAAAAAAAAAAAAAA 1

RESULT 2469  
CF301101  
LOCUS  
DEFINITION CF301101 20 bp mRNA linear EST 15-AUG-2003  
7LEAF--05-N04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--05-N04, mRNA sequence.  
ACCESSION CF301101  
VERSION CF301101.1 GI:33672862  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 20)

REFERENCE  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source Location/Qualifiers  
1. .20  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--05-N04"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"

/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2166 TTTTCTTTTCTTTTCTTCT 2185  
|||||  
Db 1 TTTTCTTTTCTTTTCTTCT 20

RESULT 2470  
AZ343730 20 bp DNA linear GSS 29-SEP-2000  
LOCUS  
DEFINITION IM0077E20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0077E20 F, genomic survey sequence.

ACCESSION AZ343730  
VERSION AZ343730.1 GI:10422288  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausen,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0077 row: E column: 20  
Seq primer: CGTTGTAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source  
1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0077E20"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Ti-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2166 TTTTCTTTTCTTTTCTTCT 2185  
|||||  
Db 1 TTTTCTTTTCTTTTCTTCT 20

RESULT 2471  
AW333777 20 bp mRNA linear EST 31-JAN-2000  
LOCUS  
DEFINITION S25H10 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.  
ACCESSION AW333777  
VERSION AW333777.1 GI:6830134  
KEYWORDS EST.  
SOURCE Pneumocystis carinii  
ORGANISM Pneumocystis carinii  
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;  
Pneumocystidaceae; Pneumocystis.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,  
Edman,J.C., Kovacs,J. and Cushion,M.  
TITLE Expressed sequence tags from Pneumocystis carinii  
JOURNAL Unpublished (2000)  
COMMENT Contact: Staben C  
School of Biological Sciences  
University of Kentucky  
101 Morgan Building, University of Kentucky, Lexington, KY  
40506-0225, USA  
Tel: 606 257 2161  
Fax: 606 257 1717  
Email: staben@pop.uky.edu.

FEATURES  
source  
1. .20  
/organism="Pneumocystis carinii"  
/mol\_type="mRNA"  
/db\_xref="taxon:4754"  
/lab\_host="E. coli"  
/clone\_lib="AGS-1"  
/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;  
P. carinii organisms (3x10e9) from a single rat (99-1-6,  
sacrificed on 3/17/99) at Cincinnati VA facilities.  
Trizol extracted RNA. Oligo dT priming, standard  
conditions described by vendor, Stratagene. Further  
details see www.uky.edu/Project/Pneumocystis/"

Query Match 0.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2168 TTTTCTTTTCTTTTCTTCT 2187  
|||||  
Db 1 TTTTCTTTTCTTTTCTTCT 20

RESULT 2472  
CF282165/c 20 bp mRNA linear EST 14-AUG-2003  
LOCUS  
DEFINITION CF282165 14ETL--09-122.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa cDNA clone 14ETL--09-122, mRNA sequence.  
ACCESSION CF282165  
VERSION CF282165.1 GI:33659552  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Query Match 0.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2168 TTTTCTTTTCTTTTCTTCT 2187  
|||||  
Db 1 TTTTCTTTTCTTTTCTTCT 20

REFERENCE  
AUTHORS Ehrhartoidae; Oryzae; Oryza.  
1 (bases 1 to 20)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@ggbio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

source

1. .20  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="14ETL-09-122"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice etiolated leaf plasmid cDNA library  
(14ETL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."  
Query Match 0.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2781 AATTGAAAAAAAAAAAAAAAAA 2800  
Db 20 ATTTGAAAAAAAAAAAAAAAAA 1

## RESULT 2473

CF298018

LOCUS 20 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--01-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--01-D19, mRNA sequence.

ACCESSION CF298018

VERSION CF298018.1 GI:33669779

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoidae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 20)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@ggbio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

source

1. .20  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--01-D19"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"

/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTTTT 2185

Db 1 TTTTTTTTTTTTTTTTGATT 20

## RESULT 2474

CF298018/c

LOCUS

DEFINITION 20 bp mRNA linear EST 15-AUG-2003  
7LEAF--01-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--01-D19, mRNA sequence.

ACCESSION CF298018

VERSION CF298018.1 GI:33669779

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoidae; Oryzae; Oryza.

REFERENCE 1 (bases 1 to 20)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@ggbio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

source

1. .20  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
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/db\_xref="taxon:4530"  
/clone="7LEAF--01-D19"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAAAA 2800

Db 20 AATCAAAAAAAAAAAAAAAAAA 1

## RESULT 2475

CF300961

LOCUS

DEFINITION 20 bp mRNA linear EST 15-AUG-2003  
7LEAF--05-K03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--05-K03, mRNA sequence.

ACCESSION CF300961

VERSION CF300961.1 GI:33672722

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM





ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0489 row: G column: 12  
Seq primer: CGTTGTAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0489G12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."  
Query Match 0.6%; Score 16.8; DB 1; Length 20;  
Best Local Similarity 90.0%; Pred. No. 1.7e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 2166 TTTTTTTTTTTTTTTTTT 2185  
Db 20 TTTCGTTT TTTTTTTTTT 1  
RESULT 2479  
CF293087/c  
LOCUS CF293087 21 bp mRNA linear EST 14-AUG-2003  
DEFINITION 30DGS--02-C07.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--02-C07, mRNA sequence.  
ACCESSION CF293087  
VERSION CF293087.1 GI:33662120  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
1..21  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="30DGS--02-C07"  
/tissue\_type="leaf"  
/dev\_stage="30 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."  
Query Match 0.6%; Score 16.8; DB 1; Length 21;  
Best Local Similarity 90.0%; Pred. No. 1.9e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 2783 TTGAAAAA AAAAAAAAAA 2802  
Db 20 TTGTCAAA AAAAAAAAAA 1  
RESULT 2480  
AW246884  
LOCUS AW246884 22 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2822626.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2822626 3', mRNA sequence.  
ACCESSION AW246884  
VERSION AW246884.1 GI:6589877  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other ESTs: 2822626.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-re@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross\_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 20 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 22 contiguous distinct peaks following vector sequence.  
Plate: LLCW9. row: 0 column: 11





electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.8; DB 1; Length 22;  
Best Local Similarity 90.0%; Pred. No. 2.1e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2173 TTTTCTTTTCTTTTAACTTT 2192  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1 TTTTCTTTTCTTTTGGCTTT 20

RESULT 2483  
TA330H07Q/c  
LOCUS TA330H07Q 22 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 330h07, reverse sequence,  
genomic survey sequence.

ACCESSION AL492002  
VERSION AL492002.1 GI:11868302  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.

REFERENCE 1 (bases 1 to 22)  
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,  
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,  
Melville,S.E., Rajandream,M.A. and Barrell,B.G.

TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nhl@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

FEATURES  
source  
1..22  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="330h07"

Query Match 0.6%; Score 16.8; DB 1; Length 22;  
Best Local Similarity 90.0%; Pred. No. 2.1e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2315 ATTTGTGCTGCTTGTCACC 2334  
| | | | | | | | | | | | | | | | | | | | | |  
Db 20 ATTTGTGCTAGTTGTCACC 1

RESULT 2484  
AL048695  
LOCUS AL048695 23 bp mRNA linear EST 04-SEP-2003  
DEFINITION DKFZp566D063\_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone  
DKFZp566D063, mRNA sequence.

ACCESSION AL048695  
VERSION AL048695.1 GI:4727766  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.  
EST (Koehrer, et al.)  
JOURNAL Unpublished (1999)  
COMMENT Contact: MIPS  
MIPS

FEATURES  
source  
1..23  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKFZp566D063"  
/tissue\_type="kidney"  
/dev\_stage="fetal"  
/lab\_host="Xl-2blue"  
/clone\_lib="566 (synonym: hfkd2)"  
/note="Vector: pAMP1; Site\_1: NotI; Site\_2: SalI"

Query Match 0.6%; Score 16.8; DB 1; Length 23;  
Best Local Similarity 90.0%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2784 TGAATAAAAAAAAAAAAAA 2803  
| | | | | | | | | | | | | | | | | | | | | |  
Db 4 TCAAAAAAAAAAAAAAGAAA 23

RESULT 2485  
CF302134  
LOCUS CF302134 23 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--07-F21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--07-F21, mRNA sequence.

ACCESSION CF302134  
VERSION CF302134.1 GI:33673895  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 23)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1..23  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--07-F21"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for

\*\*\*\*\*





SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)  
REFERENCE  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0103 row: J column: 11  
Seq primer: CGTTGTAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 24.  
FEATURES  
source Location/Qualifiers  
1..24  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0103J11"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.8; DB 1; Length 24;  
Best Local Similarity 90.0%; Pred. No. 2.5e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2166 TTTTGTGTTTTTTTTTTT 2185  
Db TTTTGTGTTTTTTTTTTT 24

RESULT 2492  
BZ765670/c 25 bp DNA linear GSS 13-MAR-2003  
LOCUS SALK\_133356.14.20.x Arabidopsis thaliana TDNA insertion lines  
DEFINITION Arabidopsis thaliana genomic clone SALK\_133356.14.20.x, genomic survey sequence.  
ACCESSION BZ765670  
VERSION BZ765670.1 GI:28938223  
KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi. 1 (bases 1 to 25)  
REFERENCE  
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmermann,J. and Ecker,J.R.  
TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
JOURNAL Unpublished (2001)  
COMMENT Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of TDNA.  
Class: TDNA tagged.  
FEATURES  
source Location/Qualifiers  
1..25  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_133356.14.20.x"  
/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna\_protocols.html"

Query Match 0.6%; Score 16.8; DB 1; Length 25;  
Best Local Similarity 90.0%; Pred. No. 2.6e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2785 GAAAAAATAAAAAA 2804  
Db GAAAAAATAAAAAA 5

RESULT 2493  
AZ404619/c 25 bp DNA linear GSS 03-OCT-2000  
LOCUS 1M0173L20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0173L20 F, genomic survey sequence.  
DEFINITION  
ACCESSION AZ404619  
VERSION AZ404619.1 GI:10528632  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 25)  
REFERENCE  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0173 row: L column: 20  
Seq primer: CGTTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 25.  
Location/Qualifiers  
1. .25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="CS7BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0173L20"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.8; DB 1; Length 25;  
Best Local Similarity 90.0%; Pred. No. 2.6e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1869 TAGCCATTCAAATGTCAAAT 1888  
Db 22 TAGCCATTCAAATATCAAAT 3

RESULT 2494  
CF300303/c  
LOCUS 27 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--04-K11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--04-K11, mRNA sequence.  
ACCESSION CF300303  
VERSION CF300303.1 GI:33672064  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 27)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
1. .27  
/organism="Oryza sativa"

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0173 row: L column: 20  
Seq primer: CGTTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 25.  
Location/Qualifiers  
1. .25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="CS7BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0173L20"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.8; DB 1; Length 25;  
Best Local Similarity 90.0%; Pred. No. 2.6e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1869 TAGCCATTCAAATGTCAAAT 1888  
Db 22 TAGCCATTCAAATATCAAAT 3

RESULT 2494  
CF300303/c  
LOCUS 27 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--04-K11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--04-K11, mRNA sequence.  
ACCESSION CF300303  
VERSION CF300303.1 GI:33672064  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 27)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
1. .27  
/organism="Oryza sativa"

/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--04-K11"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 16.8; DB 1; Length 27;  
Best Local Similarity 90.0%; Pred. No. 2.8e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAAAAAAAAA 2800  
Db 20 AAGTAAAAAAAAAAAAA 1

RESULT 2495  
AI971979  
LOCUS 28 bp mRNA linear EST 27-OCT-1999  
DEFINITION WV30h06.x1 NCI CGAP Ov18 Homo sapiens cDNA clone IMAGE:2531099 3' similar to TR:O63545 O63545 NADH DEHYDROGENASE SUBUNIT 5 ; contains TAR1.b1 TAR1 repetitive element ;, mRNA sequence.  
ACCESSION AI971979  
VERSION AI971979.1 GI:5768805  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 28)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .28  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2531099"  
/tissue\_type="fibrotheoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NCI CGAP\_Ov18"  
/note="Organ: ovary; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCGACATTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 0.6%; Score 16.8; DB 1; Length 28;

Best Local Similarity 90.0%; Pred. No. 2.9e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 3 GAAAAAAAAACAAACAAAAA 22

RESULT 2496  
AL953605/c

LOCUS  
DEFINITION AL953605 30 bp DNA linear GSS 30-NOV-2002  
Arabidopsis thaliana T-DNA flanking sequence GK-352E12-016361,  
genomic survey sequence.

ACCESSION AL953605  
VERSION AL953605.1 GI:24410227  
KEYWORDS GSS.

SOURCE  
ORGANISM Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE  
AUTHORS Strizhov,N., Li,Y., Rosso,M., Viehoveer,P., Dekker,K., Saedler,H.  
and Weisshaar,B.

TITLE A pipeline for automated high-throughput generation of FSTs  
(flanking sequence tags) from Arabidopsis thaliana T-DNA  
transformed lines

JOURNAL  
REFERENCE Unpublished  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE Unpublished  
AUTHORS  
TITLE  
JOURNAL  
COMMENT Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer  
Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany  
This sequence is recovered from the left border of the T-DNA. It  
indicates an insertion within the locus defined by clone F2K11. The  
sequences are generated at the MPI for Plant Breeding Research in  
the context of the GABI-Kat project. GABI-Kat is part of the German  
Plant Genomics program designated 'GABI'. Information on line  
availability can be found at:  
<http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES  
source  
1. 30  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="GK-352E12-016361"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
/note="PCR was performed on DNA from Arabidopsis thaliana  
plants (T1) which were transformed with the T-DNA from  
vector pAC161. The lines contain one or more T-DNA  
insertions. The DNA fragment(s) resulting from the PCR  
were directly sequenced to determine the genomic sequence  
flanking the insertion. Sequences displaying significant  
similarity to the A. thaliana nuclear genome sequence were  
processed for submission. T-DNA derived sequences were  
removed"

Query Match 0.6%; Score 16.8; DB 1; Length 30;  
Best Local Similarity 90.0%; Pred. No. 2.9e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2784 TGAAAAAAAAAAAAAAAAAAAAA 2803  
|||||  
Db 30 TGAACAAACAAATAAAAAA 11

RESULT 2497

AU265130  
LOCUS  
DEFINITION AU265130 VS Dictyostelium discoideum cDNA clone VSF372 5', mRNA  
sequence.

ACCESSION AU265130  
VERSION AU265130.1 GI:20523928  
KEYWORDS EST.

SOURCE  
ORGANISM Dictyostelium discoideum  
Dictyostelium discoideum  
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
1 (bases 1 to 34)  
Urushihara,H., Morio,T., Saito,T., Koriiki,E., Ochiai,H., Maeda,M.,  
Takeuchi,I., Kohara,Y. and Tanaka,Y.  
Population analysis of cDNAs from unicellular and multicellular  
stages of Dictyostelium discoideum  
Unpublished (2002)  
Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: hideko@biol.tsukuba.ac.jp.

FEATURES  
source  
1. 34  
/organism="Dictyostelium discoideum"  
/mol\_type="mRNA"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="VSF372"  
/sex="mat A"  
/dev\_stage="vegetative"  
/clone\_lib="VS"

Query Match 0.6%; Score 16.8; DB 1; Length 34;  
Best Local Similarity 72.4%; Pred. No. 2.7e+03;  
Matches 21; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2776 GTTAGAATTGAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 GTAATATATAAAAAAAAAAAAAAAAAATTNAAAA 29

RESULT 2498  
BF239380  
LOCUS  
DEFINITION BF239380 35 bp mRNA linear EST 14-NOV-2000  
601906237F1 NIH\_MGC\_54 Homo sapiens cDNA clone IMAGE:4134224 5',  
mRNA sequence.

ACCESSION BF239380  
VERSION BF239380.1 GI:11153302  
KEYWORDS EST.

SOURCE  
ORGANISM Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 35)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: CLONETECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM1036 row: i column: 09  
High quality sequence stop: 3.  
Location/Qualifiers  
1. 35  
/organism="Homo sapiens"



/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4134224"  
/tissue\_type="from chronic myelogenous leukemia"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_54"  
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);  
Site\_1: SfiI (ggcgctcgcc); Site\_2: SfiI  
(ggccattatggcc); Double-stranded cDNA was prepared from  
cell line RNA. 5' and 3' adaptors were used in cloning as  
follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and  
3' adaptor sequence:  
5'-ATTCTAGAGCGGAGCGCGCCGACATG-dT(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size  
1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained  
inserts by PCR. This library was enriched for full-length  
clones and was constructed by Clontech Laboratories (Palo  
Alto, CA)."

Query Match 0.6%; Score 16.8; DB 1; Length 35;  
Best Local Similarity 90.0%; Pred. No. 2.6e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2782 ATTGAAAAAAAAAAAAAAAA 2801  
1 |||||||  
Db 6 ATAGAAAAAAAAAGAAAAA 25

RESULT 2499  
CF290998  
LOCUS  
DEFINITION  
14ROOT--01-E03.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-E03, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 23)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1..23  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="14ROOT--01-E03"  
/tissue\_type="root"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: pCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.6%; Score 16.6; DB 1; Length 23;  
Best Local Similarity 82.6%; Pred. No. 2.4e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAAA 2803

Db  
1 AACAGCAAAAAAAAAAAAAA 23  
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RESULT 2500  
AW249550  
LOCUS  
DEFINITION  
2821204.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821204 3',  
mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 23)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2821204.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 9 contiguous  
PHRED high quality bases following vector sequence. Very Low  
Quality Sequence: Trace file contained 23 contiguous distinct peaks  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: L1CM6 row: D column: 5  
High quality sequence stop: 9.  
Location/Qualifiers  
1..23  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821204"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.6%; Score 16.6; DB 1; Length 23;  
Best Local Similarity 82.6%; Pred. No. 2.4e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2177 TTTTCTTTTAACTTTGAAAGTT 2199  
|||||  
Db 1 TTTTCTTTTAACTTTAAATTT 23  
|||||

RESULT 2501  
AZ330773  
LOCUS  
DEFINITION  
1M0056008F Mouse 10kb plasmid UUGC1m library Mus musculus genomic

Query Match 0.6%; Score 16.6; DB 1; Length 23;  
Best Local Similarity 82.6%; Pred. No. 2.4e+03;  
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

















```

Db      1 TTTTTTTTTTTTTTCT 18

RESULT 2516
CF320046/c
LOCUS   CF320046               18 bp   mRNA   linear   EST 15-AUG-2003
DEFINITION HD--10-M11.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--10-M11, mRNA sequence.
ACCESSION CF320046
VERSION   CF320046.1 GI:33691807
KEYWORDS EST.
SOURCE   Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
               1..18
               /organism="Oryza sativa"
               /mol_type="mRNA"
               /cultivar="Nackdong"
               /db_xref="taxon:4530"
               /clone="HD--10-M11"
               /tissue_type="callus"
               /dev_stage="proliferated callus on 2N6 media for 2 weeks"
               /lab_host="E.coli DH10B"
               /clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
               cDNA library (HD)"
               /note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
               treated with ABA(20um) for 1hr. Oligo-capped mRNA was
               reverse transcribed and then used for PCR. mRNA was
               derived from rice Histone Deacetylase overexpression
               line."

               Query Match      0.6%;   Score 16.4;   DB 1;   Length 18;
               Best Local Similarity 94.4%;   Pred. No. 1.4e+03;
               Matches 17;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAA 2803
Db      18 ATAAAAAAAAAAAAAAAA 1

RESULT 2517
AL048754
LOCUS   AL048754               18 bp   mRNA   linear   EST 04-SEP-2003
DEFINITION DKFZp566L173.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
            DKFZp566L173, mRNA sequence.
ACCESSION AL048754
VERSION   AL048754.1 GI:4727825
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

               Query Match      0.6%;   Score 16.4;   DB 1;   Length 18;
               Best Local Similarity 94.4%;   Pred. No. 1.4e+03;
               Matches 17;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAA 2803
Db      18 ATAAAAAAAAAAAAAAAA 1

RESULT 2518
AL048754/c
LOCUS   AL048754               18 bp   mRNA   linear   EST 04-SEP-2003
DEFINITION DKFZp566L173.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
            DKFZp566L173, mRNA sequence.
ACCESSION AL048754
VERSION   AL048754.1 GI:4727825
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS

               Query Match      0.6%;   Score 16.4;   DB 1;   Length 18;
               Best Local Similarity 94.4%;   Pred. No. 1.4e+03;
               Matches 17;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      2170 TTTTTTTTTTTTTTTT 2187
Db      18 TTTTTTTTTTTTTTGA 1

RESULT 2519
BM658677
LOCUS   BM658677               18 bp   mRNA   linear   EST 27-FEB-2002
DEFINITION LZV602768363.R1 CSEQFXL37 pig adrenal Sus scrofa cDNA, mRNA
            sequence.
ACCESSION BM658677
VERSION   BM658677.1 GI:18958948
KEYWORDS EST.
SOURCE   Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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FEATURES             source
               1..18
               /organism="Homo sapiens"
               /mol_type="mRNA"
               /db_xref="taxon:9606"
               /clone="DKFZp566L173"
               /tissue_type="kidney"
               /dev_stage="fetal"
               /lab_host="X1-2blue"
               /clone_lib="566 (synonym: hfkd2)"
               /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

               Query Match      0.6%;   Score 16.4;   DB 1;   Length 18;
               Best Local Similarity 94.4%;   Pred. No. 1.4e+03;
               Matches 17;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      2784 TGAATAAAAAAAAAAAAA 2801
Db      1 TCAAAAAAAAAAAAAAAAAA 18

RESULT 2518
AL048754/c
LOCUS   AL048754               18 bp   mRNA   linear   EST 04-SEP-2003
DEFINITION DKFZp566L173.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
            DKFZp566L173, mRNA sequence.
ACCESSION AL048754
VERSION   AL048754.1 GI:4727825
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 18)
AUTHORS Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS

               Query Match      0.6%;   Score 16.4;   DB 1;   Length 18;
               Best Local Similarity 94.4%;   Pred. No. 1.4e+03;
               Matches 17;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      2170 TTTTTTTTTTTTTTTT 2187
Db      18 TTTTTTTTTTTTTTGA 1

RESULT 2519
BM658677
LOCUS   BM658677               18 bp   mRNA   linear   EST 27-FEB-2002
DEFINITION LZV602768363.R1 CSEQFXL37 pig adrenal Sus scrofa cDNA, mRNA
            sequence.
ACCESSION BM658677
VERSION   BM658677.1 GI:18958948
KEYWORDS EST.
SOURCE   Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE 1 (bases 1 to 18)  
AUTHORS Adelson,D.L. and Gill,C.A.  
TITLE Porcine ESTs  
JOURNAL Unpublished (2002)  
COMMENT Contact: David L. Adelson  
Animal Breeding and Genetics  
Texas A&M University  
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,  
USA  
Tel: 9798452616  
Fax: 9798456970  
Email: david.adelson@tamu.edu.  
Location/Qualifiers  
1. .18  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone\_lib="CSEQFXL37 pig adrenal"  
/note="Organ: adrenal gland; Vector: pBluescript SK+;  
Site 1: NotI; Site 2: EcoRI; sequence 5' of the insert  
(5'-NNN...NNNinsert)  
GCGAATGGAGCTCCACCGGTCGGCGCGGCTCGAG. Sequence 3' of  
the inserts (AAGAATTCGATATCAAGCTTATCGATACGTCGACCTCGAG.  
non-normalized library, sequenced 3' with M13R primer."

Query Match 0.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTTCCTTTTTCCTTTTTCCTTTT 2183  
|||||||  
Db 1 TTTTTCCTTTTTCCTTTTTCCTTTT 18

RESULT 2520  
BM658677/c  
LOCUS BM658677 18 bp mRNA linear EST 27-FEB-2002  
DEFINITION LZV602768363.R1 CSEQFXL37 pig adrenal Sus scrofa cDNA, mRNA  
sequence.  
ACCESSION BM658677 GI:18958948  
VERSION EST.  
KEYWORDS  
SOURCE Sus scrofa (pig)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Adelson,D.L. and Gill,C.A.  
TITLE Porcine ESTs  
JOURNAL Unpublished (2002)  
COMMENT Contact: David L. Adelson  
Animal Breeding and Genetics  
Texas A&M University  
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,  
USA  
Tel: 9798452616  
Fax: 9798456970  
Email: david.adelson@tamu.edu.  
Location/Qualifiers  
1. .18  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone\_lib="CSEQFXL37 pig adrenal"  
/note="Organ: adrenal gland; Vector: pBluescript SK+;  
Site 1: NotI; Site 2: EcoRI; sequence 5' of the insert  
(5'-NNN...NNNinsert)  
GCGAATGGAGCTCCACCGGTCGGCGCGGCTCGAG. Sequence 3' of  
the inserts (AAGAATTCGATATCAAGCTTATCGATACGTCGACCTCGAG.  
non-normalized library, sequenced 3' with M13R primer."

Query Match 0.6%; Score 16.4; DB 1; Length 18;

Best Local Similarity 94.4%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
|||||||  
Db 18 AAAAAAAAAAGAAAAAAAAA 1

RESULT 2521  
CF309376  
LOCUS CF309376 18 bp mRNA linear EST 15-AUG-2003  
DEFINITION ABF--03-I19.b1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--03-I19, mRNA sequence.  
ACCESSION CF309376  
VERSION CF309376.1 GI:33681137  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
1. .18  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="ABF--03-I19"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid  
cDNA library (ABF)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2173 TTTTTCCTTTTTCCTTTTTCCTTTT 2190  
|||||||  
Db 1 TTTTTCCTTTTTCCTTTTTCCTTTT 18

RESULT 2522  
CF329285  
LOCUS CF329285 18 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--04-I22.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--04-I22, mRNA sequence.  
ACCESSION CF329285  
VERSION CF329285.1 GI:33806806  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.



REFERENCE  
AUTHORS 1 (bases 1 to 18)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
Location/Qualifiers  
1..18  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="NACL--04-I22"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2170 TTTTCTTTTCTTTTCTTA 2187  
|||||  
DB 1 TTTTCTTTTCTTTTCTTA 18

RESULT 2523  
CF329285/c  
LOCUS CF329285 18 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--04-I22.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--04-I22, mRNA sequence.

ACCESSION CF329285  
VERSION CF329285.1 GI:33806806  
KEYWORDS EST.

SOURCE  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS 1 (bases 1 to 18)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
Location/Qualifiers  
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/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
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/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2783 TTGAAAAA 2800  
|||||  
DB 18 TAGAAAAA 1

RESULT 2524  
CF329484  
LOCUS CF329484 18 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--04-N06.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--04-N06, mRNA sequence.

ACCESSION CF329484  
VERSION CF329484.1 GI:33807207  
KEYWORDS EST.

SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS 1 (bases 1 to 18)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
Location/Qualifiers  
1..18

/organism="Oryza sativa"  
/mol\_type="mRNA"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.6%; Score 16.4; DB 1; Length 18;  
Best Local Similarity 94.4%; Pred. No. 1.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2173 TTTTCTTTTCTTTTAACT 2190  
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DB 1 TTTTCTTTTCTTTTAACT 18

RESULT 2525  
CF329485/c  
LOCUS CF329485 18 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--04-N06.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--04-N06, mRNA sequence.

ACCESSION CF329485  
VERSION CF329485.1 GI:33807209  
KEYWORDS EST.

SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;



VERSION AZ360314.1 GI:10474014  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0103 row: G column: 03  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0103G03"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2166 TTTTTCCTTTTCTTTT 2183  
Db 19 TTTTTCCTTTTCTTTT 2

RESULT 2529  
CF278272/c  
LOCUS 14ETL--04-C01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)  
DEFINITION Oryza sativa cDNA clone 14ETL--04-C01, mRNA sequence.  
ACCESSION CF278272  
VERSION CF278272.1 GI:33655658

KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
1 (bases 1 to 19) Ehrhartoidae; Oryzeae; Oryza.  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
1. .19  
/organism="Oryza sativa"  
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/clone\_lib="Rice etiolated leaf plasmid cDNA library  
(14ETL)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.6%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2783 TTGAAAAAATAAAAAA 2800  
Db 18 TTTAAAAAATAAAAAA 1

RESULT 2530  
CF295672  
LOCUS 30DGS--05-L12.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
DEFINITION sativa cDNA clone 30DGS--05-L12, mRNA sequence.  
ACCESSION CF295672  
VERSION CF295672.1 GI:33664705  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
1 (bases 1 to 19) Ehrhartoidae; Oryzeae; Oryza.  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
1. .19  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"





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source
1. .19
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/tissue_type="callus"
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/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.6%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2171 TTTTTCCTTTTCTTTTAA 2188
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Db 1 TTTTTCCTTTTCTTTTGA 18

RESULT 2534
CF319596/c
LOCUS
DEFINITION
HD--10-C14.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--10-C14, mRNA sequence.
ACCESSION
CF319596
VERSION
CF319596.1 GI:33691357
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .19
/organism="Oryza sativa"
/mol_type="mRNA"
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/db_xref="taxon:4530"
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/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.6%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

FEATURES
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/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
Query Match 0.6%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 2783 TTGAAAAA 2800
|||
Db 18 TTCAAAAAA 1

RESULT 2535
CF326845
LOCUS
DEFINITION
NACL--01-B12.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--01-B12, mRNA sequence.
ACCESSION
CF326845
VERSION
CF326845.1 GI:33801944
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .19
/organism="Oryza sativa"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.6%; Score 16.4; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2783 TTGAAAAA 2800
|||
Db 2 TAGAAAAA 19

RESULT 2536
CF326845/c
LOCUS
DEFINITION
NACL--01-B12.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--01-B12, mRNA sequence.
ACCESSION
CF326845
VERSION
CF326845.1 GI:33801944
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers  
1. .19  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="NACL--01-B12"  
/tissue\_type="callus"  
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/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.6%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2170 TTTTCTTTTCTTTTCTA 2187

Db 19 TTTTCTTTTCTTTTCTA 2

RESULT 2537

AZ465954

LOCUS

DEFINITION

AZ465954 19 bp DNA linear GSS 04-OCT-2000  
1M0276E16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0276E16 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0276 row: E column: 16  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES

source

Location/Qualifiers  
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/clone="UUGC1M0276E16"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2162 CTCCTTTTCTTTTCTT 2179

Db 2 CCCCCTTTTCTTTTCTT 19

RESULT 2538

AZ766990/c

LOCUS

DEFINITION

AZ766990 19 bp DNA linear GSS 16-FEB-2001  
1M0564H19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0564H19 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0564 row: H column: 19  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES

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Location/Qualifiers  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0564H19"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.



musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 19;  
Best Local Similarity 94.4%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2163 TCCATTTTTCCTTTTTCCTTTT 2180  
Db 18 TCCATTTTTCCTTTTTCCTTTT 1

RESULT 2539  
CF319428/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CF319428 20 bp mRNA linear EST 15-AUG-2003  
HD--09-O20.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--09-O20, mRNA sequence.

CF319428 GI:33691189  
EST.  
Oryza sativa

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 20)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1..20  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="HD--09-O20"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.6%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 1.9e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2784 TGAATAAAAAAAAAAAAAA 2801  
Db 19 TCAAAAAAAAAAAAAA 2

RESULT 2540  
CF317946  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CF317946 20 bp mRNA linear EST 15-AUG-2003  
HD--07-N06.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--07-N06, mRNA sequence.

CF317946 GI:33689707  
EST.  
Oryza sativa

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 20)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1..20  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="HD--07-N06"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.6%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 52 CGCGGGGGCGCGCGCAG 69  
Db 1 CGCGGGGGCGCGCGCAG 18

RESULT 2541  
AZ368518/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

AZ368518 20 bp DNA linear GSS 02-OCT-2000  
1M0118G09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0118G09 R, genomic survey sequence.

AZ368518 GI:10482218  
GSS.  
Mus musculus (house mouse)

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausen,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0118 row: G column: 09  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

FEATURES

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1. .20  
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/db\_xref="taxon:10090"  
/clone="UUGC1M0118G09"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 20;  
Best Local Similarity 94.4%; Pred. No. 1.9e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2171 TTTTGTGTTTTTTTAA 2188  
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Db 20 TTTTGTGTTTTTTTAA 3

RESULT 2542  
CF319625  
LOCUS CF319625 21 bp mRNA linear EST 15-AUG-2003  
DEFINITION HD--10-D06.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--10-D06, mRNA sequence.  
ACCESSION CF319625  
VERSION CF319625.1 GI:33691386  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

TITLE  
JOURNAL  
COMMENT

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES

source

1. .21  
/organism="Oryza sativa"  
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/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.6%; Score 16.4; DB 1; Length 21;  
Best Local Similarity 94.4%; Pred. No. 2.2e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2803  
|||||  
Db 4 ATAAAAAAAAAAAAA 21

RESULT 2543  
CF293087

LOCUS CF293087 21 bp mRNA linear EST 14-AUG-2003  
DEFINITION 30DGS--02-C07.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa cDNA clone 30DGS--02-C07, mRNA sequence.

ACCESSION CF293087  
VERSION CF293087.1 GI:33662120  
KEYWORDS EST.  
SOURCE Oryza sativa

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

TITLE

JOURNAL

COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES

source

1. .21  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 16.4; DB 1; Length 21;  
Best Local Similarity 94.4%; Pred. No. 2.2e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2172 TTTT TTTT TTTT TTTT TTTT AAC 2189  
|||||  
Db 1 TTTT TTTT TTTT TTTT TGAC 18

RESULT 2544  
CF319122/c

LOCUS CF319122 21 bp mRNA linear EST 15-AUG-2003  
DEFINITION HD--09-I07.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--09-I07, mRNA sequence.

ACCESSION CF319122  
VERSION CF319122.1 GI:33690883  
KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..21

/organism="Oryza sativa"

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/cultivar="Nackdong"

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/clone="HD--09-I07"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_host="E.coli DH10B"

/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16.4; DB 1; Length 21;  
Best Local Similarity 94.4%; Pred. No. 2.2e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAA AAAAAA AAAAAA 2802  
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Db 18 GAAAAA AAAAAA AAAAAA 1

RESULT 2545

CF318882

LOCUS

DEFINITION HD--09-C23.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--09-C23, mRNA sequence.

ACCESSION CF318882

VERSION CF318882.1 GI:33690643

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..22

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

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/clone="HD--09-C23"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_host="E.coli DH10B"

/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16.4; DB 1; Length 22;

Best Local Similarity 94.4%; Pred. No. 2.4e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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|||||

Db 1 TTTT TTTT TTTT TTTT TTTT GAA 18

RESULT 2546

AZ307896/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

22 bp DNA linear GSS 29-SEP-2000  
IM0010N18F Mouse 10kb plasmid UUGClm library Mus musculus genomic clone UUGClm0010N18 F, genomic survey sequence.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00



Plate: 0010 row: N column: 18  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.

FEATURES  
source

Location/Qualifiers  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 22;  
Best Local Similarity 94.4%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 22 AAAAAAAAAAAACAAA 5

RESULT 2547  
BQ591193/c

LOCUS  
DEFINITION  
BQ591193 22 bp mRNA linear EST 06-DEC-2002  
CDNA clone 024-017-D14 T7 MP1Z-ADIS-024-storage root Beta vulgaris

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Beta vulgaris  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 22)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698  
Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaam@mpiz-koeln.mpg.de  
Insert length: 22 Std Error: 0.00  
Plate: 17 row: D column: 14

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

REFERENCE  
AUTHORS

Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES  
source

Location/Qualifiers  
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/clone="024-017-D14"  
/tissue\_type="storage root"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-storage root"  
/note="Vector: PCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 16.4; DB 1; Length 22;  
Best Local Similarity 94.4%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2782 ATTGAAAAAAAAAAAA 2799  
Db 18 ATTAATAAAAAAAAAAAA 1

RESULT 2548  
AZ330773/c

LOCUS  
DEFINITION

AZ330773 23 bp DNA linear GSS 29-SEP-2000  
IM0056O08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0056O08 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 23)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0056 row: O column: 08  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 23.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source

Location/Qualifiers  
1. .23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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/db\_xref="taxon:10090"  
/clone="UUGC1M0056O08"

/sex="Male"  
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 23;  
Best Local Similarity 94.4%; Pred. No. 2.6e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2171 TTTTTTTTTTTTTTTTAA 2188  
|||||  
Db 23 TTTTTTTTTTTTTTGAA 6

RESULT 2549

BX560037

LOCUS

DEFINITION BX560037 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse47e08\_plc, mRNA sequence.

ACCESSION BX560037

VERSION BX560037.1 GI:33368052

KEYWORDS EST.

SOURCE

ORGANISM

Glossina morsitans morsitans  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 23)

AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)

MEDLINE 22881942

PUBMED 14519198

COMMENT Contact: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J.Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES

source

Location/Qualifiers

1..23

/organism="Glossina morsitans morsitans"

/mol\_type="mRNA"

/sub\_species="morsitans"

/db\_xref="taxon:37546"

/clone="Tse47e08\_plc"

/tissue type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected gut"  
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.6%; Score 16.4; DB 1; Length 23;  
Best Local Similarity 94.4%; Pred. No. 2.6e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2171 TTTTTTTTTTTTTTTTAA 2188

|||||

Db 1 TTTTTTTTTTTTTTCTAA 18

RESULT 2550

AZ308447

LOCUS

DEFINITION

AZ308447 23 bp DNA linear GSS 29-SEP-2000

1M0011J24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0011J24 F, genomic survey sequence.

ACCESSION AZ308447

VERSION AZ308447.1 GI:10348452

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 23)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0011 row: J column: 24

Seq primer: CGTTGTAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1..23

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0011J24"

/sex="Male"

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and









/db\_xref="taxon:10090"  
/clone="UUGC1M0547I04"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 24;  
Best Local Similarity 94.4%; Pred. No. 2.7e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 105 CGCTTGGGGCTGGGGG 122  
|||  
Db 1 CGCTTGGGGCGGGGG 18

RESULT 2558  
AZ329925  
LOCUS  
DEFINITION  
1M0054N14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0054N14 R, genomic survey sequence.

ACCESSION  
AZ329925  
VERSION  
AZ329925.1 GI:10391126  
KEYWORDS  
GSS.

SOURCE  
Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
1 (bases 1 to 25)

AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL

COMMENT  
Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0054 row: N column: 14

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 25.

Location/Qualifiers

1. .25

FEATURES

source

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0054N14"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 25;  
Best Local Similarity 94.4%; Pred. No. 2.9e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAAAGAAAAA 2802  
|||  
Db 8 GAAGAAAAA 25

RESULT 2559

AZ515233

LOCUS

DEFINITION

1M0054N14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0054N14 F, genomic survey sequence.

ACCESSION

AZ515233

VERSION

AZ515233.1 GI:10696549

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 25)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL

COMMENT  
Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0054 row: N column: 14

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 25.

Location/Qualifiers

1. .25

FEATURES

source

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0054N14"



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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

Query Match	0.6%;	Score 16.4;	DB 1;	Length 25;
Best Local Similarity	94.4%;	Pred. No. 2.9e+03;		
Matches 17;	Conservative	0;	Mismatches 1;	Indels
			0;	Gaps 0;
QY	2785	GAAGAAAAA	AAAAAAAAA	2802
Dd	8	GAAGAAAAA	AAAAAAAAA	25

RESULT	2560
AZ997733/c	
LOCUS	AZ997733
DEFINITION	2M0284E22F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0284E22 F, genomic survey sequence.
	25 bp DNA linear
	GSS 27-APR-2001

```

FEATURES
source
1. .25
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0284E22"
/sex="Female"

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/lab host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match	0.6%;	Score 16.4;	DB 1;	Length 25;
Best Local Similarity	94.4%;	Pred. NO. 2.9e+03;		
Matches 17;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps 0;				
Qy	2162	CTCCTTTT	TTTTTTT	2179
db	18	CCCCCCCC	TTTTTTTT	1

RESULT	2561
BM658913/c	
LOCUS	
DEFINITION	BM658913 26 bp mRNA linear EST 27-FEB-2002 LQG602768282.R1 CSEQFXL36 fetal brain Sus scrofa cDNA, mRNA sequence.
ACCESSION	BM658913
VERSION	BM658913.1 GI:18959184
KEYWORDS	EST.
SOURCE	Sus scrofa (pig)
ORGANISM	Sus scrofa

REFERENCE	1 (bases 1 to 26)
AUTHORS	Adelson, D.L. and Gill, C.A.
TITLE	Porcine ESTs
JOURNAL	Unpublished (2002)
COMMENT	Contact: David L. Adelson

## FEATURES

Query Match 0.6%; Score 16.4; DB 1; Length 26;  
Best Local Similarity 94.4%; Pred. No. 3e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
| | | | | | | | | | | | | | | | | |  
Db 26 AAAAAAAAAAAAAAAAAAGAA 9

RESULT 2562  
AU265518/c  
LOCUS  
DEFINITION AU265518 VS Dictyostelium discoideum cDNA clone VSP623 5', mRNA  
sequence.  
ACCESSION AU265518  
VERSION AU265518.1 GI:20524316  
KEYWORDS EST.  
SOURCE Dictyostelium discoideum  
ORGANISM Dictyostelium discoideum  
REFERENCE Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,  
Takeuchi,I., Kohara,Y. and Tanaka,Y.  
TITLE Population analysis of cDNAs from unicellular and multicellular  
stages of Dictyostelium discoideum  
JOURNAL Unpublished (2002)  
COMMENT Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: hideko@biol.tsukuba.ac.jp.

FEATURES  
source  
1. .26  
/organism="Dictyostelium discoideum"  
/mol\_type="mRNA"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="VSP623"  
/sex="mat A"  
/dev\_stage="vegetative"  
/clone\_lib="VS"

Query Match 0.6%; Score 16.4; DB 1; Length 26;  
Best Local Similarity 94.4%; Pred. No. 3e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
| | | | | | | | | | | | | | | | | |  
Db 26 AAAAAAAAAAAAAAAAAAGA 9

RESULT 2563  
BX563414/c  
LOCUS  
DEFINITION BX563414 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tse66e05\_plc, mRNA sequence.  
ACCESSION BX563414  
VERSION BX563414.1 GI:33430654  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 2281942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source  
1. .26  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse66e05\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.6%; Score 16.4; DB 1; Length 26;  
Best Local Similarity 76.9%; Pred. No. 3e+03;  
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAAAAAAAAAAAAAA 2804  
| | | | | | | | | | | | | | | | | |  
Db 26 AAAAAAAAAAACCAAAAAAAAAAAAA 1

RESULT 2564  
AU265398  
LOCUS  
DEFINITION AU265398 VS Dictyostelium discoideum cDNA clone VSP546 5', mRNA  
sequence.  
ACCESSION AU265398  
VERSION AU265398.1 GI:20524196  
KEYWORDS EST.  
SOURCE Dictyostelium discoideum  
ORGANISM Dictyostelium discoideum  
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,  
Takeuchi,I., Kohara,Y. and Tanaka,Y.  
TITLE Population analysis of cDNAs from unicellular and multicellular  
stages of Dictyostelium discoideum  
JOURNAL Unpublished (2002)  
COMMENT Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: hideko@biol.tsukuba.ac.jp.

FEATURES  
source  
1. .27  
/organism="Dictyostelium discoideum"  
/mol\_type="mRNA"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="VSP546"  
/sex="mat A"  
/dev\_stage="vegetative"  
/clone\_lib="VS"

Query Match 0.6%; Score 16.4; DB 1; Length 27;  
Best Local Similarity 76.9%; Pred. No. 3e+03;  
Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAAAAAAAAAAAAAA 2804  
| | | | | | | | | | | | | | | | | |

Db 2 AAATTTTAAATAATAATAAAAAAAA 27

RESULT 2565

CF318113

LOCUS

DEFINITION

HD--08-B07.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--08-B07, mRNA sequence.

CF318113

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Eukarya

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 27)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .27

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="HD--08-B07"

/tissue type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_host="E.coli DH10B"

/clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16.4; DB 1; Length 27;

Best Local Similarity 76.9%; Pred. No.3e+03;

Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAAATAAAAAA 2804

Db 1 AAAAAAAACCAAAAAA 26

RESULT 2566

AW250467

LOCUS

DEFINITION

AW250467

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 27)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other ESTs: 2822354.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 27 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 27 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LLCM9 row: D column: 3

High quality sequence stop: 27.

Location/Qualifiers

1. .27

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2822354"

/tissue type="small cell carcinoma"

/cell\_line="MGC3"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC 7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.6%; Score 16.4; DB 1; Length 27;

Best Local Similarity 76.9%; Pred. No.3e+03;

Matches 20; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTTTTAACTT 2191

Db 2 TTTTTTTTCTTATATTTACTT 27

RESULT 2567

AZ827060/c

LOCUS

DEFINITION

2M0103F17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0103F17 F, genomic survey sequence.

AZ827060

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 29)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA







cdna library (HD) "  
/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

```

Query Match      0.6%; Score 16.4; DB 1; Length 34;
Best Local Similarity 94.4%; Pred. No. 2.7e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 2786 AAAAAAAAAAAAAAAAAA 2803  
 |||||  
 db 1 AAAAAAAAAAAAAAAAAA 18

RESULT	2573				
AZ339890					
LOCUS	AZ339890	39 bp	DNA	linear	GSS 29-SEP-2000
DEFINITION	1M0071L05R	Mouse 10kb	plasmid	UUGC1M library	Mus musculus genomic
				clone UUGC1M0071L05 R.	genomic survey sequence.

AZ339890  
 AZ339890.1  
 GI:10414608  
 GSS

SOURCE	ORGANISM
U.S.S.R.	
Mus musculus (house mouse)	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Mus musculus	

REFERENCE  
AUTHORS

1 (bases 1 to 39)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D.: Weiss, R.

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb  
Niederhausem,A. and Wllync,D.:;weiss,K.

TIME  
MOUSE WIRE  
plasmid inserts

JOURNAL  
Unpublished (2000)

CONTACT: Robert B. Weiss

CONTACT: ROBERT D. WEISS  
University of Utah Genome Center

University of Utah

UNIVERSITY OF UTAH  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

RM: 306, B  
84172, USA

04112, USA  
Tel.: 801 585 5606

TEL: 801 363 3606  
FAX: 801 585 7177

Fax: 801 383 7177  
Email: ddunn@genetics.utah.edu

Email: [dunning@genetics.ucall.edu](mailto:dunning@genetics.ucall.edu)  
Insert Length: 10000 Std Error: 0.00

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Insert Length: 10000
plate: 0071 row: 1 column: 05

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Plate: 0071 Row: L Column: 05  
See image: 00000000000000000000

seq primer: CACACAG

Class: plasmid ends

High quality sequence stop:

## FEATURES

## Source

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Location/Qualifiers
1. .39
  /organism="Mus musculus"
  /mol_type="genomic DNA"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="UUGC1M0071L05"
  /sex="Male"
  /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
  /clone_lib="Mouse 10kb plasmid UUGC1m library"
  /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

```



purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.4; DB 1; Length 40;  
Best Local Similarity 94.4%; Pred. No. 2.3e+03;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 39 AAAAAAAAAACAAAAAAAAA 22

RESULT 2575  
CF330439/c  
LOCUS  
DEFINITION  
NACL--06-C12.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--06-C12, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa

CF330439 21 bp mRNA linear EST 18-AUG-2003  
NACL--06-C12.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--06-C12, mRNA sequence.  
CF330439  
EST.  
CF330439.1 GI:33809110  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
1 (bases 1 to 21)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
Location/Qualifiers  
1..21  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="NACL--06-C12"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2784 TGAAAAAAAAAAAAAAAAAA 2804  
Db 21 TGTATAAAAAAAAAAAAAAAAA 1

RESULT 2576  
CF319122  
LOCUS  
DEFINITION  
HD--09-I07.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--09-I07, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
1 (bases 1 to 21)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
Location/Qualifiers  
1..21  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="HD--09-I07"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OsHDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16.2; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 2.3e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2166 TTTTATTTTTTTTTTTTTTTT 2186  
Db 1 TTTTATTTTTTTTTTTTCGTT 21

RESULT 2577  
AZ316019/c  
LOCUS  
DEFINITION  
AZ316019 21 bp DNA linear GSS 29-SEP-2000  
1M0033C05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0033C05 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AZ316019.1 GI:10363426  
GSS.  
Mus musculus (house mouse)  
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
1 (bases 1 to 21)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0033 row: C column: 05  
Seq primer: CACACAGGAACACGCTATGACC

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Class: plasmid ends
High quality sequence stop: 21.
FEATURES
    Location/Qualifiers
        source            1..21

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FEATURES  
source

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1. 21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0033C05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

```

Query Match          0.6%;   Score 16.2;   DB 1;   Length 21;
Best Local Similarity 85.7%;   Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

Qy 2161 TCTCCCTTTTTTTT 2181  
pb 21 TGCGGTTTTTTTTT 1

RESULT	2578
AZ345540	
LOCUS	AZ345540
DEFINITION	1M0080P05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080P05 F, genomic survey sequence.
	21 bp DNA linear GSS 29-SEP-2000

AZ345540  
 AZ345540.1  
 GI:10424777  
 GSS.  
 Mus musculus (house mouse)

ORGANISM	Mus musculus (house mouse)
SOURCE	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 21)
	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

High quality sequence stop: 21.  
Location/Qualifiers

FEATURES	SOURCE
1. <b>Age</b>	1. <b>Age</b>
2. <b>Gender</b>	2. <b>Gender</b>
3. <b>Marital Status</b>	3. <b>Marital Status</b>
4. <b>Education</b>	4. <b>Education</b>
5. <b>Income</b>	5. <b>Income</b>
6. <b>Occupation</b>	6. <b>Occupation</b>
7. <b>Religion</b>	7. <b>Religion</b>
8. <b>Political Affiliation</b>	8. <b>Political Affiliation</b>
9. <b>Health Status</b>	9. <b>Health Status</b>
10. <b>Travel History</b>	10. <b>Travel History</b>
11. <b>Family Size</b>	11. <b>Family Size</b>
12. <b>Home Ownership</b>	12. <b>Home Ownership</b>
13. <b>Employment Status</b>	13. <b>Employment Status</b>
14. <b>Language Spoken</b>	14. <b>Language Spoken</b>
15. <b>Religious Beliefs</b>	15. <b>Religious Beliefs</b>
16. <b>Political Views</b>	16. <b>Political Views</b>
17. <b>Health Habits</b>	17. <b>Health Habits</b>
18. <b>Travel Preferences</b>	18. <b>Travel Preferences</b>
19. <b>Family Values</b>	19. <b>Family Values</b>
20. <b>Home Environment</b>	20. <b>Home Environment</b>
21. <b>Employment History</b>	21. <b>Employment History</b>
22. <b>Language Proficiency</b>	22. <b>Language Proficiency</b>
23. <b>Religious Practices</b>	23. <b>Religious Practices</b>
24. <b>Political Engagement</b>	24. <b>Political Engagement</b>
25. <b>Health Insurance</b>	25. <b>Health Insurance</b>
26. <b>Travel Insurance</b>	26. <b>Travel Insurance</b>
27. <b>Family Income</b>	27. <b>Family Income</b>
28. <b>Home Address</b>	28. <b>Home Address</b>
29. <b>Employment Type</b>	29. <b>Employment Type</b>
30. <b>Language of Origin</b>	30. <b>Language of Origin</b>
31. <b>Religious Community</b>	31. <b>Religious Community</b>
32. <b>Political Party</b>	32. <b>Political Party</b>
33. <b>Health Care Access</b>	33. <b>Health Care Access</b>
34. <b>Travel Agency</b>	34. <b>Travel Agency</b>
35. <b>Family Traditions</b>	35. <b>Family Traditions</b>
36. <b>Home Decor</b>	36. <b>Home Decor</b>
37. <b>Employment Sector</b>	37. <b>Employment Sector</b>
38. <b>Language Skills</b>	38. <b>Language Skills</b>
39. <b>Religious Festivals</b>	39. <b>Religious Festivals</b>
40. <b>Political Movements</b>	40. <b>Political Movements</b>
41. <b>Health Services</b>	41. <b>Health Services</b>
42. <b>Travel Packages</b>	42. <b>Travel Packages</b>
43. <b>Family Budget</b>	43. <b>Family Budget</b>
44. <b>Home Location</b>	44. <b>Home Location</b>
45. <b>Employment Duration</b>	45. <b>Employment Duration</b>
46. <b>Language Fluency</b>	46. <b>Language Fluency</b>
47. <b>Religious Groups</b>	47. <b>Religious Groups</b>
48. <b>Political Candidates</b>	48. <b>Political Candidates</b>
49. <b>Health Facilities</b>	49. <b>Health Facilities</b>
50. <b>Travel Destinations</b>	50. <b>Travel Destinations</b>
51. <b>Family Members</b>	51. <b>Family Members</b>
52. <b>Home Amenities</b>	52. <b>Home Amenities</b>
53. <b>Employment Benefits</b>	53. <b>Employment Benefits</b>
54. <b>Language Learning</b>	54. <b>Language Learning</b>
55. <b>Religious Events</b>	55. <b>Religious Events</b>
56. <b>Political Issues</b>	56. <b>Political Issues</b>
57. <b>Health Programs</b>	57. <b>Health Programs</b>
58. <b>Travel Agencies</b>	58. <b>Travel Agencies</b>
59. <b>Family Values</b>	59. <b>Family Values</b>
60. <b>Home Environment</b>	60. <b>Home Environment</b>
61. <b>Employment History</b>	61. <b>Employment History</b>
62. <b>Language Proficiency</b>	62. <b>Language Proficiency</b>
63. <b>Religious Practices</b>	63. <b>Religious Practices</b>
64. <b>Political Engagement</b>	64. <b>Political Engagement</b>
65. <b>Health Insurance</b>	65. <b>Health Insurance</b>
66. <b>Travel Insurance</b>	66. <b>Travel Insurance</b>
67. <b>Family Income</b>	67. <b>Family Income</b>
68. <b>Home Address</b>	68. <b>Home Address</b>
69. <b>Employment Type</b>	69. <b>Employment Type</b>
70. <b>Language of Origin</b>	70. <b>Language of Origin</b>
71. <b>Religious Community</b>	71. <b>Religious Community</b>
72. <b>Political Party</b>	72. <b>Political Party</b>
73. <b>Health Care Access</b>	73. <b>Health Care Access</b>
74. <b>Travel Agency</b>	74. <b>Travel Agency</b>
75. <b>Family Traditions</b>	75. <b>Family Traditions</b>
76. <b>Home Decor</b>	76. <b>Home Decor</b>
77. <b>Employment Sector</b>	77. <b>Employment Sector</b>
78. <b>Language Skills</b>	78. <b>Language Skills</b>
79. <b>Religious Festivals</b>	79. <b>Religious Festivals</b>
80. <b>Political Movements</b>	80. <b>Political Movements</b>
81. <b>Health Services</b>	81. <b>Health Services</b>
82. <b>Travel Packages</b>	82. <b>Travel Packages</b>
83. <b>Family Budget</b>	83. <b>Family Budget</b>
84. <b>Home Location</b>	84. <b>Home Location</b>
85. <b>Employment Duration</b>	85. <b>Employment Duration</b>
86. <b>Language Fluency</b>	86. <b>Language Fluency</b>
87. <b>Religious Groups</b>	87. <b>Religious Groups</b>
88. <b>Political Candidates</b>	88. <b>Political Candidates</b>
89. <b>Health Facilities</b>	89. <b>Health Facilities</b>
90. <b>Travel Destinations</b>	90. <b>Travel Destinations</b>
91. <b>Family Members</b>	91. <b>Family Members</b>
92. <b>Home Amenities</b>	92. <b>Home Amenities</b>
93. <b>Employment Benefits</b>	93. <b>Employment Benefits</b>
94. <b>Language Learning</b>	94. <b>Language Learning</b>
95. <b>Religious Events</b>	95. <b>Religious Events</b>
96. <b>Political Issues</b>	96. <b>Political Issues</b>
97. <b>Health Programs</b>	97. <b>Health Programs</b>
98. <b>Travel Agencies</b>	98. <b>Travel Agencies</b>
99. <b>Family Values</b>	99. <b>Family Values</b>
100. <b>Home Environment</b>	100. <b>Home Environment</b>

```

1. /organism="Mus musculus"
2. /mol_type="genomic DNA"
3. /strain="C57BL/6J"
4. /db_xref="taxon:10090"
5. /clone="UUGC1M0080P05"
6. /sex="Male"
7. /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
8. /clone_lib="Mouse 10kb plasmid UUGC1M library"
9. /note="Vector: PWD42nv; Purified genomic DNA from M.
    musculus C57BL/6J (male) was obtained from the Jackson
    Laboratory Mouse DNA Resource
    (http://www.jax.org/resources/documents/dnares/). The DNA
    was hydrodynamically sheared by repeated passage through a
    0.005 inch orifice at constant velocity. The sheared DNA
    was blunt end-repaired with T4 DNA polymerase and T4
    polynucleotide kinase. Adaptor oligonucleotides were
    ligated to the blunt ends in high molar excess. The
    adaptor DNA was purified and size-selected for a 9.5 to
    10.5 kb range using preparative agarose gel
    electrophoresis. Vector DNA was prepared from a derivative
    of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
    inducible derivative of plasmid R1. The vector was ligated
    with adaptors complementary to the insert adaptors and
    purified. The sheared, adaptor mouse DNA was annealed to
    adaptor vector DNA, and transformed into
    chemically-competent E. coli XL10-Gold (Stratagene) cells
    and selected for ampicillin resistance."

```

```

Query Match          0.6%;   Score 16.2;   DB 1;   Length 21;
Best Local Similarity 85.7%;   Pred. No. 2.3e+03;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

Qy 2165 CTTTTTTTTTTTTTTTTT 2185  
 ||||| ||||| ||||| |||||  
 pb 1 CTTTTCTTTTTTCTCTCTT 21

RESULT 2579  
AZ346717

**LOCUS** AZ346717 21 bp DNA linear GSS 29-SEP-2000  
**DEFINITION** 1M0082002F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0082002 F, genomic survey sequence.

AZ346717  
 AZ346717.1  
 GI:10425954  
 GSS.  
 Mus musculus (house mouse)

**SOURCE**  
**ORGANISM**

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 21)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.

FEATURES

source

Location/Qualifiers

1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0082002"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity

Matches

0.6%; Score 16.2; DB 1; Length 21;  
85.7%; Pred. No. 2.3e+03;  
18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy

2165 CTTTCTTTCTTTCTTTT 2185

Db

1 CTTTCTTTCTTTCTTTT 21

RESULT 2580

AZ625662/c

LOCUS

DEFINITION

IM0465C23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0465C23 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AZ625662 21 bp DNA linear GSS 13-DEC-2000  
IM0465C23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0465C23 F, genomic survey sequence.  
AZ625662 GI:11747852  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0465 row: C column: 23  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers

FEATURES

source

source

1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0465C23"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity

Matches

0.6%; Score 16.2; DB 1; Length 21;  
85.7%; Pred. No. 2.3e+03;  
18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy

2167 TTTTTTTTTTTTTTTT 2187

Db

21 TATATATTTTTTTTTTT 1

RESULT 2581

AZ316361/c

LOCUS

DEFINITION

1M0034I16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0034I16 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AZ316361 22 bp DNA linear GSS 29-SEP-2000  
1M0034I16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0034I16 F, genomic survey sequence.  
AZ316361 GI:10364110  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0034 row: I column: 16  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers  
1. .22





Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2166 TTTT... 2186  
Db 3 TTTT... 23

RESULT 2584  
CF337747/c

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source

CF337747 24 bp mRNA linear EST 18-AUG-2003  
JMT--08-F05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--08-F05, mRNA sequence.

CF337747  
CF337747.1 GI:33823871

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 24)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers  
1..24  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="JMT--08-F05"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="AtJMT-overexpressing transgenic rice plasmid  
cDNA library (JMT)"  
/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Oligo-capped mRNA  
was reverse transcribed and then used for PCR. mRNA was  
prepared from Arabidopsis Jasmoinate Carboxyl  
methyltransferase overexpression line."

Query Match 0.6%; Score 16.2; DB 1; Length 24;  
Best Local Similarity 85.7%; Pred. No. 2.9e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2782 ATTG... 2802  
Db 21 ATATAC... 1

RESULT 2585  
CF328535

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS

CF328535 24 bp mRNA linear EST 18-AUG-2003  
NACL--03-H21.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--03-H21, mRNA sequence.

CF328535  
CF328535.1 GI:33805314

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 24)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

TITLE  
JOURNAL  
COMMENT

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers  
1..24  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
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/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: pCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.6%; Score 16.2; DB 1; Length 24;  
Best Local Similarity 85.7%; Pred. No. 2.9e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2165 CTTT... 2185  
Db 1 CTTT... 21

RESULT 2586  
AZ308225

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS

TITLE  
JOURNAL  
COMMENT

FEATURES  
source

AZ308225 24 bp DNA linear GSS 29-SEP-2000  
1M0011E06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0011E06 F, genomic survey sequence.

AZ308225  
AZ308225.1 GI:10348004

GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 24)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0011 row: E column: 06  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers  
1..24  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"

/clone="UUGC1M0011E06"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 16.2; DB 1; Length 24;  
Best Local Similarity 85.7%; Pred. No. 2.9e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT 2186  
||||| ||||| ||||| ||||| |||||  
Db 3 TTTT TTTT TTTT TTTT TTTT TTTT 23

RESULT 2587  
AI445764  
LOCUS AI445764.1 GI:4290493  
DEFINITION 25 bp mRNA linear EST 13-APR-1999  
tj09g10.x1 NCI CGAP Gas4 Homo sapiens CDNA clone IMAGE:2141058 3', similar to SW:YM04 PARTE P15605 HYPOTHETICAL 18.8 KD PROTEIN ;contains element L1 repetitive element ;, mRNA sequence.

ACCESSION AI445764  
VERSION AI445764.1 GI:4290493  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Insert Length: 715 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers

FEATURES  
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/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
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/tissue\_type="poorly differentiated adenocarcinoma with

signet ring cell features"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Gas4"  
/note="Organ: stomach; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"

Query Match 0.6%; Score 16.2; DB 1; Length 25;  
Best Local Similarity 85.7%; Pred. No. 3e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA AAAAAA AAAAAA 2801  
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Db 1 AAATAAAAAA AAAAAA AAAAAA 21

RESULT 2588  
CF308158/c  
LOCUS CF308158 25 bp mRNA linear EST 15-AUG-2003  
DEFINITION ABF--01-N19.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--01-N19, mRNA sequence.

ACCESSION CF308158  
VERSION CF308158.1 GI:33679919  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1. .25  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="ABF--01-N19"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"  
/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.6%; Score 16.2; DB 1; Length 25;  
Best Local Similarity 85.7%; Pred. No. 3e+03;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1970 TTTACCTTGAAAAA AAAAAA 1990  
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Db 23 TTTATCTTAAAAA AAAAAA 3

RESULT 2589  
AV740046/c  
LOCUS AV740046 25 bp mRNA linear EST 17-OCT-2000  
DEFINITION AV740046 CB Homo sapiens cDNA clone CBFANF04 5', mRNA sequence.





Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2181  
Db 1 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2592  
BQ590166/c

LOCUS  
DEFINITION BQ590166 16 bp mRNA linear EST 06-DEC-2002  
CDNA clone 024-019-K18-T7 MP1Z-ADIS-024-storage root Beta vulgaris

ACCESSION BQ590166  
VERSION BQ590166  
KEYWORDS BQ590166.1 GI:26119749  
SOURCE EST.  
ORGANISM Beta vulgaris

REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 16)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698

COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 16 Std Error: 0.00  
Plate: 19 row: K column: 18  
Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES  
source  
1. .16  
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/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:189955"  
/db\_xref="taxon:161934"  
/clone="024-019-K18"  
/tissue\_type="storage root"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-storage root"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2801  
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 2593

BQ590507  
LOCUS  
DEFINITION BQ590507 16 bp mRNA linear EST 06-DEC-2002  
CDNA clone 024-019-M04-T7 MP1Z-ADIS-024-storage root Beta vulgaris

ACCESSION BQ590507  
VERSION BQ590507.1 GI:26120090  
KEYWORDS EST.  
SOURCE BQ590507.1  
ORGANISM Beta vulgaris

REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 16)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698

COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 16 Std Error: 0.00  
Plate: 19 row: M column: 04  
Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES  
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1. .16  
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line)"  
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cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2172 TTTT TTTT TTTT TTTT TTTT 2187  
Db 1 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2594  
BQ592600

LOCUS  
DEFINITION BQ592600 16 bp mRNA linear EST 06-DEC-2002  
CDNA clone 024-028-F08-SP6R MP1Z-ADIS-024-developing root Beta  
vulgaris

ACCESSION BQ592600  
VERSION BQ592600.1 GI:26122183  
KEYWORDS EST.  
SOURCE BQ592600.1  
ORGANISM Beta vulgaris

REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE 1 (bases 1 to 16)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@piz-koeln.mpg.de  
Insert Length: 16 Std Error: 0.00  
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SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2801  
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Db 1 AAAAAAAAAAAAAA 16

RESULT 2595  
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LOCUS S013686-024-028-F08-SP6R MPIZ-ADIS-024-developing root Beta vulgaris  
DEFINITION vulgaris cDNA clone 024-028-F08 5-PRIME, mRNA sequence.  
ACCESSION BQ592600  
VERSION BQ592600.1 GI:26122183  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 16)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189

PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@piz-koeln.mpg.de  
Insert Length: 16 Std Error: 0.00  
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SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2181  
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Db 16 TTTT TTTT TTTT TTTT TTTT 1

RESULT 2596  
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DEFINITION cDNA clone 024-028-A01 3-PRIME, mRNA sequence.  
ACCESSION BQ592965  
VERSION BQ592965.1 GI:26122548  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 16)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@piz-koeln.mpg.de  
Insert Length: 16 Std Error: 0.00  
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Seq primer: T7; GTAATACGACTCACTATAGGCG.



FEATURES  
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Location/Qualifiers  
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SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTTTTTTTTTTTT 16

RESULT 2597  
BQ592965/C

LOCUS  
DEFINITION  
BQ592965  
BQ592965.1 GI:26122548

EST.  
Beta vulgaris  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 16)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698

COMMENT  
Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@piz-koeln.mpg.de  
Insert Length: 16 Std Error: 0.00  
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FEATURES  
source

Location/Qualifiers  
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SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2801  
Db 16 AAAAAAAAAAAAAA 1

RESULT 2598

BQ595369  
LOCUS  
DEFINITION  
BQ595369  
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EST.  
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Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 16)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698

COMMENT  
Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@piz-koeln.mpg.de  
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Seq primer: T7; GTAATACGACTCACTATAGGCG.

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SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator:

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SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator:

FEATURES  
source  
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SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator:

FEATURES  
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Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTT-----TTT 16

RESULT 2599  
BQ595717 16 bp mRNA linear EST 06-DEC-2002  
LOCUS  
DEFINITION  
E012692-024-022-H07-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
cDNA clone 024-022-H07 5-PRIME, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Beta vulgaris  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE  
AUTHORS  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL  
MEDLINE  
PUBMED  
Plant J. 32 (5), 845-857 (2002)

COMMENT  
Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: [weisshaar@mpiz-koeln.mpg.de](mailto:weisshaar@mpiz-koeln.mpg.de)  
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Seq primer: SP6; CATACGATTAGGTGACACTATAG.

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cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2801  
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Db 1 AAAAAAAAAAAAAA 16

RESULT 2600  
BQ595717/c 16 bp mRNA linear EST 06-DEC-2002  
LOCUS  
DEFINITION  
E012692-024-022-H07-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
cDNA clone 024-022-H07 5-PRIME, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Beta vulgaris  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE  
AUTHORS  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL  
MEDLINE  
PUBMED  
Plant J. 32 (5), 845-857 (2002)

COMMENT  
Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: [weisshaar@mpiz-koeln.mpg.de](mailto:weisshaar@mpiz-koeln.mpg.de)  
Insert Length: 16 Std Error: 0.00  
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Seq primer: SP6; CATACGATTAGGTGACACTATAG.

FEATURES  
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cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT-----TTT 2181  
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Db 16 TTTT-----TTT 1

RESULT 2601  
CF279325 16 bp mRNA linear EST 14-AUG-2003  
LOCUS  
DEFINITION  
14ETL--05-J09.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa cDNA clone 14ETL--05-J09, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
CF279325  
CF279325.1 GI:33656711  
EST.

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SOURCE      Oryza sativa
ORGANISM     Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 16)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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            /db_xref="taxon:4530"
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            /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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Query Match      0.6%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT-----TTT 2181
Db      1 TTTT-----TTT 16

RESULT 2602
CF279325/c
LOCUS      CF279325      16 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION Oryza sativa cDNA clone 14ETL--05-J09, mRNA sequence.
ACCESSION  CF279325.1 GI:33656711
VERSION     CF279325
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 16)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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            /mol_type="mRNA"
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SOURCE      Oryza sativa
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 16)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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RT-PCR."

Query Match      0.6%; Score 16; DB 1; Length 16;
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2801
Db      16 AAAAAAAAAAAAAA 1

RESULT 2603
CF296130
LOCUS      CF296130      16 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION 30DGS--06-F22.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--06-F22, mRNA sequence.
ACCESSION  CF296130
VERSION     CF296130.1 GI:33665163
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 16)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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QY      2172 TTTT-----TTT 2187
Db      1 TTTT-----TTT 16

RESULT 2604
CF311057
LOCUS      CF311057      16 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION ABF--06-C03.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--06-C03, mRNA sequence.
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/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2181  
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Db 1 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2610  
CF315789/c

LOCUS CF315789 16 bp mRNA linear EST 15-AUG-2003

DEFINITION HD--04-N10.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--04-N10, mRNA sequence.

ACCESSION CF315789

VERSION CF315789.1 GI:33687550

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 16)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .16

/organism="Oryza sativa"

/mol\_type="mRNA"

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/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 16;  
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2801  
| | | | | | | | | | | | | | | |  
Db 16 AAAAAA AAAAAA AAAAAA 1

RESULT 2611  
CF316056

LOCUS CF316056 16 bp mRNA linear EST 15-AUG-2003

DEFINITION HD--05-D07.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--05-D07, mRNA sequence.

ACCESSION CF316056

CF316056.1 GI:33687817

EST.

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 16)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

Contact: Nahm B.H.

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .16

/organism="Oryza sativa"

/mol\_type="mRNA"

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/db\_xref="taxon:4530"

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/lab\_host="E.coli DH10B"

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/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
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QY 2166 TTTT TTTT TTTT TTTT TTTT 2181  
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Db 1 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2612  
CF316056/c

LOCUS CF316056 16 bp mRNA linear EST 15-AUG-2003

DEFINITION HD--05-D07.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--05-D07, mRNA sequence.

ACCESSION CF316056

VERSION CF316056.1 GI:33687817

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 16)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

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Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .16

source

FEATURES



/organism="Oryza sativa"  
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line."

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2801  
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16 AAAAAAAAAAAAAAAAAA 1

RESULT 2613  
CF317718 16 bp mRNA linear EST 15-AUG-2003  
LOCUS  
DEFINITION  
HD--07-I05.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--07-I05, mRNA sequence.  
ACCESSION  
CF317718.1 GI:33689479  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 16)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES  
source  
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line."

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTT 2181

Db 1 TTTTTTTTTTTTTTTT 16

RESULT 2614  
CF317718/c 16 bp mRNA linear EST 15-AUG-2003  
LOCUS  
DEFINITION  
HD--07-I05.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--07-I05, mRNA sequence.  
ACCESSION  
CF317718.1 GI:33689479  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 16)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

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line."

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2801  
|  
16 AAAAAAAAAAAAAAAAAA 1

RESULT 2615  
CF320356 16 bp mRNA linear EST 15-AUG-2003  
LOCUS  
DEFINITION  
HD--11-D14.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--11-D14, mRNA sequence.  
ACCESSION  
CF320356.1 GI:33692117  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 16)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs

REFERENCE  
AUTHORS  
TITLE

JOURNAL  
COMMENT  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2181  
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Db 1 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2616  
CF320356/c  
LOCUS  
DEFINITION  
HD--11-D14.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--11-D14, mRNA sequence.

ACCESSION  
CF320356.1 GI:33692117  
VERSION  
CF320356  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 16)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2801  
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Db 16 AAAAAA AAAAAA AAAAAA 1

RESULT 2617  
CF327722  
LOCUS  
DEFINITION  
CF327722 16 bp mRNA linear EST 18-AUG-2003  
NACL--02-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--02-F06, mRNA sequence.

ACCESSION  
CF327722  
VERSION  
CF327722.1 GI:33803695  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 16)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2181  
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Db 1 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2618  
CF327722/c  
LOCUS  
DEFINITION  
CF327722 16 bp mRNA linear EST 18-AUG-2003  
NACL--02-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--02-F06, mRNA sequence.

ACCESSION  
CF327722  
VERSION  
CF327722.1 GI:33803695  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa  
ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS

1 (bases 1 to 16)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

## COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

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Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

source

Location/Qualifiers

1..16

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="NACL--02-F06"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 30 days"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

## Query Match

Best Local Similarity 0.6%; Score 16; DB 1; Length 16;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2801

|||||

Db 16 AAAAAAAAAAAAAA 1

## RESULT 2619

CF329320

## LOCUS

CF329320 NACL--04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza

sativa cDNA clone NACL--04-J17, mRNA sequence.

## ACCESSION

CF329320

## VERSION

CF329320.1 GI:33806877

## KEYWORDS

EST.

## SOURCE

Oryza sativa

## ORGANISM

Oryza sativa

## REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 16)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

source

Location/Qualifiers

1..16

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

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/tissue\_type="callus"

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/lab\_host="E.coli DH10B"

/clone\_lib="Rice callus plasmid cDNA library (NACL)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

## Query Match

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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2172 TTTTTTTTTTTTTTTA 2187

|||||

Db 1 TTTTTTTTTTTTTTTA 16

## RESULT 2620

CF333386

## LOCUS

CF333386 JMT--02-E05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa cDNA clone JMT--02-E05, mRNA sequence.

## ACCESSION

CF333386

## VERSION

CF333386.1 GI:33815044

## KEYWORDS

EST.

## SOURCE

Oryza sativa

## ORGANISM

Oryza sativa

## REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 16)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

source

Location/Qualifiers

1..16

/organism="Oryza sativa"

/mol\_type="mRNA"

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/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="AtJMT-overexpressing transgenic rice plasmid

cDNA library (JMT)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA

was reverse transcribed and then used for PCR. mRNA was

prepared from Arabidopsis Jasmonate Carboxyl

methyltransferase overexpression line."

QY 2786 AAAAAAAAAAAAAA 2801

|||||

Db 1 AAAAAAAAAAAAAA 16

## RESULT 2621

CF333386/c

## LOCUS

CF333386 JMT--02-E05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA

library (JMT) Oryza sativa cDNA clone JMT--02-E05, mRNA sequence.

## ACCESSION

CF333386

## VERSION

CF333386.1 GI:33815044



KEYWORDS  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1. .16  
/organism="Oryza sativa"  
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/cultivar="Nackdong"  
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cDNA library (JMT)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; Oligo-capped mRNA  
was reverse transcribed and then used for PCR. mRNA was  
prepared from Arabidopsis Jasmonate Carboxyl  
methyltransferase overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2181  
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Db 16 TTTT TTTT TTTT TTTT TTTT 1

RESULT 2622  
BQ590128/c  
LOCUS BQ590128 17 bp mRNA linear EST 06-DEC-2002  
DEFINITION E012843-024-019-E19-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
cDNA clone 024-019-E19 3-PRIME, mRNA sequence.  
ACCESSION BQ590128  
VERSION BQ590128.1 GI:26119711  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radclouf,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@mpiz-koeln.mpg.de  
Insert Length: 17 Std Error: 0.00

KEYWORDS  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1. .17  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
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line)"  
/db\_xref="GABI:189986"  
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/clone="024-019-E19"  
/tissue\_type="storage root"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-storage root"  
/note="Vector: pCMVSPORT6; Site 1: SaliI; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAAA 2801  
|||||  
Db 16 AAAAAA AAAAAA AAAAAA 1

RESULT 2623  
CF294668/c  
LOCUS CF294668 17 bp mRNA linear EST 14-AUG-2003  
DEFINITION 30DGS--04-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa cDNA clone 30DGS--04-E17, mRNA sequence.  
ACCESSION CF294668  
VERSION CF294668.1 GI:33663701  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1. .17  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Gyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1..17  
 /organism="Oryza sativa"  
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 /db\_xref="taxon:4530"  
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 /tissue\_type="leaf"  
 /dev\_stage="7 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: PCR4-TOPO; Site1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.6%; Score 16; DB 1; Length 17;  
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 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2181  
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 Db 1 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2626  
 CF313013

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Gyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1. .17  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
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 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="ABF3-overexpressing transgenic rice plasmid  
 cDNA library (ABF)"  
 /note="Vector: pCB4-TACO. Site 1: EcoRI. Leaf was dried

for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT 2181  
|||||  
Db 1 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2627  
CF336950/c  
LOCUS  
DEFINITION JMT--07-D04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--07-D04, mRNA sequence.  
ACCESSION CF336950  
VERSION CF336950.1 GI:33822280  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.  
FEATURES  
source Location/Qualifiers  
1..17  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="JMT--07-D04"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2801  
|||||  
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 2628  
BQ591181  
LOCUS  
DEFINITION BQ591181 17 bp mRNA linear EST 06-DEC-2002  
E012715-024-017-H16-T7 MP1Z-ADIS-024-storage root Beta vulgaris cDNA clone 024-017-H16 3-PRIME, mRNA sequence.  
ACCESSION BQ591181  
VERSION BQ591181.1 GI:26120764  
KEYWORDS EST.

SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 17 Std Error: 0.00  
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Seq primer: T7; GTATACGACTCACTATAGGCG.  
FEATURES  
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1..17  
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/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:188932"  
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/clone\_lib="MPIZ-ADIS-024-storage root"  
/note="Vector: pCMVSPORT6; Site 1: Sall; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sall-NotI, primer sites and orientation:  
SP6-Sall-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2172 TTTT TTTT TTTT TTTT TTTT 2187  
|||||  
Db 1 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2629  
CF295807  
LOCUS  
DEFINITION CF295807 17 bp mRNA linear EST 14-AUG-2003  
30DGS--05-O12.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--05-O12, mRNA sequence.  
ACCESSION CF295807  
VERSION CF295807.1 GI:33664840  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 17)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)



COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES Location/Qualifiers

source  
1.17  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="30DGS--05-O12"  
/tissue\_type="leaf"  
/dev\_stage="30 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2181  
|||||  
Db 1 TTTT TTTT TTTT TTTT TTTT 16

## RESULT 2630

CF295807/c  
LOCUS CF295807 17 bp mRNA linear EST 14-AUG-2003  
DEFINITION 30DGS--05-O12.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa cDNA clone 30DGS--05-O12, mRNA sequence.

ACCESSION CF295807  
VERSION CF295807.1 GI:33664840  
KEYWORDS EST.

## SOURCE Oryza sativa

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 17)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

Location/Qualifiers

source  
1.17  
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/mol\_type="mRNA"  
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/clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.6%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAA 2801  
|||||  
Db 16 AAAAAAAAAAAAAA 1

## RESULT 2631

CF299639  
LOCUS CF299639 17 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--03-L20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--03-L20, mRNA sequence.

ACCESSION CF299639

VERSION CF299639.1 GI:33671400

KEYWORDS EST.

## SOURCE Oryza sativa

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 17)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

COMMENT Contact: Nahm B.H.

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Fax: 82 31 321 6355

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## FEATURES

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Location/Qualifiers

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with oligoribonucleotides and then used as templates for

RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1.4e+03;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2181

|||||

Db 1 TTTT TTTT TTTT TTTT TTTT 16

## RESULT 2632

CF299639/c

LOCUS CF299639 17 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--03-L20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--03-L20, mRNA sequence.

ACCESSION CF299639

VERSION CF299639.1 GI:33671400

KEYWORDS EST.

## SOURCE Oryza sativa

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 17)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL  
COMMENT Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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RT-PCR."

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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2801  
Db 16 AAAAAAAAAAAAAAAAAA 1

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CF299997/c  
LOCUS 7LEAF--04-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--04-D19, mRNA sequence.

ACCESSION CF299997  
VERSION CF299997.1 GI:33671758  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 17)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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RT-PCR."

Query Match 0.6%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2800  
Db 16 GAAAAAAAAAAAAAAAAA 1

RESULT 2634  
CF311499  
LOCUS ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--06-L20, mRNA sequence.

ACCESSION CF311499  
VERSION CF311499.1 GI:33683260  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 17)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.6%; Score 16; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.4e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2172 TTTTTTTTTTTTTTTA 2187  
Db 1 TTTTTTTTTTTTTTTA 16

RESULT 2635  
CF319075  
LOCUS HD--09-H06.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (HD) Oryza sativa cDNA clone HD--09-H06, mRNA sequence.

ACCESSION CF319075  
VERSION CF319075.1 GI:33690836  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.







LOCUS CF311668 19 bp mRNA linear EST 15-AUG-2003  
DEFINITION ABF--07-A05.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--07-A05, mRNA sequence.  
ACCESSION CF311668  
VERSION CF311668.1 GI:33683429  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source

1..19  
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Query Match 0.6%; Score 16; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2181  
|||||  
Db 16 TTTT TTTT TTTT TTTT TTTT 1

RESULT 2642  
CF327587  
LOCUS NACL--02-C04.b1 19 bp mRNA linear EST 18-AUG-2003  
DEFINITION sativa cDNA clone NACL--02-C04, mRNA sequence.

ACCESSION CF327587  
VERSION CF327587.1 GI:33803426  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 19)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193

Query Match 0.6%; Score 16; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2801  
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Db 16 AAAAAAAAAAAAAA 1

FEATURES  
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2181  
|||||  
Db 1 TTTT TTTT TTTT TTTT TTTT 16

RESULT 2643  
CF327587/c

LOCUS NACL--02-C04.b1 19 bp mRNA linear EST 18-AUG-2003  
DEFINITION sativa cDNA clone NACL--02-C04, mRNA sequence.

ACCESSION CF327587  
VERSION CF327587.1 GI:33803426  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 19)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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Query Match 0.6%; Score 16; DB 1; Length 19;  
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2801  
|||||  
Db 16 AAAAAAAAAAAAAA 1





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RESULT 2646
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LOCUS          AZ316019          21 bp    DNA          linear          GSS 29-SEP-2000
DEFINITION    1M0033C05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
               clone UUGC1M0033C05 R, genomic survey sequence.
ACCESSION     AZ316019
VERSION       AZ316019.1  GI:10363426
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE     1 (bases 1 to 21)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhauser,A. and Wright,D.,Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL
COMMENT       Unpublished (2000)
               Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0033 row: C column: 05
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               Laboratory Mouse DNA Resource
               (http://www.jax.org/resources/documents/dnares/). The DNA
               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
               was blunt end-repaired with T4 DNA polymerase and T4
               polynucleotide kinase. Adaptor oligonucleotides were
               ligated to the blunt ends in high molar excess. The
               adaptored DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adaptored mouse DNA was annealed to
               adaptored vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."
               Query Match          0.6%; Score 16; DB 1; Length 21;
               Best Local Similarity 100.0%; Pred. No. 2.5e+03;
               Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2801
Db 1 AAAAAAAAAAAAAAAAAA 16

RESULT 2647
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CF309614
LOCUS          CF309614          21 bp    mRNA          linear          EST 15-AUG-2003
DEFINITION    ABF--03-N20.g1 ABF3-overexpressing transgenic rice plasmid cDNA
               library (ABF) Oryza sativa cDNA clone ABF--03-N20, mRNA sequence.
ACCESSION     CF309614
VERSION       CF309614.1  GI:33681375
KEYWORDS      EST.
SOURCE        Oryza sativa
ORGANISM      Oryza sativa
REFERENCE     1 (bases 1 to 21)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, MyongJi University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES      Location/Qualifiers
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               then used for PCR. mRNA was prepared from ABA-responsive
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               line."
               Query Match          0.6%; Score 16; DB 1; Length 21;
               Best Local Similarity 100.0%; Pred. No. 2.5e+03;
               Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2165 CTTTTTTTTTTTTTTT 2180
Db 3 CTTTTTTTTTTTTTTT 18

RESULT 2648
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LOCUS          CF310806          22 bp    mRNA          linear          EST 15-AUG-2003
DEFINITION    ABF--05-K20.g1 ABF3-overexpressing transgenic rice plasmid cDNA
               library (ABF) Oryza sativa cDNA clone ABF--05-K20, mRNA sequence.
ACCESSION     CF310806
VERSION       CF310806.1  GI:33682567
KEYWORDS      EST.
SOURCE        Oryza sativa
ORGANISM      Oryza sativa
REFERENCE     1 (bases 1 to 22)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL       Unpublished (2003)
COMMENT       Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, MyongJi University
               Yongin, Kyeonggi, Korea
```

Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES

source

1. .22  
/organism="Oryza sativa"  
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/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
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cDNA library (ABF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried  
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then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.6%; Score 16; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2801  
|||||  
Db 22 AAAAAAAAAAAAAA 7

RESULT 2649

AZ316361

LOCUS

DEFINITION AZ316361 22 bp DNA linear GSS 29-SEP-2000  
1M0034116F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0034116 F, genomic survey sequence.

ACCESSION AZ316361

VERSION AZ316361.1 GI:10364110

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 22)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0034 row: I column: 16  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.

FEATURES

source

1. .22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0034116"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.6%; Score 16; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2801  
|||||  
Db 1 AAAAAAAAAAAAAA 16

RESULT 2650

AZ307559

LOCUS

DEFINITION AZ307559 22 bp DNA linear GSS 29-SEP-2000

1M0009020F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0009020 F, genomic survey sequence.

ACCESSION AZ307559

VERSION AZ307559.1 GI:10346680

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 22)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
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JOURNAL Unpublished (2000)

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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0009 row: O column: 20  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.

FEATURES

source

1. .22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0009020"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.















ACCESSION AW247153  
VERSION AW247153.1 GI:6590146  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 25)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2819969.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
<http://www.genome.washington.edu> Low Quality Sequence: 7 contiguous  
PHRED high quality bases following vector sequence. Very Low  
Quality Sequence: Trace file contained 25 contiguous distinct peaks  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LLCW2 row: P column: 18  
High quality sequence stop: 7.  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2819969"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC 7"  
/note="Organ: lung; Vector: POTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
Query Match 0.6%; Score 16; DB 1; Length 25;  
Best Local Similarity 79.2%; Pred.No. 3.1e+03;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 2781 AATTGAAAAA...AAAAA 2804  
Db 25 AATAAACACAAACAAAAA 2  
RESULT 2663  
TA324F07P  
LOCUS TA324F07P 25 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 324f07, forward sequence,  
genomic survey sequence.  
ACCESSION AL493403  
VERSION AL493403.1 GI:11867768  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.  
1 (bases 1 to 25)  
REFERENCE

AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,  
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,  
Melville,S.E., Rajandream,M.A. and Barrell,B.G.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: [barrell@sanger.ac.uk](mailto:barrell@sanger.ac.uk) and  
[nhl@sanger.ac.uk](mailto:nhl@sanger.ac.uk)  
COMMENT Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (  
4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).  
Email: [nelsayed@tigr.org](mailto:nelsayed@tigr.org)  
Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).  
Location/Qualifiers  
1..25  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="324f07"  
Query Match 0.6%; Score 16; DB 1; Length 25;  
Best Local Similarity 100.0%; Pred.No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2166 TTTT...TTTTT 2181  
Db 1 TTTT...TTTTT 16  
RESULT 2664  
AZ437459/c  
LOCUS AZ437459 26 bp DNA linear GSS 03-OCT-2000  
DEFINITION 1M0225B15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0225B15 R, genomic survey sequence.  
ACCESSION AZ437459  
VERSION AZ437459.1 GI:10561472  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 26)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
Insert length: 10000 Std Error: 0.00  
Plate: 0225 row: B column: 15  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 26.  
Location/Qualifiers  
1..26  
/organism="Mus musculus"  
FEATURES  
source





COMMENT

Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES

source

Location/Qualifiers  
1. .26  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tsel23b02\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match

Best Local Similarity 0.6%; Score 16; DB 1; Length 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2801

Db 26 AAAAAAAAAAAAAA 11

RESULT 2668

BX553653/c

LOCUS

DEFINITION BX553653 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tsel2h01\_plc, mRNA sequence.

ACCESSION BX553653

VERSION BX553653.1 GI:33377798

KEYWORDS

SOURCE

ORGANISM

Glossina morsitans morsitans  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
1 (bases 1 to 26)

REFERENCE

AUTHORS

Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Genome Biol. 4 (10), R63 (2003)  
22881942  
14519198  
Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxtton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES

source

Location/Qualifiers  
1. .26  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"

/db\_xref="taxon:37546"  
/clone="Tsel2h01\_plc"

/tissue\_type="adult infected gut"

/clone\_lib="Glossina morsitans morsitans adult infected  
gut"

/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match

Best Local Similarity 0.6%; Score 16; DB 1; Length 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2801

Db 26 AAAAAAAAAAAAAA 11

RESULT 2669

BX553888/c

LOCUS

DEFINITION BX553888 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tsel13b10\_plc, mRNA sequence.

ACCESSION BX553888

VERSION BX553888.1 GI:33378008

KEYWORDS

SOURCE

ORGANISM

Glossina morsitans morsitans  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
1 (bases 1 to 26)

REFERENCE

AUTHORS

Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
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Genome Biol. 4 (10), R63 (2003)

22881942

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COMMENT

Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
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Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5'  
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the 3' end.

FEATURES

source

Location/Qualifiers

1. .26  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
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/clone="Tsel13b10\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match

Best Local Similarity 0.6%; Score 16; DB 1; Length 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2801

Db 26 AAAAAAAAAAAAAA 11

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RESULT 2670
BX557791/c
LOCUS
DEFINITION
BX557791 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse34g02_plc, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 26)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
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Pathogen Sequencing Unit
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Hinxtan, Cambridge, CB10 1SA, UK
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Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.
FEATURES
source
Location/Qualifiers
1..26
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse34g02_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"
Query Match 0.6%; Score 16; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2801
|||||
Db 26 AAAAAAAAAAAAAAAAAA 11
RESULT 2671
BX566514/c
LOCUS
DEFINITION
BX566514 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse82f08_plc, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 26)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
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Hinxtan, Cambridge, CB10 1SA, UK
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Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.
FEATURES
source
Location/Qualifiers
1..26
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse34g02_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"
Query Match 0.6%; Score 16; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2801
|||||
Db 26 AAAAAAAAAAAAAAAAAA 11
RESULT 2672
BX567795/c
LOCUS
DEFINITION
BX567795 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse8b03_plc, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 26)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
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response genes
Genome Biol. 4 (10), R63 (2003)
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Pathogen Sequencing Unit
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Hinxtan, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
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School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.
FEATURES
source
Location/Qualifiers
1..26
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse82f08_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"
Query Match 0.6%; Score 16; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2801
|||||
Db 26 AAAAAAAAAAAAAAAAAA 11
RESULT 2673
BX567795/c
LOCUS
DEFINITION
BX567795 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse8b03_plc, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 26)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
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morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
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Hinxtan, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.
FEATURES
source
Location/Qualifiers
1..26
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse82f08_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"
Query Match 0.6%; Score 16; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2801
|||||
Db 26 AAAAAAAAAAAAAAAAAA 11
```

```
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxtan, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.
FEATURES
source
Location/Qualifiers
1..26
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse82f08_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"
Query Match 0.6%; Score 16; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2801
|||||
Db 26 AAAAAAAAAAAAAAAAAA 11
RESULT 2672
BX567795/c
LOCUS
DEFINITION
BX567795 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse8b03_plc, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 26)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxtan, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.
FEATURES
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Location/Qualifiers
1..26
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse82f08_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"
Query Match 0.6%; Score 16; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2801
|||||
Db 26 AAAAAAAAAAAAAAAAAA 11
RESULT 2673
BX567795/c
LOCUS
DEFINITION
BX567795 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse8b03_plc, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 26)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxtan, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.
FEATURES
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Location/Qualifiers
1..26
/organism="Glossina morsitans morsitans"
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/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse82f08_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"
Query Match 0.6%; Score 16; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2786 AAAAAAAAAAAAAAAAAA 2801
|||||
Db 26 AAAAAAAAAAAAAAAAAA 11
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FEATURES
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Location/Qualifiers
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/clone="Tse8b03_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.6%; Score 16; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2801
Db 26 AAAAAAAAAAAAAAAAAA 11

RESULT 2673
AU267251
LOCUS
DEFINITION AU267251 VS Dictyostelium discoideum cDNA clone VSH318 5', mRNA
sequence.
ACCESSION AU267251
VERSION AU267251.1 GI:20526049
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
REFERENCE Dictyostelium discoideum; Dictyosteliida; Dictyostelium.
AUTHORS Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 27)
Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
Takeuchi,I., Kohara,Y. and Tanaka,Y.
TITLE Population analysis of cDNAs from unicellular and multicellular
stages of Dictyostelium discoideum
JOURNAL Unpublished (2002)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
Location/Qualifiers
1. .27
/organism="Dictyostelium discoideum"
/mol_type="mrna"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSH318"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

Query Match 0.6%; Score 16; DB 1; Length 27;
Best Local Similarity 79.2%; Pred. No. 3.1e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAAAA 2804
Db 2 AAATAATAATAAAGTAAAAAAAA 25

RESULT 2674
CF329137
LOCUS
DEFINITION CF329137 19 bp mrna linear EST 18-AUG-2003
NACL--04-F15.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-F15, mRNA sequence.
ACCESSION CF329137
VERSION CF329137.1 GI:33806511
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KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 5355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 19
/organism="Oryza sativa"
/mol_type="mrna"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--04-F15"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.6%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804
Db 1 AAAGATAAAAAAAAAA 19

RESULT 2675
AZ345499/c
LOCUS
DEFINITION AZ345499 19 bp DNA linear GSS 29-SEP-2000
clone UUGClM0080F06 F, genomic survey sequence.
ACCESSION AZ345499
VERSION AZ345499.1 GI:10424736
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
TITLE Unpublished (2000)
JOURNAL Contact: Robert B. Weiss
COMMENT University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0080 row: F column: 06
Seq primer: CGTTGTAACGACGCCAGT
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Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source

Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0080F06"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.1e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804

Db 19 AAAAAAAAAAGAGAAAAA 1

RESULT 2676  
AZ447251/c

LOCUS  
DEFINITION 1M0244J19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0244J19 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0244 row: J column: 19  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends

FEATURES  
source

High quality sequence stop: 19.  
Location/Qualifiers  
1. .19  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0244J19"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.1e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2783 TTGAAAAAAAAAAAAAAAAAAAA 2801

Db 19 TTATAAAAAAAAAAAAAAAAAA 1

RESULT 2677  
AZ786336/c

LOCUS  
DEFINITION 2M0031H17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0031H17 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)

REFERENCE

AUTHORS

TITLE

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0031 row: H column: 17  
Seq primer: CACACAGCAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

JOURNAL

COMMENT

FEATURES  
source

Location/Qualifiers  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0031H17"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.1e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
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Db 19 AAAAAAAAAAGAGAAAAA 1

RESULT 2678  
CF298472/c

LOCUS  
DEFINITION  
7LEAF--01-001.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--01-001, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CF298472 19 bp mRNA linear EST 15-AUG-2003  
CF298472  
EST.  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers  
1. .19  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
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/clone="7LEAF--01-001"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"

FEATURES  
source

Location/Qualifiers

1. .19  
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/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
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/tissue\_type="leaf"  
/dev\_stage="7 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.1e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2782 ATTGAAAAAAAAAAAAAAAA 2800  
|||  
Db 19 ATATAAAAAAAAAAAAAA 1

RESULT 2679  
CF298134/c

LOCUS  
DEFINITION  
7LEAF--01-G09.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--01-G09, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers  
1. .19  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--01-G09"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"

FEATURES  
source

Location/Qualifiers

1. .19  
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/mol\_type="mRNA"  
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/db\_xref="taxon:4530"  
/clone="7LEAF--01-G09"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"

/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.6%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.1e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2166 TTTTTCCTT 2184  
|||||  
Db 19 TTTTTCCTT 1

RESULT 2680  
CF300236

LOCUS  
DEFINITION  
7LEAF--04-I24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--04-I24, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE

CF300236 19 bp mRNA linear EST 15-AUG-2003  
CF300236  
EST.  
Oryza sativa

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..19  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--04-I24"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.6%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.1e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2184

Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 2681

CF300236/c

LOCUS 7LEAF--04-I24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--04-I24, mRNA sequence.

ACCESSION CF300236

VERSION CF300236.1 GI:33671997

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..19  
Location/Qualifiers  
/organism="Oryza sativa"  
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/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
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/lab\_host="E.coli DH10B"

/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.6%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.1e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA AAAAAA 2799

Db 19 AATCAAAAAA AAAAAA 1

RESULT 2682

CF309858/c

LOCUS

DEFINITION

ABF--04-D16.g1 ABF3-overexpressing transgenic rice plasmid cDNA

library (ABF) Oryza sativa cDNA clone ABF--04-D16, mRNA sequence.

ACCESSION CF309858

VERSION CF309858.1 GI:33681619

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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/mol\_type="mRNA"

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/clone\_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.6%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.1e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2169 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2187

Db 19 TATGTTT TTTT TTTT TTTT 1

RESULT 2683

AZ509929

LOCUS

DEFINITION

IM0354A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0354A07 F, genomic survey sequence.

AZ509929  
IM0354A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0354A07 F, genomic survey sequence.



ACCESSION AZ509929  
VERSION AZ509929.1 GI:10691245  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0354 row: A column: 07  
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Class: plasmid ends  
High quality sequence stop: 19.  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.1e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
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Db 1 AAAAAAAAAAAAAAAAAATTAA 19

RESULT 2684  
AZ509929/c  
LOCUS AZ509929 19 bp DNA linear GSS 05-OCT-2000  
DEFINITION 1M0354A07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0354A07 F, genomic survey sequence.  
ACCESSION AZ509929

VERSION AZ509929.1 GI:10691245  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0354 row: A column: 07  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.1e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2184  
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Db 19 TTAATTTTTTTTTTTTTTTT 1

RESULT 2685  
AZ611602  
LOCUS AZ611602 19 bp DNA linear GSS 13-DEC-2000  
DEFINITION 1M0438G03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0438G03 F, genomic survey sequence.  
ACCESSION AZ611602  
VERSION AZ611602.1 GI:11733792

KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0438 row: G column: 03  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
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/sex="Male"  
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.  
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JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0438 row: G column: 03  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
FEATURES Location/Qualifiers  
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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.1e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2166 TTTTGTGTTTTTTTTTTT 2184  
||||| |||||||  
Db 1 TTTTGTGTTTTTTTTTTT 19

RESULT 2686  
AZ611602/c  
LOCUS AZ611602 19 bp DNA linear GSS 13-DEC-2000  
DEFINITION IM0438G03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0438G03 F, genomic survey sequence.  
ACCESSION AZ611602  
VERSION AZ611602.1 GI:11733792  
KEYWORDS GSS.

Query Match 0.6%; Score 15.8; DB 1; Length 19;  
Best Local Similarity 89.5%; Pred. No. 2.1e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
||||| |||||||  
Db 19 AAAAAAAAAAACCAAAA 1

RESULT 2687  
AW333777/c  
LOCUS AW333777 20 bp mRNA linear EST 31-JAN-2000  
DEFINITION S25H10 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.  
ACCESSION AW333777  
VERSION AW333777.1 GI:6830134  
KEYWORDS EST.  
SOURCE Pneumocystis carinii  
ORGANISM Pneumocystis carinii





adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 20;  
Best Local Similarity 89.5%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
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Db 1 AAAAAAAAAAAACCA 19

RESULT 2690  
AZ368518  
LOCUS AZ368518 20 bp DNA linear GSS 02-OCT-2000  
DEFINITION IM0118G09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0118G09 R, genomic survey sequence.

ACCESSION AZ368518  
VERSION AZ368518.1 GI:10482218  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0118 row: G column: 09  
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Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers

FEATURES  
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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into

Chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 20;  
Best Local Similarity 89.5%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2782 ATTGAAAAAAAAAAAA 2800  
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Db 2 ATTAACAAAAAACAAAA 20

RESULT 2691  
CF336815/c  
LOCUS CF336815 20 bp mRNA linear EST 18-AUG-2003  
DEFINITION JMT--07-A04.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--07-A04, mRNA sequence.

ACCESSION CF336815  
VERSION CF336815.1 GI:33822012  
KEYWORDS EST.  
SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source 1..20  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
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/tissue\_type="leaf"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.6%; Score 15.8; DB 1; Length 20;  
Best Local Similarity 89.5%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2803  
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Db 19 GAGCAAAAAAAAAAAAA 1

RESULT 2692  
CF340627  
LOCUS CF340627 20 bp mRNA linear EST 18-AUG-2003  
DEFINITION RCL1--08-K02.g1 Regenerated callus lambda phage cDNA library (RCL1) Oryza sativa cDNA clone RCL1--08-K02, mRNA sequence.

ACCESSION CF340627  
VERSION CF340627.1 GI:33829609  
KEYWORDS EST.  
SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

1..20  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
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/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli SOLR"  
/clone\_lib="Regenerated callus lambda phage cDNA library (RCL1)"  
/note="Vector: pBluescript SK(+); Site 1: SstI; Site 2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.6%; Score 15.8; DB 1; Length 20;  
Best Local Similarity 89.5%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2155 TTTTTCCTCCTTTT 2173  
Db 2 TTTTTCCTCCTTTT 20

RESULT 2693  
AW248782/c  
LOCUS AW248782 21 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2821017.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821017 3', mRNA sequence.  
ACCESSION AW248782  
VERSION AW248782.1 GI:6591775  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other\_ESTs: 2821017.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html  
Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 21

contiguous PHRED high quality bases following vector sequence. Very

Low Quality Sequence: Trace file contained 21 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LCM5 row: L column: 10  
High quality sequence stop: 21.

FEATURES Location/Qualifiers

1..21  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821017"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.6%; Score 15.8; DB 1; Length 21;  
Best Local Similarity 89.5%; Pred. No. 2.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 20 AAAAAAAAAATAAAAAAAAA 2

RESULT 2694  
AZ597932/c

LOCUS AZ597932 21 bp DNA linear GSS 13-DEC-2000  
DEFINITION IM0412D23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0412D23 F, genomic survey sequence.

ACCESSION AZ597932  
VERSION AZ597932.1 GI:11720122  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE Unpublished (2000)

JOURNAL Contact: Robert B. Weiss  
COMMENT University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0412 row: D column: 23  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.

FEATURES Location/Qualifiers

1..21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"





/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 22;  
Best Local Similarity 89.5%; Pred. No. 2.8e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
||||| |||||||  
Db 22 AAAAAAAAAAAAAAAAAA 4

RESULT 2697  
AZ345485/c  
LOCUS  
DEFINITION  
AZ345485 22 bp DNA linear GSS 29-SEP-2000  
1M0080C02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0080C02 F, genomic survey sequence.

ACCESSION  
AZ345485  
VERSION  
AZ345485.1 GI:10424722  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0080 row: C column: 02  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0080C02"  
/sex="Male"

FEATURES  
source  
1. .22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0080C02"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 22;  
Best Local Similarity 89.5%; Pred. No. 2.8e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
||||| |||||||  
Db 22 AAAAAATTAAAAAAAAAA 4

RESULT 2698  
AZ355624/c  
LOCUS  
DEFINITION  
AZ355624 22 bp DNA linear GSS 02-OCT-2000  
1M0095E22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0095E22 F, genomic survey sequence.

ACCESSION  
AZ355624  
VERSION  
AZ355624.1 GI:10468133  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0095 row: E column: 22  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0095E22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

FEATURES  
source  
1. .22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0095E22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 22;  
Best Local Similarity 89.5%; Pred. No. 2.8e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2179 TTTTAAAACTTTGAAAG 2197  
|||||  
Db 22 TTTTAAAACTTTGAAAG 4

RESULT 2699  
AZ447220  
LOCUS  
DEFINITION  
AZ447220 1M0244E15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0244E15 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0244 row: E column: 15  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 23.

FEATURES  
source  
1. .23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
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/clone="UUGC1M0244E15"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 23;  
Best Local Similarity 89.5%; Pred. No. 3e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAATAAAAAA 2804  
|||||  
Db 2 AAAAAAATAAAAAA 20

RESULT 2700  
BX560037/c  
LOCUS  
DEFINITION  
BX560037 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse47e08\_plc, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Glossina morsitans morsitans

REFERENCE  
AUTHORS  
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Genome Biol. 4 (10), R63 (2003)  
22881942  
14519198

Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES  
Location/Qualifiers  
1. .23  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse47e08\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected gut"

/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.6%; Score 15.8; DB 1; Length 23;  
Best Local Similarity 89.5%; Pred. No. 3e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2783 TTGAAAAA 2801  
Db 19 TTTAGAAAAA 1

RESULT 2701  
AZ514388/c  
LOCUS  
DEFINITION 24 bp DNA linear GSS 05-OCT-2000  
1M0361H04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0361H04 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 24)

AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0361 row: H column: 04  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 24.

FEATURES  
source  
1. .24  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0361H04"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.6%; Score 15.8; DB 1; Length 24;  
Best Local Similarity 89.5%; Pred. No. 3.1e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAA 2804  
Db 24 AAAAAAAGAGA 6

RESULT 2702  
AZ814559/c  
LOCUS  
DEFINITION 24 bp DNA linear GSS 20-FEB-2001  
2M0082P18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0082P18 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 24)

AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0082 row: P column: 18  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 24.

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0082P18"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."







ORGANISM Pneumocystis carinii  
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;  
Pneumocystidaceae; Pneumocystis.

REFERENCE 1 (bases 1 to 23)  
AUTHORS Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,  
Edman,J.C., Kovacs,J. and Cushion,M.  
TITLE Expressed sequence tags from Pneumocystis carinii  
JOURNAL Unpublished (2000)  
COMMENT Contact: Staben C  
School of Biological Sciences  
University of Kentucky  
101 Morgan Building, University of Kentucky, Lexington, KY  
40506-0225, USA  
Tel: 606 257 2161  
Fax: 606 257 1717  
Email: staben@pop.uky.edu.

FEATURES  
source  
1: .23  
/organism="Pneumocystis carinii"  
/mol\_type="mrna"  
/db\_xref="taxon:4754"  
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/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;  
P. carinii organisms (3x10e9) from a single rat (99-1-6,  
sacrificed on 3/17/99) at Cincinnati VA facilities.  
Trizol extracted RNA. Oligo dT priming, standard  
conditions described by vendor, Stratagene. Further  
details see www.uky.edu/Project/Pneumocystis/"

Query Match 0.6%; Score 15.6; DB 1; Length 23;  
Best Local Similarity 81.8%; Pred. No. 3.1e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2780 GAATTGAAAAAATAAAAAA 2801  
||||| ||||| ||||| ||||| |||||  
Db 2 GAATTAAAGAAAGATAAAAAA 23

RESULT 2709  
AZ632757  
LOCUS AZ632757 23 bp DNA linear GSS 13-DEC-2000  
DEFINITION IM0487M05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0487M05 R, genomic survey sequence.

ACCESSION AZ632757  
VERSION AZ632757.1 GI:11754947  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 23)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0487 row: M column: 05  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 23.  
Location/Qualifiers

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0487M05"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.6%; Score 15.6; DB 1; Length 23;  
Best Local Similarity 81.8%; Pred. No. 3.1e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2161 TCTCCTTTTCTTTTCTTTTCTTTT 2182  
||||| ||||| ||||| ||||| |||||  
Db 2 TCTCTTTTCTTTTCTTTTCTTTT 23

RESULT 2710  
AW247816/c  
LOCUS AW247816 24 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2820481.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2820481 3',  
mRNA sequence.

ACCESSION AW247816  
VERSION AW247816.1 GI:6590809  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 24)  
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other\_ESTs: 2820481.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu/low Quality Sequence: 10  
contiguous PHRED high quality bases followed by vector sequence. Very  
Low Quality Sequence: Trace file contained 24 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was





JOURNAL  
COMMENT  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
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Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 33.  
Location/Qualifiers  
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/db\_xref="taxon:10090"  
/clone="UUGC1M0082114"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.6%; Score 15.6; DB 1; Length 33;  
Best Local Similarity 81.8%; Pred. No. 2.7e+03;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAAATAAAAAA 2800  
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Db 8 AAAATTAAAAATAAATAAAAAA 29

RESULT 2714  
BQ591181/c  
LOCUS  
DEFINITION  
E012715-024-017-H16-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-017-H16 3-PRIME, mRNA sequence.

ACCESSION  
BQ591181  
VERSION  
BQ591181.1 GI:26120764  
KEYWORDS  
EST.  
SOURCE  
Beta vulgaris  
ORGANISM  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
REFERENCE  
1 (bases 1 to 17)  
AUTHORS  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
TITLE  
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698  
Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaar@mpiz-koeln.mpg.de  
Insert Length: 17 Std Error: 0.00  
Plate: 17 row: H column: 16  
Seq primer: T7; GTAATACGACTCATATAGGC.  
Location/Qualifiers  
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/db\_xref="taxon:161934"  
/clone="024-017-H16"  
/tissue\_type="storage root"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-storage root"  
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAATAAAAAA 2802  
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Db 17 ATAAAAAATAAAAAA 1

RESULT 2715  
CF299997  
LOCUS  
DEFINITION  
7LEAF--04-D19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa CDNA clone 7LEAF--04-D19, mRNA sequence.

ACCESSION  
CF299997  
VERSION  
CF299997.1 GI:33671758  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
1 (bases 1 to 17)  
AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE  
Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
1. .17  
/organism="Oryza sativa"  
/mol\_type="mRNA"

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/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--04-D19"
/tissue_type="leaf"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.5%;   Score 15.4;   DB 1;   Length 17;
Best Local Similarity 94.1%;   Pred. No. 1.8e+03;
Matches 16;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      2166 TTTT-----TTT-----TTT 2182
Db      1 TTTT-----TTT-----TTTCT 17

RESULT 2716
CF311499/c
LOCUS      CF311499      17 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--06-L20, mRNA sequence.
ACCESSION  CF311499
VERSION     CF311499.1 GI:33683260
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
     source
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     /organism="Oryza sativa"
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     /db_xref="taxon:4530"
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     /tissue_type="leaf"
     /dev_stage="14 days after germination"
     /lab_host="E.coli DH10B"
     /clone_lib="ABF3-overexpressing transgenic rice plasmid
     cDNA library (ABF)"
     /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
     for 2hrs. Oligo-capped mRNA was reverse transcribed and
     then used for PCR. mRNA was prepared from ABA-responsive
     element binding transcription factor 3 overexpression
     line."

Query Match      0.5%;   Score 15.4;   DB 1;   Length 17;
Best Local Similarity 94.1%;   Pred. No. 1.8e+03;
Matches 16;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      2785 GAAAAA-----AAAAA 2801
Db      17 GTAAAAA-----AAAAA 1

RESULT 2717
CF311499/c
LOCUS      CF311499      17 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--06-L20, mRNA sequence.
ACCESSION  CF311499
VERSION     CF311499.1 GI:33683260
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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     /organism="Oryza sativa"
     /mol_type="mRNA"
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     /dev_stage="14 days after germination"
     /lab_host="E.coli DH10B"
     /clone_lib="ABF3-overexpressing transgenic rice plasmid
     cDNA library (ABF)"
     /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
     for 2hrs. Oligo-capped mRNA was reverse transcribed and
     then used for PCR. mRNA was prepared from ABA-responsive
     element binding transcription factor 3 overexpression
     line."

Query Match      0.5%;   Score 15.4;   DB 1;   Length 17;
Best Local Similarity 94.1%;   Pred. No. 1.8e+03;
Matches 16;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      2785 GAAAAA-----AAAAA 2801
Db      17 GTAAAAA-----AAAAA 1

RESULT 2717
CF311499/c
LOCUS      CF311499      17 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION ABF--06-L20.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--06-L20, mRNA sequence.
ACCESSION  CF311499
VERSION     CF311499.1 GI:33683260
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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     /organism="Oryza sativa"
     /mol_type="mRNA"
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     cDNA library (ABF)"
     /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
     for 2hrs. Oligo-capped mRNA was reverse transcribed and
     then used for PCR. mRNA was prepared from ABA-responsive
     element binding transcription factor 3 overexpression
     line."

Query Match      0.5%;   Score 15.4;   DB 1;   Length 17;
Best Local Similarity 94.1%;   Pred. No. 1.8e+03;
Matches 16;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      2786 AAAAAA-----AAAAA 2802
Db      17 ATAAAAA-----AAAAA 1

RESULT 2718
AW245664
LOCUS      AW245664      17 bp      mRNA      linear      EST 07-JAN-2000
DEFINITION 2822994.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822994 3',
            mRNA sequence.
ACCESSION  AW245664
VERSION     AW245664.1 GI:6588657
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 17)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Other ESTs: 2822994.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-re@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
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CF319075/c
LOCUS      CF319075      17 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION HD--09-H06.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa cDNA clone HD--09-H06, mRNA sequence.
ACCESSION  CF319075
VERSION     CF319075.1 GI:33690836
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
     source
     1..17
     /organism="Oryza sativa"
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     /db_xref="taxon:4530"
     /clone="HD--09-H06"
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     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
     /lab_host="E.coli DH10B"
     /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
     cDNA library (HD)"
     /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
     reverse transcribed and then used for PCR. mRNA was
     derived from rice Histone Deacetylase overexpression
     line."

Query Match      0.5%;   Score 15.4;   DB 1;   Length 17;
Best Local Similarity 94.1%;   Pred. No. 1.8e+03;
Matches 16;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      2786 AAAAAA-----AAAAA 2802
Db      17 ATAAAAA-----AAAAA 1

RESULT 2718
AW245664
LOCUS      AW245664      17 bp      mRNA      linear      EST 07-JAN-2000
DEFINITION 2822994.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822994 3',
            mRNA sequence.
ACCESSION  AW245664
VERSION     AW245664.1 GI:6588657
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 17)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Other ESTs: 2822994.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-re@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
```



project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 0 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence.

Plate: LLCM10 row: N column: 19.

FEATURES  
source

1. .17  
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/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2163 TCCTTTTTCCTTTTTCCTTTT 2179  
|||||  
Db 1 TCCTGTTTTCCTTTTTCCTTTT 17

RESULT 2719  
AW248574

LOCUS AW248574 17 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2821096.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821096 3', mRNA sequence.  
ACCESSION AW248574  
VERSION AW248574.1 GI:6591567  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2821096.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 8 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated. Plate: LLCM5 row: O column: 17  
High quality sequence stop: 8.

FEATURES  
source

1. .17  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821096"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTTCCTTTTTCCTTTTTCCTTTT 2182  
|||||  
Db 1 TTTTTCCTTTTTCCTTTTTCCTTTT 17

RESULT 2720  
AW248574/c

LOCUS AW248574 17 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2821096.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821096 3', mRNA sequence.  
ACCESSION AW248574  
VERSION AW248574.1 GI:6591567  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2821096.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 8 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source

1. .17  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"

/db\_xref="taxon:9606"  
/clone="IMAGE:2821096"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
Db 17 AAAAAACAAAAAAAAAAA 1

RESULT 2721  
BQ591588  
LOCUS BQ591588 17 bp mRNA linear EST 06-DEC-2002  
DEFINITION E012616-024-017-C15-SP6 MP1Z-ADIS-024-storage root Beta vulgaris cDNA clone 024-017-C15 5-PRIME, mRNA sequence.  
ACCESSION BQ591588  
VERSION BQ591588.1 GI:26121171  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 17)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698  
Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 17 Std Error: 0.00  
Plate: 17 row: C column: 15  
Seq primer: SP6; CATACGATTAGGTGACACTATAG.  
Location/Qualifiers  
1. .17  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:188532"  
/db\_xref="taxon:161934"  
/clone="024-017-C15"  
/tissue\_type="storage root"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-storage root"  
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Query Match 0.5%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802

Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2182  
Db 1 TTAT TTTT TTTT TTTT TTTT TTTT TTTT 17

RESULT 2722  
BQ591588/c  
LOCUS BQ591588 17 bp mRNA linear EST 06-DEC-2002  
DEFINITION E012616-024-017-C15-SP6 MP1Z-ADIS-024-storage root Beta vulgaris cDNA clone 024-017-C15 5-PRIME, mRNA sequence.  
ACCESSION BQ591588  
VERSION BQ591588.1 GI:26121171  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 17)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698  
Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 17 Std Error: 0.00  
Plate: 17 row: C column: 15  
Seq primer: SP6; CATACGATTAGGTGACACTATAG.  
Location/Qualifiers  
1. .17  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:188532"  
/db\_xref="taxon:161934"  
/clone="024-017-C15"  
/tissue\_type="storage root"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-storage root"  
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 15.4; DB 1; Length 17;  
Best Local Similarity 94.1%; Pred. No. 1.8e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802

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Db      17 AAAAAAAAAAAAAAAAAATAA 1
|||||
CF276637      17 bp      mRNA      linear      EST 14-AUG-2003
LOCUS      14ETL--01-N18.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION      Oryza sativa cDNA clone 14ETL--01-N18, mRNA sequence.
ACCESSION      CF276637
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--01-N18"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.5%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2166 TTTTGTGTGTGTGTGTGT 2182
Db      17 TTTTGTGTGTGTGTGTGT 1

RESULT 2723
CF291802
LOCUS      CF291802      17 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION      14ROOT--02-G05.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--02-G05, mRNA sequence.
ACCESSION      CF291802
VERSION      CF291802.1 GI:336660835
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--01-N18"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.5%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAA 2802
Db      1 AAAAAACAAAAAAAAAAAAA 17
|||||

RESULT 2724
CF276637/c
LOCUS      14ETL--01-N18.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
DEFINITION      Oryza sativa cDNA clone 14ETL--01-N18, mRNA sequence.
ACCESSION      CF276637
VERSION      CF276637.1 GI:33654023
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--01-N18"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.5%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAA 2802
Db      1 AAAAAACAAAAAAAAAAAAA 17
|||||

RESULT 2725
CF291802
LOCUS      CF291802      17 bp      mRNA      linear      EST 14-AUG-2003
DEFINITION      14ROOT--02-G05.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--02-G05, mRNA sequence.
ACCESSION      CF291802
VERSION      CF291802.1 GI:336660835
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 17)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1..17
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--02-G05"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.5%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2166 TTTTGTGTGTGTGTGTGT 2182
Db      17 TTTTGTGTGTGTGTGTGT 1
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Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTT... 2182  
 Db 1 TGT... 17

RESULT 2726  
 CF291802/c  
 LOCUS  
 DEFINITION 14ROOT--02-G05.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--02-G05, mRNA sequence.  
 ACCESSION CF291802  
 VERSION CF291802.1 GI:33660835  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1. .17  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /culturivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="14ROOT--02-G05"  
 /tissue\_type="root"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 1.8e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
 Db 17 AAAAAAAAAAAAAAAAAACA 1

RESULT 2727  
 CF297251  
 LOCUS  
 DEFINITION 30DGS--07-P12.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--07-P12, mRNA sequence.  
 ACCESSION CF297251  
 VERSION CF297251.1 GI:33666284  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1. .17  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /culturivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="30DGS--07-P12"  
 /tissue\_type="leaf"  
 /dev\_stage="30 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 1.8e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2171 TTTT... 2187  
 Db 1 TTTT... 17

RESULT 2728  
 CF297251/c  
 LOCUS  
 DEFINITION 30DGS--07-P12.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--07-P12, mRNA sequence.  
 ACCESSION CF297251  
 VERSION CF297251.1 GI:33666284  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1. .17  
 /organism="Oryza sativa"  
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 /lab\_host="E.coli DH10B"  
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 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 15.4; DB 1; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 1.8e+03;  
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

	Best Local Similarity	94.1%;	Pred. NO. 1.8e+03;	
	Matches	16;	Mismatches	1;
		Conservative	Indels	0; Gaps
QY	2784	TGAAAAAAAAAAAAA	2800	
Dd	17	TCAAAAAAAAAAAAA	1	

RESULT 2729  
CF298341/c  
LOCUS  
DEFINITION  
CF298341  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

17 bp mRNA linear EST 15-AUG-2003  
7LEAF--01-K24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--01-K24, mRNA sequence.  
CF298341  
CF298341.1 GI:33670102  
EST.  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 17)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Query Match	0.5%;	Score 15.4;	DB 1;	Length 17;
Best Local Similarity	94.1%;	Pred. No. 1.8e+03;		
Matches 16;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;

  

QY	2785	GAAAAA	AAAAAAAAAA	2801
Db	17	GCAAAA	AAAAAAAAAA	1

  

RESULT 2730				
CF299675				
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DEFINITION	7LEAF--03-M14.g1 Rice leaf plasmid cDNA library II (7LEAF)	Oryza sativa cDNA clone 7LEAF--03-M14,	mRNA sequence.	EST 15-AUG-2003
ACCESSION	CF299675			
VERSION	CF299675.1	GI:33671436		
KEYWORDS	EST.			
SOURCE	Oryza sativa			
ORGANISM	Oryza sativa			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
	Ehrhartoideae; Oryzeae; Oryza.			
REFERENCE	1 (bases 1 to 17)			
AUTHORS	Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.			

**TITLE** Large-scale Sequencing Analysis of Rice ESTs  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.myongji.ac.kr.

RESULT 2731  
CF299675/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CF299675  
7LEAF--03-M14.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--03-M14, mRNA sequence.  
CF299675  
CF299675.1 GI:33671436  
EST.  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 17)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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            /organism="Oryza sativa"
            /mol_type="mRNA"
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            /db_xref="taxon:4530"
            /clone="7LEAF--03-M14"
            /tissue_type="leaf"
            /dev_stage="7 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
            /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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Best Local Similarity 94.1%; Pred. NO. 2.1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 2785 GAAAAAAAAAAAAAAAAA 2801  
Db 2 GTAAAAAAAAAAAAAAAAA 18

RESULT	2735
CF329020	
LOCUS	CF329020
DEFINITION	18 bp mRNA linear EST 18-AUG-2003
	NACL--04-D03.b1 Rice callus plasmid cDNA library (NACL) Oryza
	sativa cDNA clone NACL--04-D03, mRNA sequence.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

<b>AUTHORS</b>	Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
<b>TITLE</b>	Large-scale Sequencing Analysis of Rice ESTs
<b>JOURNAL</b>	Unpublished (2003)

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: [bhnaem@ggbio.com](mailto:bhnaem@ggbio.com), [bhnaem@bio.myongji.ac.kr](mailto:bhnaem@bio.myongji.ac.kr).

FEATURES	Location/Qualifiers
source	1. .18

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/organism="Oryza sativa"
/mol_type="mRNA"
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/db_xref="taxon:4530"
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/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match	0.5%	Score 15.4;	DB 1;	Length 18;
Best Local Similarity	94.1%;	Pred. No. 2.1e+03;		
Matches 16;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

QY	2174	TTTTTTTTTTTAACT	2190
Db	1	TTTTTTTTTTTAACT	17

RESULT	2736
CF301222/c	
LOCUS	CF301222
DEFINITION	20 bp mRNA linear EST 15-AUG-2003 7LEAF--05-P21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--05-P21, mRNA sequence.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 20)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.myongji.ac.kr.

FEATURES	Location/Qualifiers
source	1. .20

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/organism="Oryza sativa"
/mol_type="mRNA"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Query Match	0.5%	Score 15.4;	DB 1;	Length 20;
Best Local Similarity	94.1%;	Pred. No. 2.7e+03;		
Matches 16;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

Qy 2784 TGAAAAAAAAAAAAAAAA 2800  
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Db 18 TGTAAAAAAAAAAAAAAAA 2

RESULT 2737  
AZ589400

LOCUS	AZ589400	21 bp	DNA	linear	GSS 13-DEC-2000
DEFINITION	1M0398C23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0398C23 F, genomic survey sequence.				

ACCESSION      AZ589400

VERSION AZ589400.1 GI:11711590

**KEYWORDS**

SOURCE	Mus musculus (house mouse)
OPCANTCM	Mus musculus

ORGANISM MUS MUSCULUS  
Eukaryota: M

REFERENCE

1 (bases 1 to 21)

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

Sukariyola; Metazoa; Chordata; Vertebrata; Eucercostomi;

**AUTHORS**

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT  
Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah

University of Utah  
Rm 308 Biomedical Polymers Bldg

KIM: 308, BIOMEDICAL POLYMERS RESEARCH, INC.  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@gene

Insert Length: 10000	Std Err
Insert Length: 10000	Std Err

plate: 0398 row: C column: 23

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seq primer: CGTGTAAACGACGGCA
class: nlasmid ends
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Class: piasm14 ends  
High quality sequence stop: 21.

## FEATURES

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source 1. .21
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/organism="Mus musculus"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15.4; DB 1; Length 21;  
Best Local Similarity 94.1%; Pred. No. 2.9e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2162 CTCCTTTTTTTTTTTT 2178  
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Db 5 CCCCTTTTTTTTTTTT 21

RESULT 2738  
AZ8433343/c  
LOCUS AZ8433343 21 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0142K10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0142K10 F, genomic survey sequence.  
ACCESSION AZ8433343 GI:13013251  
VERSION AZ8433343.1  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0142 row: K column: 10  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
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Location/Qualifiers  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15.4; DB 1; Length 21;  
Best Local Similarity 94.1%; Pred. No. 2.9e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAAATAAAAAAAAAA 2801  
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Db 17 GAGAAAAAATAAAAAAAAAA 1

RESULT 2739  
CF297521  
LOCUS CF297521 22 bp mRNA linear EST 14-AUG-2003  
DEFINITION 30DGS--08-H01.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--08-H01, mRNA sequence.  
ACCESSION CF297521 GI:33666554  
VERSION CF297521.1  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.  
FEATURES  
Location/Qualifiers  
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/db\_xref="taxon:4530"  
/clone="30DGS--08-H01"  
/tissue\_type="leaf"  
/dev\_stage="30 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
/note="Vector: pCR4-TOPO; Site\_1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 15.4; DB 1; Length 22;  
Best Local Similarity 94.1%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2172 TTTTCTTTTCTTTTCTTAA 2188  
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Db 1 TTTTCTTTTCTTTTCTTCAA 17

RESULT 2740  
AZ307559/c  
LOCUS  
DEFINITION  
AZ307559 1M0009O20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0009O20 F, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0009 row: 0 column: 20  
Seq primer: CGTTGTAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.

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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.5%; Score 15.4; DB 1; Length 22;  
Best Local Similarity 94.1%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2783 TTGAAAAA 2799  
|||  
Db 22 TTTAAAAA 6

RESULT 2741  
TA367G08P/c  
LOCUS  
DEFINITION  
TA367G08P 22 bp DNA linear GSS 13-DEC-2000  
T. brucei sheared genomic DNA clone 367g08, forward sequence,  
genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Trypanosoma brucei  
Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.  
REFERENCE  
AUTHORS  
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,  
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,  
Melville,S.E., Rajandream,M.A. and Barrell,B.G.  
TITLE  
JOURNAL  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nhl@sanger.ac.uk  
COMMENT  
Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available  
at http://www.sanger.ac.uk/Projects/T\_brucei/.

FEATURES  
source  
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Query Match 0.5%; Score 15.4; DB 1; Length 22;  
Best Local Similarity 94.1%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2783 TTGAAAAA 2799  
|||  
Db 17 TTTAAAAA 1

RESULT 2742  
AZ470212/c  
LOCUS  
DEFINITION  
AZ470212 1M0284L09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0284L09 F, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
  
QY 2783 TTGAAAAA 2799  
|||  
Db 17 TTTAAAAA 1



REFERENCE 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0284 row: L column: 09  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid Ri. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15.4; DB 1; Length 22;  
Best Local Similarity 94.1%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2785 GAAAAAAAAAAAAAAAAA 2801  
|||||  
Db 22 GAAAAAAAAAAGAAA 6

RESULT 2743  
AL587602/c  
LOCUS AL587602 BP Chicken Brain Library Gallus cdna clone  
DEFINITION ROS059F08, mRNA sequence.  
ACCESSION AL587602  
VERSION AL587602.1 GI:13192636  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 23)  
AUTHORS Murray,F.  
TITLE BP Chicken Brain Library  
JOURNAL Unpublished (2001)  
COMMENT Contact: Frazer Murray  
Dept. Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UK  
Tel: +44 (0)131 527 4200  
Fax: +44 (0)131 440 0434  
Email: frazer.murray@bbsrc.ac.uk  
CGGGCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech (\*6854-  
Seq primer: M13F.  
Location/Qualifiers  
1. .23  
/organism="Gallus gallus"  
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/dev\_stage="Unknown"  
/lab\_host="DH10B"  
/clone\_lib="BP Chicken Brain Library"  
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. 5' adaptor sequence: 5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5' GCGGCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clontech (\*6854-1)"

Query Match 0.5%; Score 15.4; DB 1; Length 23;  
Best Local Similarity 88.9%; Pred. No. 3.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803  
|||||  
Db 23 AAAAAAAAAAAGAGA 6

RESULT 2744  
AZ662734 23 bp DNA linear GSS 14-DEC-2000  
LOCUS IM0542D04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0542D04 F, genomic survey sequence.  
DEFINITION AZ662734  
ACCESSION AZ662734.1 GI:11799880  
VERSION  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0542 row: D column: 04  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 23.  
Location/Qualifiers

source

1. .23  
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/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.5%; Score 15.4; DB 1; Length 23;  
Best Local Similarity 94.1%; Pred. No. 3.2e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
Db 7 AATAAAAAAAAAAAAAA 23

RESULT 2745

LOCUS CF280704 23 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ETL--07-H17.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa cDNA clone 14ETL--07-H17, mRNA sequence.  
ACCESSION CF280704  
VERSION CF280704.1 GI:33658090  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 23)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1. .23  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="14ETL--07-H17"  
/tissue type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"

/clone lib="Rice etiolated leaf plasmid cDNA library  
(14ETL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 15.4; DB 1; Length 23;  
Best Local Similarity 94.1%; Pred. No. 3.2e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2783 TTGAAAAAAAAAAAAA 2799  
Db 7 TTTAAAAAAAAAAAAA 23

RESULT 2746

LOCUS TA367D08P/c 23 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 367d08, forward sequence,  
genomic survey sequence.  
ACCESSION AL493509  
VERSION AL493509.1 GI:11870519  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.

REFERENCE 1 (bases 1 to 23)  
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,  
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,  
Melville,S.E., Rajandream,M.A. and Barrell,B.G.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nhl@sanger.ac.uk

COMMENT

Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available  
at http://www.sanger.ac.uk/Projects/T\_brucei/.

FEATURES

source

1. .23  
/organism="Trypanosoma brucei"  
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Query Match 0.5%; Score 15.4; DB 1; Length 23;  
Best Local Similarity 94.1%; Pred. No. 3.2e+03;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2783 TTGAAAAAAAAAAAAA 2799  
Db 17 TTTAAAAAAAAAAAAA 1

RESULT 2747

AZ615086  
LOCUS AZ615086 23 bp DNA linear GSS 13-DEC-2000  
DEFINITION 1M0444C14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0444C14 F, genomic survey sequence.  
ACCESSION AZ615086  
VERSION AZ615086.1 GI:11737276  
KEYWORDS GSS.

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SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 23)
AUTHORS
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0444 row: C column: 14
Seq primer: CGTTGTAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
FEATURES
source
Location/Qualifiers
1..23
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0444C14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.5%; Score 15.4; DB 1; Length 23;
Best Local Similarity 94.1%; Pred. No. 3.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2162 CTCCTTTT TTTT TTTT TTTT 2178
| | | | | | | | | | | | | |
Db 7 CCCCTTTT TTTT TTTT TTTT 23
RESULT 2748
AZ819376/c
LOCUS AZ819376 23 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0089P23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0089P23 R, genomic survey sequence.
ACCESSION AZ819376
VERSION AZ819376.1 GI:12989284
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

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CDNA library (JMT)"  
/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.5%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 2.8e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2185  
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Db 1 TTTTTTTTTTTTGTCTCT 20

RESULT 2754  
AZ316368/c  
LOCUS  
DEFINITION  
AZ316368  
1M0034L22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0034L22 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 20)

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0034 row: L column: 22  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
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/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and

FEATURES  
source  
1. .20  
/organism="Mus musculus"  
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/db\_xref="taxon:10090"  
/clone="UUGC1M0034L22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. Coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.5%; Score 15.2; DB 1; Length 20;  
Best Local Similarity 85.0%; Pred. No. 2.8e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTTTTTT 2185  
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Db 20 TTAATAATTTTTTTTTTTT 1

RESULT 2755  
AZ843343  
LOCUS  
DEFINITION  
AZ843343  
2M0142K10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0142K10 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 21)

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0142 row: K column: 10  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to

FEATURES  
source  
1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to





and selected for ampicillin resistance."

Query Match 0.5%; Score 15.2; DB 1; Length 21;  
Best Local Similarity 85.0%; Pred. No. 3.1e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
Qy 289 CCCCAGCGCACCCCTCTCCC 308  
Db 20 CCCCAGCGCCCCCCCCCCCC 1

RESULT 2758  
D20705/c  
LOCUS D20705 22 bp mRNA linear EST 30-JUL-1996  
DEFINITION HUMGS01681 Human promyelocyte Homo sapiens cDNA clone pm2012 3', mRNA sequence.  
ACCESSION D20705 GI:501801  
VERSION D20705.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Kojima,Y., Yoshinari,H., Arimoto,J. and Matsubara,K.  
TITLE Gene expression of human promyelocytic cell line HL60 before and after induction of differentiation. A new application of 3'directed cDNA sequencing  
JOURNAL Unpublished (1993)  
COMMENT Contact: Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Kojima,Y., Yoshinari,H., Arimoto,J. and Matsubara,K.  
Institute for Molecular and Cellular Biology  
Osaka University  
3-1 Yamada-oka,Suita,Osaka 565,Japan.  
Location/Qualifiers

FEATURES  
source 1..22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="pm2012"  
/clone\_lib="Human promyelocyte"  
/note="Female, adult, cell\_line = HL60, cell\_type = promyelocyte."

Query Match 0.5%; Score 15.2; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 3.2e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2469 TTAATATTAACTTTTAATGGT 2489  
Db 22 TTTATTTNACTTTTAATGAT 2

RESULT 2759  
TA181E11P/c  
LOCUS TA181E11P 22 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 181e11, forward sequence, genomic survey sequence.  
ACCESSION AL474328  
VERSION AL474328.1 GI:11839616  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

COMMENT  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk  
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/projects/T\\_brucei/](http://www.sanger.ac.uk/projects/T_brucei/).

FEATURES  
source 1..22  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="181e11"

Query Match 0.5%; Score 15.2; DB 1; Length 22;  
Best Local Similarity 85.0%; Pred. No. 3.2e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1769 GCITTTTITTTTGAACCCC 1788  
Db 21 GGITTTTITTTTGGCCCCC 2

RESULT 2760  
AU267211  
LOCUS AU267211 23 bp mRNA linear EST 10-MAY-2002  
DEFINITION AU267211 VS Dictyostelium discoideum cDNA clone VSH291 5', mRNA sequence.  
ACCESSION AU267211 GI:20526009  
VERSION AU267211.1  
KEYWORDS EST.  
SOURCE Dictyostelium discoideum  
ORGANISM Dictyostelium discoideum  
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriaki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.  
TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum  
JOURNAL Unpublished (2002)  
COMMENT Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: hideko@biol.tsukuba.ac.jp.

FEATURES  
source 1..23  
/organism="Dictyostelium discoideum"  
/mol\_type="mRNA"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="VSH291"  
/sex="mat A"  
/dev\_stage="vegetative"  
/clone\_lib="V5"

Query Match 0.5%; Score 15.2; DB 1; Length 23;  
Best Local Similarity 85.0%; Pred. No. 3.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2781 AATTGAAAAAATAAAAAA 2800  
Db 4 AATTGTATACAAAAAATAA 23

RESULT 2761  
AW245956  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AW245956  
2823002.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2823002 3',  
mRNA sequence.  
AW245956  
AW245956.1 GI:6588949  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 23)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2823002.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
<http://www.genome.washington.edu> Low Quality Sequence: 9 contiguous  
PHRED high quality bases following vector sequence. Very Low  
Quality Sequence: Trace file contained 23 contiguous distinct peaks  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LCM10 row: O column: 3  
High quality sequence stop: 9.  
Location/Qualifiers  
1..23  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2823002"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: POTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 15.2; DB 1; Length 23;  
Best Local Similarity 85.0%; Pred. No. 3.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2166 TTTTCTTTTCTTTATTTT 2185  
Db 1 TTTTCTTTTCTTTATTTT 20

RESULT 2762  
CF292525/c  
LOCUS  
DEFINITION  
ACCESSION

CF292525  
30DGS--01-G03.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa cDNA clone 30DGS--01-G03, mRNA sequence.  
CF292525

VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CF292525.1 GI:33661558  
EST.  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 23)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: [bnahm@ggbio.com](mailto:bnahm@ggbio.com), [bnahm@bio.myongji.ac.kr](mailto:bnahm@bio.myongji.ac.kr).  
Location/Qualifiers  
1..23  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="30DGS--01-G03"  
/tissue\_type="leaf"  
/dev\_stage="30 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 15.2; DB 1; Length 23;  
Best Local Similarity 85.0%; Pred. No. 3.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2780 GAATTGAAAAA 2799  
Db 20 GTAATGCAAAAAA 1

RESULT 2763  
CK277017  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CK277017  
EST723095 potato abiotic stress cDNA library Solanum tuberosum cDNA  
clone POADx19 3' end, mRNA sequence.  
CK277017  
CK277017.1 GI:39833995  
EST.  
Solanum tuberosum (potato)  
Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Solanaceae; Solanum.  
1 (bases 1 to 23)  
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.  
Generation of ESTs from abiotic stressed potato tissue  
Unpublished (2003)  
Other\_ESTs: EST723094  
Contact: Robin Buell  
The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: [potato-array@tigr.org](mailto:potato-array@tigr.org)  
Clones can be requested from TIGR via [potato@tigr.org](mailto:potato@tigr.org)  
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.  
Location/Qualifiers  
1..23  
/organism="Solanum tuberosum"  
/mol\_type="mRNA"  
/cultivar="Kennebec"  
/db\_xref="taxon:4113"

FEATURES  
source





REFERENCE 1 (bases 1 to 24)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other\_ESTs: 2820481.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 10 contiguous PHRED high quality bases followed vector sequence. Very Low Quality Sequence: Trace file contained 24 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LLCM4 row: F column: 2  
High quality sequence stop: 10.  
Location/Qualifiers  
1. .24  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2820481"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: POTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 15.2; DB 1; Length 24;  
Best Local Similarity 85.0%; Pred. No. 3.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2177 TTTTCTTTTAACTTTGAA 2196  
|||||||  
Db 1 TTTTCTTTTCACTTTTACA 20

RESULT 2767  
AZ9533355/c  
LOCUS AZ9533355 27 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0218M01R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0218M01 R, genomic survey sequence.  
ACCESSION AZ9533355  
VERSION AZ9533355.1 GI:13824582  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 27)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 24)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2820481.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 10 contiguous PHRED high quality bases followed vector sequence. Very Low Quality Sequence: Trace file contained 24 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LLCM4 row: F column: 2  
High quality sequence stop: 10.  
Location/Qualifiers  
1. .24  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2820481"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: POTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 15.2; DB 1; Length 24;  
Best Local Similarity 85.0%; Pred. No. 3.4e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2177 TTTTCTTTTAACTTTGAA 2196  
|||||||  
Db 1 TTTTCTTTTCACTTTTACA 20

RESULT 2767  
AZ9533355/c  
LOCUS AZ9533355 27 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0218M01R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0218M01 R, genomic survey sequence.  
ACCESSION AZ9533355  
VERSION AZ9533355.1 GI:13824582  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 27)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0218 row: M column: 01  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 27.  
Location/Qualifiers  
1. .27  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0218M01"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15.2; DB 1; Length 27;  
Best Local Similarity 85.0%; Pred. No. 3.3e+03;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2785 GAAAAAAGAAAAA 2804  
|||||||  
Db 27 GAAAAAAGAAAAAAGA 8

RESULT 2768  
AV741507/c  
LOCUS AV741507 27 bp mRNA linear EST 17-OCT-2000  
DEFINITION AV741507 CB Homo sapiens cDNA clone CBMAMC05 5', mRNA sequence.  
ACCESSION AV741507  
VERSION AV741507.1 GI:10859088  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 27)  
Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z., Chen,S., Mao,M. and Chen,Z.  
Homo sapiens CB library cDNA clones  
Unpublished (2000)  
Contact: Zhu Chen  
Shanghai Institute of Hematology, Rui-Jin Hospital  
197 Rui-Jin II Road, Shanghai 200025, P. R. China





PUBMED  
COMMENT  
12472698  
Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@mpiz-koeln.mpg.de  
Insert Length: 15 Std Error: 0.00  
Plate: 7 row: B column: 02  
Seq primer: T7; GTAATACGACTCACTATAGGCG.  
Location/Qualifiers  
1. .15  
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/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:184162"  
/db\_xref="taxon:161934"  
/clone="024-007-B02"  
/tissue\_type="inflorescence"  
/lab\_host="EMDH10B"  
/clone\_lib="MPIZ-ADIS-024-inflorescence"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2180  
Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2772  
BQ582543/c  
LOCUS  
DEFINITION  
BQ582543  
VERSION  
BQ582543.1 GI:26112120  
KEYWORDS  
SOURCE  
ORGANISM  
Beta vulgaris  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 15)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
PUBMED  
COMMENT  
Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@mpiz-koeln.mpg.de  
Insert Length: 15 Std Error: 0.00  
Plate: 7 row: B column: 02  
Seq primer: T7; GTAATACGACTCACTATAGGCG.

PUBMED  
COMMENT  
12472698  
Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@mpiz-koeln.mpg.de  
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Location/Qualifiers  
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SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION  
BQ582543  
VERSION  
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SOURCE  
ORGANISM  
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Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 15)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
PUBMED  
COMMENT  
Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@mpiz-koeln.mpg.de  
Insert Length: 15 Std Error: 0.00  
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Seq primer: T7; GTAATACGACTCACTATAGGCG.

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SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

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DEFINITION  
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VERSION  
BQ585820.1 GI:26115402  
KEYWORDS  
SOURCE  
ORGANISM  
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Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 15)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
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22362189  
12472698  
COMMENT  
Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@mpiz-koeln.mpg.de  
Insert Length: 15 Std Error: 0.00  
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Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
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RZPD/GABI-Primary database:http://gabi.rzpd.de"

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RESULT 2774  
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LOCUS BQ585820 15 bp mRNA linear EST 06-DEC-2002  
DEFINITION E012533-024-014-H17-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone  
ACCESSION BQ585820  
VERSION BQ585820.1 GI:26115402  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
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fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@mpiz-koeln.mpg.de  
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Seq primer: SP6; CATACGATTAGGTGACACTATAG.

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cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:

Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database:http://gabi.rzpd.de"  
Query Match 0.5%; Score 15; DB 1; Length 15;  
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RESULT 2775  
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DEFINITION E012844-024-019-M08-T7 MPIZ-ADIS-024-storage root Beta vulgaris  
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ACCESSION BQ590410  
VERSION BQ590410.1 GI:26119993  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
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MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@mpiz-koeln.mpg.de  
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cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 15; DB 1; Length 15;  
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Db 1 TTTT TTTT TTTT TTTT TTTT 15

SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

RESULT 2776  
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LOCUS  
DEFINITION E012844-024-019-M08-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
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ACCESSION BQ590410  
VERSION BQ590410.1 GI:26119993  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
JOURNAL 22362189  
MEDLINE  
PUBMED  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@piz-koeln.mpg.de  
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Seq primer: T7; GTAATACGACTCACTATAGGCG.  
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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
CDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 15; DB 1; Length 15;  
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Db 15 AAAAAAAAAAAAAA 1

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ACCESSION BQ590656  
VERSION BQ590656.1 GI:26120239  
KEYWORDS EST.

Query Match 0.5%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 15 AAAAAAAAAAAAAA 1

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ACCESSION BQ590656  
VERSION BQ590656.1 GI:26120239  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
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TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide

SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
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AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
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JOURNAL 22362189  
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COMMENT Contact: Weisshaar B  
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Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaa@piz-koeln.mpg.de  
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CDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
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Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
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Db 1 TTTTTTTTTTTTTT 15

RESULT 2778  
BQ590656/c  
LOCUS  
DEFINITION BQ590656  
S015086-024-018-L13-SP6 MP1Z-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-018-L13 5-PRIME, mRNA sequence.  
ACCESSION BQ590656  
VERSION BQ590656.1 GI:26120239  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
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TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide



JOURNAL  
MEDLINE  
PUBMED  
COMMENT

fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698  
Contact: Weissshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
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Email: weissshaampiz-koeln.mpg.de  
Insert Length: 15 Std Error: 0.00  
Plate: 18 row: L column: 13  
Seq primer: SP6; CATACGATTAGTGACACTATAG.  
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1. .15  
/organism="Beta vulgaris"  
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SP6-Sali-CCACGGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

FEATURES  
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Query Match 0.5%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800  
Db 15 AAAAAAAAAAAAAA 1

RESULT 2779  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

BQ591170  
E012715-024-017-N18-T7 MPIZ-ADIS-024-storage root Beta vulgaris  
cDNA clone 024-017-N18 3-PRIME, mRNA sequence.  
BQ591170  
BQ591170.1 GI:26120753  
EST.  
Beta vulgaris  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
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Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
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22362189  
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Contact: Weissshaar B  
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Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaampiz-koeln.mpg.de

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SP6-Sali-CCACGGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

FEATURES  
source

Query Match 0.5%; Score 15; DB 1; Length 15;  
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTT 2180  
Db 1 TTTTTTTTTTTTTT 15

RESULT 2780  
BQ591170/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

BQ591170  
E012715-024-017-N18-T7 MPIZ-ADIS-024-storage root Beta vulgaris  
cDNA clone 024-017-N18 3-PRIME, mRNA sequence.  
BQ591170  
BQ591170.1 GI:26120753  
EST.  
Beta vulgaris  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 15)  
Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698  
Contact: Weissshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaampiz-koeln.mpg.de  
Insert Length: 15 Std Error: 0.00  
Plate: 17 row: N column: 18  
Seq primer: T7; GTAATACGACTACTATAGGC.  
Location/Qualifiers  
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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 15; DB 1; Length 15;  
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||  
Db 15 AAAAAAAAAAAAAA 1

RESULT 2781  
BQ5911178  
LOCUS  
DEFINITION  
E012715-024-017-F22-T7 MPIZ-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-017-F22 3-PRIME, mRNA sequence.

ACCESSION  
BQ5911178  
VERSION  
BQ5911178.1 GI:26120761  
KEYWORDS  
EST.

SOURCE  
Beta vulgaris

ORGANISM

REFERENCE  
AUTHORS  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

22362189

PUBMED

COMMENT  
Contact: Weisshaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaar@piz-koeln.mpg.de

Insert Length: 15 Std Error: 0.00

Plate: 17 row: F column: 22

Seq primer: T7; GTAATACGACTCCTATAGGGC.

Location/Qualifiers

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line)"

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/lab\_host="EMDH10B"

/clone\_lib="MPIZ-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites Sali-NotI, primer sites and

orientation:

SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTT 2180  
|||||  
Db 1 TTTTTTTTTTTTTT 15

RESULT 2782

BQ5911178/c

LOCUS

DEFINITION  
E012715-024-017-F22-T7 MPIZ-ADIS-024-storage root Beta vulgaris

CDNA clone 024-017-F22 3-PRIME, mRNA sequence.

ACCESSION  
BQ5911178

VERSION  
BQ5911178.1 GI:26120761

KEYWORDS  
EST.

SOURCE  
Beta vulgaris

ORGANISM

REFERENCE  
AUTHORS  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

22362189

PUBMED

COMMENT  
Contact: Weisshaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

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Fax: 00492215062851

Email: weisshaar@piz-koeln.mpg.de

Insert Length: 15 Std Error: 0.00

Plate: 17 row: F column: 22

Seq primer: T7; GTAATACGACTCCTATAGGGC.

Location/Qualifiers

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/mol\_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding

line)"

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/db\_xref="taxon:161934"

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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites Sali-NotI, primer sites and

orientation:

SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:

Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800  
Db 15 AAAAAAAAAAAAAA 1

RESULT 2783

BQ591223  
LOCUS  
DEFINITION  
E012715-024-017-H02-T7 MPIZ-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-017-H02 3-PRIME, mRNA sequence.  
ACCESSION  
BQ591223  
VERSION  
BQ591223.1 GI:26120806  
KEYWORDS  
EST.  
SOURCE  
Beta vulgaris  
ORGANISM  
Beta vulgaris

REFERENCE

1 (bases 1 to 15)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698  
Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 15 Std Error: 0.00  
Plate: 17 row: H column: 02  
Seq primer: T7; GTAATACGACTCACTATAGGCG.

TITLE

1. .15  
Location/Qualifiers  
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/mol\_type="mRNA"  
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line)"  
/db\_xref="GABI:188901"  
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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

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Location/Qualifiers  
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line)"  
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cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match

Best Local Similarity 0.5%; Score 15; DB 1; Length 15;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2784

BQ591223/c

LOCUS

DEFINITION  
E012715-024-017-H02-T7 MPIZ-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-017-H02 3-PRIME, mRNA sequence.  
BQ591223  
LOCUS  
DEFINITION  
E012715-024-017-H02-T7 MPIZ-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-017-H02 3-PRIME, mRNA sequence.

ACCESSION  
BQ591223.1 GI:26120806  
VERSION  
BQ591223.1  
KEYWORDS  
EST.  
SOURCE  
Beta vulgaris  
ORGANISM  
Beta vulgaris

REFERENCE

AUTHORS

TITLE

1 (bases 1 to 15)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698  
Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 15 Std Error: 0.00  
Plate: 17 row: H column: 02  
Seq primer: T7; GTAATACGACTCACTATAGGCG.

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

1. .15  
Location/Qualifiers  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
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line)"  
/db\_xref="GABI:188901"  
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cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match

Best Local Similarity 0.5%; Score 15; DB 1; Length 15;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800  
Db 15 AAAAAAAAAAAAAA 1

RESULT 2785

BQ594689

LOCUS

DEFINITION

E012404-024-024-M05-T7 MPIZ-ADIS-024-developing root Beta vulgaris  
CDNA clone 024-024-M05 3-PRIME, mRNA sequence.  
BQ594689  
VERSION  
BQ594689.1 GI:26124272  
KEYWORDS  
EST.  
SOURCE  
Beta vulgaris  
ORGANISM  
Beta vulgaris

REFERENCE

AUTHORS

1 (bases 1 to 15)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698  
Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 15 Std Error: 0.00  
Plate: 17 row: H column: 02  
Seq primer: T7; GTAATACGACTCACTATAGGCG.



Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)

JOURNAL MEDLINE PUBMED

COMMENT Contact: Weisshaar B ADIS DNA core facility at MPIZ Max-Planck-Institute for Plant Breeding Research Carl-von-Linne Weg 10, 50829 Koeln, Germany Fax: 00492215062851

Email: weissshaam@piz-koeln.mpg.de Insert Length: 15 Std Error: 0.00 Plate: 24 row: M column: 05 Seq primer: T7; GTAATACGACTCATATAGGCG.

FEATURES

Location/Qualifiers 1..15 /organism="Beta vulgaris" /mol\_type="mRNA" /cultivar="KWS2320 (double haploid, monogerm breeding line)" /db\_xref="GABI:192163" /db\_xref="taxon:161934" /clone="024-024-M05" /tissue\_type="developing root" /lab\_host="EMDH10B" /clone\_lib="MPIZ-ADIS-024-developing root" /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation: SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 15; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 1.5e+03; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT 2180 Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2786 BQ594689/c

LOCUS E012404-024-024-M05-T7 MPIZ-ADIS-024-developing root Beta vulgaris cDNA clone 024-024-M05 3-PRIME, mRNA sequence. 15 bp mRNA linear EST 06-DEC-2002

ACCESSION BQ594689 VERSION BQ594689.1 GI:26124272 KEYWORDS EST.

SOURCE Beta vulgaris ORGANISM Beta vulgaris

REFERENCE 1 (bases 1 to 15) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes Plant J. 32 (5), 845-857 (2002)

JOURNAL MEDLINE PUBMED

COMMENT Contact: Weisshaar B ADIS DNA core facility at MPIZ Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany Fax: 00492215062851

Email: weissshaam@piz-koeln.mpg.de Insert Length: 15 Std Error: 0.00 Plate: 24 row: M column: 05 Seq primer: T7; GTAATACGACTCATATAGGCG.

FEATURES

Location/Qualifiers 1..15 /organism="Beta vulgaris" /mol\_type="mRNA" /cultivar="KWS2320 (double haploid, monogerm breeding line)" /db\_xref="GABI:192163" /db\_xref="taxon:161934" /clone="024-024-M05" /tissue\_type="developing root" /lab\_host="EMDH10B" /clone\_lib="MPIZ-ADIS-024-developing root" /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation: SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 15; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 1.5e+03; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAA AAAAAA AAAAAA 2800 Db 15 AAAAAA AAAAAA AAAAAA 1

RESULT 2787 CF277319

LOCUS CF277319 14ETL--02-M23.b1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa cDNA clone 14ETL--02-M23, mRNA sequence. 15 bp mRNA linear EST 14-AUG-2003

ACCESSION CF277319 VERSION CF277319.1 GI:33654705 KEYWORDS EST.

SOURCE Oryza sativa ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 15) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355

Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers 1..15 /organism="Oryza sativa" /mol\_type="mRNA" /cultivar="Nackdong" /db\_xref="taxon:4530" /clone="14ETL--02-M23" /tissue\_type="leaf" /dev\_stage="14 days after germination" /lab\_host="E.coli DH10B"

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/note="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."  
  
Query Match 0.5%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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|||||  
Db 1 TTTT TTTT TTTT TTTT TTTT 15  
  
RESULT 2788  
CF277319/c  
LOCUS  
DEFINITION 14ETL--02-M23.b1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa cDNA clone 14ETL--02-M23, mRNA sequence.  
CF277319  
ACCESSION CF277319.1 GI:33654705  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
  
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Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 15 AAAAAA AAAAAA AAAAAA 1  
  
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Oryza sativa cDNA clone 14ETL--09-D04, mRNA sequence.  
CF281923  
ACCESSION CF281923.1 GI:33659310  
VERSION  
KEYWORDS

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
  
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RESULT 2790  
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LOCUS  
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CF281923  
ACCESSION CF281923.1 GI:33659310  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
  
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CF281923/c  
LOCUS  
DEFINITION 14ETL--09-D04.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa cDNA clone 14ETL--09-D04, mRNA sequence.  
CF281923  
ACCESSION CF281923.1 GI:33659310  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
  
FEATURES  
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Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2794
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LOCUS
DEFINITION
14ROOT--01-E19.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-E19, mRNA sequence.
ACCESSION
CF291029
VERSION
CF291029.1 GI:33660062
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Db 15 AAAAAA AAAAAA AAAAAA 1

RESULT 2795
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DEFINITION
14ROOT--01-G10.b1 Rice root plasmid cDNA library (14ROOT) Oryza
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sativa cDNA clone 14ROOT--01-G10, mRNA sequence.
CF291103
VERSION
CF291103.1 GI:33660136
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RESULT 2796
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LOCUS
DEFINITION
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sativa cDNA clone 14ROOT--01-G10, mRNA sequence.
ACCESSION
CF291103
VERSION
CF291103.1 GI:33660136
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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LOCUS
DEFINITION
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sativa cDNA clone 14ROOT--02-G02, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Db 15 AAAAAA AAAAAA AAAAAA 1

RESULT 2801
CF292458
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LOCUS
DEFINITION
30DGS--01-E17.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2180
Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2802
CF292458/c
LOCUS
DEFINITION
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sativa cDNA clone 30DGS--01-E17, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 15)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Location/Qualifiers
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QY 2786 AAAAAAAAAAAAAA 2800
Db 15 AAAAAAAAAAAAAA 1

RESULT 2803
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LOCUS
DEFINITION
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sativa cDNA clone 30DGS--01-E19, mRNA sequence.
ACCESSION
CF292461
VERSION
CF292461.1 GI:33661494
KEYWORDS
EST.
SOURCE
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ORGANISM
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1.5e+03;
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Db 15 AAAAAAAAAAAAAA 1

RESULT 2805
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DEFINITION
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sativa cDNA clone 30DGS--04-O02, mRNA sequence.
ACCESSION
CF295100
VERSION
CF295100.1 GI:33664133
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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RT-PCR."

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Db 1 TTTT TTTT TTTT TTTT 15

RESULT 2804
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CF292461/c
LOCUS
DEFINITION
30DGS--01-E19.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
sativa cDNA clone 30DGS--01-E19, mRNA sequence.
ACCESSION
CF292461
VERSION
CF292461.1 GI:33661494
KEYWORDS
EST.
SOURCE
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ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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QY 2786 AAAAAAAAAAAAAA 2800
Db 15 AAAAAAAAAAAAAA 1

RESULT 2805
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LOCUS
DEFINITION
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sativa cDNA clone 30DGS--04-O02, mRNA sequence.
ACCESSION
CF295100
VERSION
CF295100.1 GI:33664133
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2809  
CF298630/c  
LOCUS  
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ACCESSION CF298630  
VERSION CF298630.1 GI:33670391  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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JOURNAL Unpublished (2003)  
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Db 15 AAAAAA AAAAAA AAAAAA 1

RESULT 2810  
CF298733  
LOCUS  
DEFINITION 7LEAF--02-E20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--02-E20, mRNA sequence.  
ACCESSION CF298733  
VERSION CF298733.1 GI:33670494  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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Qy 2166 TTTT TTTT TTTT TTTT TTTT 2180  
Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2811  
CF298733/c  
LOCUS  
DEFINITION 7LEAF--02-E20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--02-E20, mRNA sequence.  
ACCESSION CF298733  
VERSION CF298733.1 GI:33670494  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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## FEATURES

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QY 2786 AAAAAAAAAAAAAA 2800

Db 15 AAAAAAAAAAAAAA 1

## RESULT 2812

CF298805

LOCUS

7LEAF--02-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--02-G20, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
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Unpublished (2003)

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Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

source

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QY 2166 TTTTTTTTTTTTTT 2180

Db 1 TTTTTTTTTTTTTT 15

## RESULT 2813

CF298805/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

source

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QY 2786 AAAAAAAAAAAAAA 2800

Db 15 AAAAAAAAAAAAAA 1

## RESULT 2814

CF298889

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

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QY 2166 TTTT TTTT TTTT TTTT TTTT 2180

Db 1 TTTT TTTT TTTT TTTT TTTT 15

## RESULT 2815

CF298889/c

LOCUS

7LEAF--02-J09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--02-J09, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
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## FEATURES

source

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Db 15 AAAAAAAAAAAAAA 1

## RESULT 2816

CF299602

LOCUS

7LEAF--03-L01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--03-L01, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

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Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

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0.5%; Score 15; DB 1; Length 15;

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QY 2166 TTTT TTTT TTTT TTTT TTTT 2180

Db 1 TTTT TTTT TTTT TTTT TTTT 15

## RESULT 2817

CF299602/c

LOCUS

7LEAF--03-L01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--03-L01, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 15 AAAAAAAAAAAAAA 1

## RESULT 2818

CF299608

LOCUS

DEFINITION  
7LEAF--03-L04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--03-L04, mRNA sequence.

ACCESSION

VERSION CF299608.1 GI:33671369

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE  
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL  
Unpublished (2003)

COMMENT

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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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Db 1 TTTTTTTTTTTTTT 15

## RESULT 2819

CF299608/c

LOCUS

DEFINITION

7LEAF--03-L04.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--03-L04, mRNA sequence.

ACCESSION

VERSION CF299608.1 GI:33671369

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE  
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL  
Unpublished (2003)

COMMENT

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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

Location/Qualifiers

1. .15

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/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match

Best Local Similarity 100.0%; Score 15; DB 1; Length 15;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800

Db 15 AAAAAAAAAAAAAA 1

## RESULT 2820

CF300121

LOCUS

DEFINITION

7LEAF--04-G12.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--04-G12, mRNA sequence.

ACCESSION

VERSION CF300121

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE  
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL  
Unpublished (2003)

COMMENT

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FEATURES

source  
1. .15  
/organism="Oryza sativa"  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

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Qy 2166. TTTT TTTT TTTT TTTT TTTT 2180

Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2821

CF300121/c

LOCUS

7LEAF--04-G12.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--04-G12, mRNA sequence.

ACCESSION

CF300121

VERSION

CF300121.1 GI:33671882

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
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Contact: Nahm B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

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1. .15  
/organism="Oryza sativa"  
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Query Match 0.5%; Score 15; DB 1; Length 15;  
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2800

Db 15 AAAAAAAAAAAAAA 1

RESULT 2822

CF300361

LOCUS

7LEAF--04-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--04-L16, mRNA sequence.

ACCESSION

CF300361

VERSION

CF300361.1 GI:33672122

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

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1. .15  
/organism="Oryza sativa"  
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Query Match 0.5%; Score 15; DB 1; Length 15;  
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Qy 2166 TTTT TTTT TTTT TTTT TTTT 2180

Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2823

CF300361/c

LOCUS

7LEAF--04-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--04-L16, mRNA sequence.

ACCESSION

CF300361

VERSION

CF300361.1 GI:33672122

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

REFERENCE

AUTHORS

TITLE

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## FEATURES

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with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 15; DB 1; Length 15;  
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 15 AAAAAAAAAAAAAA 1

## RESULT 2824

CF300992

LOCUS

DEFINITION 7LEAF--05-K19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--05-K19, mRNA sequence.

ACCESSION

VERSION CF300992.1 GI:33672753

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE

JOURNAL

COMMENT

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Yongin, Kyeonggi, Korea  
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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTT 2180  
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Db 1 TTTTTTTTTTTTTT 15

## RESULT 2825

CF300992/c

LOCUS

DEFINITION 7LEAF--05-K19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--05-K19, mRNA sequence.

ACCESSION

VERSION CF300992.1 GI:33672753

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE

JOURNAL

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Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||||  
Db 15 AAAAAAAAAAAAAA 1

## RESULT 2826

CF302034

LOCUS

DEFINITION 7LEAF--07-C24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--07-C24, mRNA sequence.

ACCESSION

VERSION CF302034.1 GI:33673795

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

## TITLE

JOURNAL

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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES Location/Qualifiers

source  
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with oligoribonucleotides and then used as templates for  
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QY 2166 TTTT TTTT TTTT TTTT TTTT 2180

Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2827  
CF302034/c  
LOCUS CF302034 15 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--07-C24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--07-C24, mRNA sequence.

ACCESSION CF302034  
VERSION CF302034.1 GI:33673795  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 15)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES Location/Qualifiers

source  
1. .15  
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/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 15; DB 1; Length 15;

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAA 2800  
|||||  
Db 15 AAAAAAAAAAAAAA 1

## RESULT 2828

CF302124

LOCUS CF302124 15 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--07-F16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--07-F16, mRNA sequence.

ACCESSION CF302124

VERSION CF302124.1 GI:33673885

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 15)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

Location/Qualifiers

1. .15

/organism="Oryza sativa"

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with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2180

Db 1 TTTT TTTT TTTT TTTT TTTT 15

## RESULT 2829

CF302124/c

LOCUS CF302124 15 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--07-F16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--07-F16, mRNA sequence.

ACCESSION CF302124

VERSION CF302124.1 GI:33673885

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 15)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs



JOURNAL Unpublished (2003)  
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 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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QY 2786 AAAAAAAAAAAAAA 2800  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 2830  
 CF302182  
 LOCUS 15 bp mRNA linear EST 15-AUG-2003  
 DEFINITION 7LEAF--07-H20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 sativa cDNA clone 7LEAF--07-H20, mRNA sequence.  
 ACCESSION CF302182  
 VERSION CF302182.1 GI:33673943  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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Query Match 0.5%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1 TTTT TTTT TTTT TTTT 15

RESULT 2831  
 CF302182/c  
 LOCUS 15 bp mRNA linear EST 15-AUG-2003  
 DEFINITION 7LEAF--07-H20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 sativa cDNA clone 7LEAF--07-H20, mRNA sequence.

ACCESSION CF302182  
 VERSION CF302182.1 GI:33673943  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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 RT-PCR."

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QY 2786 AAAAAAAAAAAAAA 2800  
 Db 15 AAAAAAAAAAAAAA 1

RESULT 2832  
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 DEFINITION ABF--01-I15.b1 ABF3-overexpressing transgenic rice plasmid cDNA  
 library (ABF) Oryza sativa cDNA clone ABF--01-I15, mRNA sequence.  
 ACCESSION CF307923  
 VERSION CF307923.1 GI:33679684  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.  
 REFERENCE 1 (bases 1 to 15)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Query Match 0.5%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2180  
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Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2833  
CF307923/c  
LOCUS  
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ACCESSION CF307923  
VERSION CF307923.1 GI:33679684  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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/note="Vector: PCR4-TOPO; Site\_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.5%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
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|||||  
Db 15 AAAAAA AAAAAA AAAAAA 1

RESULT 2834  
CF311159  
LOCUS  
DEFINITION ABF--06-E11.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--06-E11, mRNA sequence.  
ACCESSION CF311159  
VERSION CF311159.1 GI:33682920  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"  
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Query Match 0.5%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
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Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2835  
CF311159/c  
LOCUS  
DEFINITION ABF--06-E11.b1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--06-E11, mRNA sequence.  
ACCESSION CF311159

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VERSION      CF311159.1  GI:33682920
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Oryza sativa
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
             Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, MyongJi University
             Yongin, Kyeonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     Location/Qualifiers
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             /mol_type="mRNA"
             /cultivar="Nackdong"
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             /tissue_type="leaf"
             /dev_stage="14 days after germination"
             /lab_host="E.coli DH10B"
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             cDNA library (ABF)"
             /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
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             then used for PCR. mRNA was prepared from ABA-responsive
             element binding transcription factor 3 overexpression
             line."

             Query Match      0.5%; Score 15; DB 1; Length 15;
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             Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800
Db 15 AAAAAAAAAAAAAA 1

RESULT 2836
CF3111907
LOCUS      CF3111907
DEFINITION ABF--07-G04.b1 ABF3-overexpressing transgenic rice plasmid cDNA
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ACCESSION  CF3111907
VERSION     CF3111907.1  GI:33683668
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     Location/Qualifiers
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             element binding transcription factor 3 overexpression
             line."

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QY 2786 AAAAAAAAAAAAAA 2800
Db 15 AAAAAAAAAAAAAA 1

RESULT 2836
CF3111907
LOCUS      CF3111907
DEFINITION ABF--07-G04.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--07-G04, mRNA sequence.
ACCESSION  CF3111907
VERSION     CF3111907.1  GI:33683668
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, MyongJi University
             Yongin, Kyeonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     Location/Qualifiers
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             line."

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QY 2786 AAAAAAAAAAAAAA 2800
Db 15 AAAAAAAAAAAAAA 1
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
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element binding transcription factor 3 overexpression
line."

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QY 2166 TTTT TTTT TTTT TTTT 2180
Db 1 TTTT TTTT TTTT TTTT 15

RESULT 2837
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LOCUS      CF3111907
DEFINITION ABF--07-G04.b1 ABF3-overexpressing transgenic rice plasmid cDNA
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ACCESSION  CF3111907
VERSION     CF3111907.1  GI:33683668
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
             Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
             Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
             of Bioscience and Bioinformatics, MyongJi University
             Yongin, Kyeonggi, Korea
             Tel: 82 31 330 6193
             Fax: 82 31 321 6355
             Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     Location/Qualifiers
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             /clone_lib="ABF3-overexpressing transgenic rice plasmid
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             line."

             Query Match      0.5%; Score 15; DB 1; Length 15;
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Db 15 |||||AAAAAAAAAAAA 1

RESULT 2838  
CF313319

LOCUS  
DEFINITION HD--01-G13.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--01-G13, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Oryza sativa

REFERENCE  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL  
COMMENT Unpublished (2003)

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

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/organism="Oryza sativa"

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/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred.No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2180

Db |||||

RESULT 2839  
CF313319/c

LOCUS  
DEFINITION HD--01-G13.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--01-G13, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Oryza sativa

REFERENCE  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL  
COMMENT Unpublished (2003)

Contact: Nahm B.H.

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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

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/organism="Oryza sativa"

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/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred.No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800

Db |||||

RESULT 2840  
CF313320

LOCUS  
DEFINITION HD--01-G13.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--01-G13, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Oryza sativa

REFERENCE  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL  
COMMENT Unpublished (2003)

Contact: Nahm B.H.

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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .15

/organism="Oryza sativa"

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/cultivar="Nackdong"

/db\_xref="taxon:4530"

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/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

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/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800  
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Db 1 AAAAAAAAAAAAAA 15

RESULT 2841  
CF313320/c

LOCUS  
DEFINITION  
HD--01-G13.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--01-G13, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE  
JOURNAL  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES  
source  
1..15  
Location/Qualifiers

/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
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/clone="HD--01-G13"  
/tissue\_type="callus"  
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/lab\_host="E.coli DH10B"  
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2180  
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Db 15 TTTT TTTT TTTT TTTT TTTT 1

RESULT 2842  
CF316251

LOCUS  
DEFINITION  
HD--05-H15.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--05-H15, mRNA sequence.

ACCESSION  
VERSION  
CF316251.1 GI:33688012

KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
1 (bases 1 to 15)

AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE  
JOURNAL  
COMMENT  
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FEATURES  
source  
1..15  
Location/Qualifiers

/organism="Oryza sativa"  
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

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Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800  
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Db 1 AAAAAAAAAAAAAA 15

RESULT 2843  
CF316251/c

LOCUS  
DEFINITION  
HD--05-H15.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--05-H15, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
1 (bases 1 to 15)  
AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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FEATURES  
source  
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Location/Qualifiers

/organism="Oryza sativa"

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derived from rice Histone Deacetylase overexpression  
line."

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Db 15 TTTT TTTT TTTT TTTT 1

RESULT 2844  
CF318035  
LOCUS  
DEFINITION HD--07-P06.b1 OSHDAc1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--07-P06, mRNA sequence.

ACCESSION CF318035  
VERSION CF318035.1 GI:33689796  
KEYWORDS EST.  
SOURCE Oryza sativa

ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 15)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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FEATURES  
Location/Qualifiers

source

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/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

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/clone\_lib="OSHDAc1-overexpressing transgenic rice plasmid  
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was

reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression

line."

Query Match 0.5%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2180  
|||||

Db 1 TTTT TTTT TTTT TTTT 15

RESULT 2845

CF318035/c

LOCUS

DEFINITION HD--07-P06.b1 OSHDAc1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--07-P06, mRNA sequence.

ACCESSION CF318035

VERSION CF318035.1 GI:33689796

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 15)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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FEATURES  
Location/Qualifiers

source

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/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

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/lab\_host="E.coli DH10B"

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/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Callus was

treated with ABA(20um) for 1hr. Oligo-capped mRNA was

reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression

line."

Query Match 0.5%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800  
|||||

Db 15 AAAAAAAAAAAAAA 1

RESULT 2846

CF327434

LOCUS

DEFINITION CF327434 15 bp mRNA linear EST 18-AUG-2003  
NACL--01-O18.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--01-O18, mRNA sequence.

ACCESSION CF327434

VERSION CF327434.1 GI:33803127

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 15)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

TITLE

JOURNAL



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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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1. .15  
/organism="Oryza sativa"  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 15; DB 1; Length 15;  
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Qy 2166 TTTT TTTT TTTT TTTT 2180  
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Db 1 TTTT TTTT TTTT TTTT 15

RESULT 2847  
CF327434/c

LOCUS CF327434 15 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--01-O18.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--01-O18, mRNA sequence.

ACCESSION CF327434.1 GI:33803127  
VERSION  
KEYWORDS EST.

## SOURCE

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 15)

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

1. .15  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 15; DB 1; Length 15;  
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2786 AAAAAAAAAAAAAA 2800  
|||||  
Db 15 AAAAAAAAAAAAAA 1

## RESULT 2848

CF330195

## LOCUS

CF330195 15 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--05-N03.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--05-N03, mRNA sequence.

ACCESSION CF330195  
VERSION CF330195.1 GI:33808618  
KEYWORDS EST.

## SOURCE

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 15)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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with oligoribonucleotides and then used as templates for  
RT-PCR."

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT 2180  
|||||  
Db 1 TTTT TTTT TTTT TTTT 15

## RESULT 2849

CF330195/c

## LOCUS

CF330195 15 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--05-N03.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--05-N03, mRNA sequence.

ACCESSION CF330195  
VERSION CF330195.1 GI:33808618  
KEYWORDS EST.

## SOURCE

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 15)

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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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JOURNAL Unpublished (2003)  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source  
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RT-PCR."

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QY 2786 AAAAAAAAAAAAAA 2800  
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Db 15 AAAAAAAAAAAAAA 1

RESULT 2850  
CF330668  
LOCUS  
DEFINITION NACL--06-H16.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--06-H16, mRNA sequence.  
ACCESSION CF330668  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzae; Oryza.  
1 (bases 1 to 15)  
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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source  
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RT-PCR."

Query Match 0.5%; Score 15; DB 1; Length 15;  
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800  
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Db 15 AAAAAAAAAAAAAA 1

RESULT 2850  
CF330668  
LOCUS  
DEFINITION NACL--06-H16.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--06-H16, mRNA sequence.  
ACCESSION CF330668  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzae; Oryza.  
1 (bases 1 to 15)  
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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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FEATURES source  
Location/Qualifiers  
1. .15  
/organism="Oryza sativa"  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2180  
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Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2851  
CF330668/c  
LOCUS  
DEFINITION NACL--06-H16.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--06-H16, mRNA sequence.  
ACCESSION CF330668  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzae; Oryza.  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source  
Location/Qualifiers  
1. .15  
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/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 15; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800  
|||||  
Db 15 AAAAAAAAAAAAAA 1

RESULT 2852  
CF332178  
LOCUS  
DEFINITION NACL--08-J10.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--08-J10, mRNA sequence.  
ACCESSION CF332178  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzae; Oryza.  
1 (bases 1 to 15)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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1. .15
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
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RT-PCR."
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Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2853  
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LOCUS CF332178 15 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--08-J10.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--08-J10, mRNA sequence.

ACCESSION CF332178.1 GI:33812580  
VERSION  
KEYWORDS  
SOURCE

ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 15)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source

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/organism="Oryza sativa"
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/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
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|||||  
Db 15 AAAAAAAAAAAAAA 1

RESULT 2854  
CF336202

LOCUS CF336202 15 bp mRNA linear EST 18-AUG-2003  
DEFINITION JMT--06-C20.b1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--06-C20, mRNA sequence.

ACCESSION CF336202  
VERSION CF336202.1 GI:33820794  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 15)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source

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/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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cDNA library (JMT)"
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was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||  
Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2855  
CF336202/c

LOCUS CF336202 15 bp mRNA linear EST 18-AUG-2003  
DEFINITION JMT--06-C20.b1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--06-C20, mRNA sequence.

ACCESSION CF336202  
VERSION CF336202.1 GI:33820794  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.



```
REFERENCE
AUTHORS      1 (bases 1 to 15)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmoinate Carboxyl
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Query Match      0.5%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
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Db      15 AAAAAAAAAAAAAA 1

RESULT 2856
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LOCUS
DEFINITION E012844-024-019-M04-T7 MP1Z-ADIS-024-storage root Beta vulgaris
CDNA clone 024-019-M04 3-PRIME, mRNA sequence.
ACCESSION BQ590507
VERSION   BQ590507.1 GI:26120090
KEYWORDS  EST.
SOURCE    Beta vulgaris
ORGANISM  Beta vulgaris
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           Caryophyllales; Amaranthaceae; Beta.
           1 (bases 1 to 16)
           Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,
           Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
           and Radelof,U.
           Construction of a 'unigene' cDNA clone set by oligonucleotide
           fingerprinting allows access to 25 000 potential sugar beet genes
           Plant J. 32 (5), 845-857 (2002)
           22362189
           PUBMED
           12472698
           COMMENT
           Contact: Weissshaar B
           ADIS DNA core facility at MP1Z
           Max-Planck-Institute for Plant Breeding Research
           Carl-von-Linne Weg 10, 50829 Koeln, Germany
           Fax: 00492215062851
           Email: weisssha@mpiz-koeln.mpg.de
           Insert Length: 16 Std Error: 0.00
           Plate: 19 row: M column: 04
           Seq primer: T7; GTAATACGACTCACTATAGGCG.
           Location/Qualifiers
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REFERENCE
AUTHORS      1 (bases 1 to 15)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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methyltransferase overexpression line."

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Best Local Similarity 100.0%; Pred. No. 1.5e+03;
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QY      2786 AAAAAAAAAAAAAA 2800
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Db      15 AAAAAAAAAAAAAA 1

RESULT 2857
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LOCUS
DEFINITION S013317-024-022-P02-T7 MP1Z-ADIS-024-developing root Beta vulgaris
CDNA clone 024-022-P02 3-PRIME, mRNA sequence.
ACCESSION BQ595369
VERSION   BQ595369.1 GI:26124952
KEYWORDS  EST.
SOURCE    Beta vulgaris
ORGANISM  Beta vulgaris
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           Caryophyllales; Amaranthaceae; Beta.
           1 (bases 1 to 16)
           Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,
           Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
           and Radelof,U.
           Construction of a 'unigene' cDNA clone set by oligonucleotide
           fingerprinting allows access to 25 000 potential sugar beet genes
           Plant J. 32 (5), 845-857 (2002)
           22362189
           PUBMED
           12472698
           COMMENT
           Contact: Weissshaar B
           ADIS DNA core facility at MP1Z
           Max-Planck-Institute for Plant Breeding Research
           Carl-von-Linne Weg 10, 50829 Koeln, Germany
           Fax: 00492215062851
           Email: weisssha@mpiz-koeln.mpg.de
           Insert Length: 16 Std Error: 0.00
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           Seq primer: T7; GTAATACGACTCACTATAGGCG.
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REFERENCE
AUTHORS      1 (bases 1 to 15)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
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/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
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/clone="024-019-M04"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      15 AAAAAAAAAAAAAA 1

RESULT 2857
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LOCUS
DEFINITION S013317-024-022-P02-T7 MP1Z-ADIS-024-developing root Beta vulgaris
CDNA clone 024-022-P02 3-PRIME, mRNA sequence.
ACCESSION BQ595369
VERSION   BQ595369.1 GI:26124952
KEYWORDS  EST.
SOURCE    Beta vulgaris
ORGANISM  Beta vulgaris
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
           Caryophyllales; Amaranthaceae; Beta.
           1 (bases 1 to 16)
           Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,
           Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
           and Radelof,U.
           Construction of a 'unigene' cDNA clone set by oligonucleotide
           fingerprinting allows access to 25 000 potential sugar beet genes
           Plant J. 32 (5), 845-857 (2002)
           22362189
           PUBMED
           12472698
           COMMENT
           Contact: Weissshaar B
           ADIS DNA core facility at MP1Z
           Max-Planck-Institute for Plant Breeding Research
           Carl-von-Linne Weg 10, 50829 Koeln, Germany
           Fax: 00492215062851
           Email: weisssha@mpiz-koeln.mpg.de
           Insert Length: 16 Std Error: 0.00
           Plate: 22 row: P column: 02
           Seq primer: T7; GTAATACGACTCACTATAGGCG.
           Location/Qualifiers
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           /mol_type="mRNA"

REFERENCE
AUTHORS      1 (bases 1 to 15)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
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Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:

SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.5%; Score 15; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 15 AAAAAAAAAAAAAA 1

RESULT 2858  
CF296130/c

LOCUS CF296130 16 bp mRNA linear EST 14-AUG-2003  
DEFINITION 30DGS--06-F22.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa cDNA clone 30DGS--06-F22, mRNA sequence.

ACCESSION CF296130  
VERSION CF296130.1 GI:33665163  
KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 16)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: [bhnam@gbio.com](mailto:bhnam@gbio.com), [bhnam@bio.myongji.ac.kr](mailto:bhnam@bio.myongji.ac.kr).

FEATURES

source

1. .16

/organism="Oryza sativa"

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/db\_xref="taxon:4530"

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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2786 AAAAAAAAAAAAAA 2800  
Db 15 AAAAAAAAAAAAAA 1

RESULT 2859

CF314013/c

LOCUS

DEFINITION HD--02-G01.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--02-G01, mRNA sequence.

ACCESSION CF314013

VERSION CF314013.1 GI:33685774

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 16)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: [bhnam@gbio.com](mailto:bhnam@gbio.com), [bhnam@bio.myongji.ac.kr](mailto:bhnam@bio.myongji.ac.kr).

FEATURES

source

1. .16

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="HD--02-G01"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_host="E.coli DH10B"

/clone\_lib="OsHDAC1-overexpressing transgenic rice plasmid

cDNA library (HD)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was

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derived from rice Histone Deacetylase overexpression

line."

Query Match 0.5%; Score 15; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2786 AAAAAAAAAAAAAA 2800

Db 15 AAAAAAAAAAAAAA 1

RESULT 2860

CF329320/c

LOCUS

DEFINITION CF329320 16 bp mRNA linear EST 18-AUG-2003

NACL--04-J17.b1 Rice callus plasmid cDNA library (NACL) Oryza

sativa cDNA clone NACL--04-J17, mRNA sequence.

ACCESSION CF329320

VERSION CF329320.1 GI:33806877

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 16)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: [bhnam@gbio.com](mailto:bhnam@gbio.com), [bhnam@bio.myongji.ac.kr](mailto:bhnam@bio.myongji.ac.kr).

FEATURES

source

1. .16

/organism="Oryza sativa"  
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/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 15; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800  
|||||  
Db 15 AAAAAAAAAAAAAA 1

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BQ590207  
LOCUS  
DEFINITION BQ590207 16 bp mRNA linear EST 06-DEC-2002  
E012843-024-019-015-T7 MPIZ-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-019-015 3-PRIME, mRNA sequence.

ACCESSION BQ590207  
VERSION BQ590207.1 GI:26119790  
KEYWORDS EST.  
SOURCE Beta vulgaris

ORGANISM  
Beta vulgaris

REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 16)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

22362189

PUBMED

COMMENT

Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaa@piz-koeln.mpg.de

Insert Length: 16 Std Error: 0.00

Plate: 19 row: 0 column: 15

Seq primer: T7; GTAATACGACTCACTATAGGCG.

Location/Qualifiers

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line)"

/db\_xref="GABI:189913"

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/lab\_host="EMDH10B"

/clone\_lib="MPIZ-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:

SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:

Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.5%; Score 15; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2180  
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Db 1 TTTT TTTT TTTT TTTT 15

RESULT 2862  
BQ590207/c

LOCUS

DEFINITION BQ590207 16 bp mRNA linear EST 06-DEC-2002

E012843-024-019-015-T7 MPIZ-ADIS-024-storage root Beta vulgaris

CDNA clone 024-019-015 3-PRIME, mRNA sequence.

ACCESSION BQ590207

VERSION BQ590207.1 GI:26119790

KEYWORDS EST.

SOURCE Beta vulgaris

ORGANISM

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 16)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

and Radelof,U.

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22362189

PUBMED

COMMENT

Contact: Weisshaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisshaa@piz-koeln.mpg.de

Insert Length: 16 Std Error: 0.00

Plate: 19 row: 0 column: 15

Seq primer: T7; GTAATACGACTCACTATAGGCG.

Location/Qualifiers

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/organism="Beta vulgaris"

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/cultivar="KWS2320 (double haploid, monogerm breeding

line)"

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/clone="024-019-015"

/tissue\_type="storage root"

/lab\_host="EMDH10B"

/clone\_lib="MPIZ-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites SalI-NotI, primer sites and

orientation:

SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:

Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.5%; Score 15; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800

|||||

Db 15 AAAAAAAAAAAAAA 1



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RESULT 2863
CF291803
LOCUS
DEFINITION
14ROOT--02-G05.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--02-G05, mRNA sequence.
ACCESSION
CF291803
VERSION
CF291803.1 GI:33660836
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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with oligoribonucleotides and then used as templates for
RT-PCR."

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAA 2799
Db 2 GAAAAAAAAAAAAA 16

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DEFINITION
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library (ABF) Oryza sativa cDNA clone ABF--08-G13, mRNA sequence.
ACCESSION
CF312586
VERSION
CF312586.1 GI:33684347
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
```

```
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
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then used for PCR. mRNA was prepared from ABA-responsive
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line."

Query Match 0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2174 TTTTNTTTTNTTTTAA 2188
Db 1 TTTTNTTTTNTTTTAA 15

RESULT 2865
CF318894
LOCUS
DEFINITION
HD--09-D06.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--09-D06, mRNA sequence.
ACCESSION
CF318894
VERSION
CF318894.1 GI:33690655
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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/organism="Oryza sativa"
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derived from rice Histone Deacetylase overexpression
line."
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Query Match      0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 TTTTttttttttttt 15

RESULT 2866
CF318894/c
LOCUS
DEFINITION
HD--09-D06.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--09-D06, mRNA sequence.
ACCESSION
CF318894
VERSION
CF318894.1 GI:33690655
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2800
Db      15 AAAAAAAAAAAAAA 1

RESULT 2867
CF327923
LOCUS
DEFINITION
NACL--02-J18.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--02-J18, mRNA sequence.
ACCESSION
CF327923
VERSION
CF327923.1 GI:33804096
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
```

```
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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/mol_type="mRNA"
/cultivar="Nackdong"
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/lab_host="E.coli DH10B"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 TTTTttttttttttt 15

RESULT 2868
CF327923/c
LOCUS
DEFINITION
NACL--02-J18.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--02-J18, mRNA sequence.
ACCESSION
CF327923
VERSION
CF327923.1 GI:33804096
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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JOURNAL
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 TTTTttttttttttt 15

RESULT 2869
CF327923/c
LOCUS
DEFINITION
NACL--02-J18.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--02-J18, mRNA sequence.
ACCESSION
CF327923
VERSION
CF327923.1 GI:33804096
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .16
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/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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RT-PCR."

Query Match      0.5%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2870
CF327923/c
LOCUS
DEFINITION
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sativa cDNA clone NACL--02-J18, mRNA sequence.
ACCESSION
CF327923
VERSION
CF327923.1 GI:33804096
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 15; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800  
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Db 15 AAAAAAAAAAAAAA 1

## RESULT 2869

CF328223  
LOCUS  
DEFINITION NACL--03-A10.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--03-A10, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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Query Match 0.5%; Score 15; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTT 2180  
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Db 1 TTTTTTTTTTTTTT 15

## RESULT 2870

CF328223/c  
LOCUS  
DEFINITION NACL--03-A10.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--03-A10, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
1 (bases 1 to 16)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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/organism="Oryza sativa"  
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/clone="NACL--03-A10"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 15; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800  
|||||  
Db 15 AAAAAAAAAAAAAA 1

## RESULT 2871

CF298341  
LOCUS  
DEFINITION 7LEAF--01-K24.b1 Rice leaf plasmid cDNA library 11 (7LEAF) Oryza  
sativa cDNA clone 7LEAF--01-K24, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source  
1. .17  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--01-K24"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"



/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 15; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT 2180  
Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2872  
CF301359 18 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--06-D05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--06-D05, mRNA sequence.

ACCESSION CF301359  
VERSION CF301359.1 GI:33673120  
KEYWORDS EST.  
SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 18)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..18  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--06-D05"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 15; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT 2180  
Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2873  
CF325356 19 bp mRNA linear EST 18-AUG-2003  
LOCUS JMT1--03-A08.g1 AtJMT-overexpressing transgenic rice lambda phage  
DEFINITION cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-A08, mRNA  
sequence.

ACCESSION CF325356  
VERSION CF325356.1 GI:33798994  
KEYWORDS EST.  
SOURCE Oryza sativa

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..19  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="JMT1--03-A08"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli SOLR"  
/clone\_lib="AtJMT-overexpressing transgenic rice lambda  
phage cDNA library (JMT1)"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'  
end with EcoRI and 3' end with XhoI site. mRNA was  
prepared from Arabidopsis Jasmonate Carboxyl  
methyltransferase overexpression line."

Query Match 0.5%; Score 15; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT 2180  
Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2874

CF325356/c

LOCUS

DEFINITION

CF325356 19 bp mRNA linear EST 18-AUG-2003  
JMT1--03-A08.g1 AtJMT-overexpressing transgenic rice lambda phage  
cDNA library (JMT1) Oryza sativa cDNA clone JMT1--03-A08, mRNA  
sequence.

ACCESSION CF325356

VERSION CF325356.1 GI:33798994

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

COMMENT

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..19  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	0.5%;	Score 15;	DB 1;	Length 19;
Best Local Similarity	100.0%;	Pred.No.	2.7e+03;	
Matches 15;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
2785	GAAGAAAAA	AAAAAAAAA	2799	
15	GAAGAAAAA	AAAAAAAAA	1	

RESULT	2876
AZ950028	
LOCUS	AZ950028
DEFINITION	2M0213L19R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0213L19 R, genomic survey sequence.
	linear DNA 19 bp
	GSS 27-APR-2001

VERSION AZ950028.1 GI:13821255  
KEYWORDS GSS.

RELAYED SOURCE	ORGANISM	CCG.
	Mus musculus	(house mouse)
	Mus musculus	

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

**JOURNAL COMMENT**  
 Unpublished (2000)  
 Contact: Robert B. Weiss

Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0213 row: L column: 19  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 19

FEATURES  
source

/sex="female"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC2M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (female) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnares/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were







adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800  
|||||  
Db 1 AAAAAAAAAAAAAA 15

RESULT 2882  
CF309614/c

LOCUS CF309614 21 bp mRNA linear EST 15-AUG-2003  
DEFINITION ABF--03-N20.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--03-N20, mRNA sequence.

ACCESSION CF309614  
VERSION CF309614.1 GI:33681375  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 21)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1..21

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="ABF--03-N20"

/tissue\_type="Leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"

/note="Vector: PCR4-TOPO; Site\_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.5%; Score 15; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800  
|||||  
Db 18 AAAAAAAAAAAAAA 4

RESULT 2883

CF282313

LOCUS

DEFINITION

14ETL--09-M08.g1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa cDNA clone 14ETL--09-M08, mRNA sequence.

ACCESSION CF282313

VERSION CF282313.1 GI:33659700

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 21)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1..21

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="14ETL--09-M08"

/tissue\_type="Leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"

/note="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 15; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800

|||||

Db 7 AAAAAAAAAAAAAA 21

RESULT 2884

CF282313/c

LOCUS

DEFINITION

14ETL--09-M08.g1 Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa cDNA clone 14ETL--09-M08, mRNA sequence.

ACCESSION CF282313

VERSION CF282313.1 GI:33659700

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 21)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnaahm@gbio.com, bhnaahm@bio.myongji.ac.kr.

FEATURES  
source

Location/Qualifiers  
1. .21  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="14ETL--09-M08"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 15; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT 2180  
Db 21 TTTT TTTT TTTT TTTT TTTT 7

RESULT 2885  
AZ785791/c

LOCUS  
DEFINITION  
1M0030019F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0030019 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0030 row: 0 column: 19  
Seq primer: CGTTGTAACACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.

FEATURES  
source

Location/Qualifiers  
1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0030019"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2785 GAAAAA AAAAAA AAAAA 2799  
Db 15 GAAAAA AAAAAA AAAAA 1

RESULT 2886  
AZ818565

LOCUS  
DEFINITION  
2M0088K10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0088K10 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0088 row: K column: 10  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.

FEATURES  
source

Location/Qualifiers  
1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0088K10"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a





polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2180  
Db 1 TTTT TTTT TTTT TTTT TTTT 15

RESULT 2889  
AZ963501/c  
LOCUS AZ963501 21 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0232M07R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0232M07 R, genomic survey sequence.

ACCESSION AZ963501  
VERSION AZ963501.1 GI:13834728  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0232 row: M column: 07  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.

FEATURES Location/Qualifiers  
1..21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0232M07"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.2e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA AAAAA 2800  
Db 15 AAAAAA AAAAAA AAAAA 1

RESULT 2890  
AZ317017/c  
LOCUS AZ317017 22 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0035P09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0035P09 F, genomic survey sequence.

ACCESSION AZ317017  
VERSION AZ317017.1 GI:10365400  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0035 row: P column: 09  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.

FEATURES Location/Qualifiers  
1..22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0035P09"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800  
|||||  
Db 22 AAAAAAAAAAAAAA 8

RESULT 2891  
CF308058/c

LOCUS CF308058 23 bp mRNA linear EST 15-AUG-2003  
DEFINITION ABF--01-L15.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--01-L15, mRNA sequence.

ACCESSION CF308058  
VERSION CF308058.1 GI:33679819  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 23)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source  
1. .23  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="ABF--01-L15"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.5%; Score 15; DB 1; Length 23;  
Best Local Similarity 78.3%; Pred. No. 3.5e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAAAAAAAAAA 2801  
|||  
Db 23 AGTGTAGTAAAAAAAAAAAAA 1

RESULT 2892

AZ390689

LOCUS

DEFINITION 1M0152A18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0152A18 F, genomic survey sequence.

ACCESSION

VERSION AZ390689.1 GI:10505732

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

REFERENCE

AUTHORS

1 (bases 1 to 23)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00

Plate: 0152 row: A column: 18

Seq primer: CGTTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

FEATURES

source

1. .23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0152A18"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to

adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match

0.5%; Score 15; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 3.5e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAA 2799

|||||

Db 9 GAAAAAAAAAAAAA 23

RESULT 2893

AZ654389/c





clone UUGC1M0573A16 F, genomic survey sequence.

AZ771221

AZ771221.1 GI:12893248

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0573 row: A column: 16

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1. .23

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0573A16"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15; DB 1; Length 23;

Best Local Similarity 100.0%; Pred. No. 3.5e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2180

Db |||||

15 TTTT TTTT TTTT TTTT TTTT 1

RESULT 2896

AZ810709/c

LOCUS

DEFINITION

2M0076M20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0076M20 F, genomic survey sequence.

AZ810709

AZ810709.1 GI:12978228

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 23)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0076 row: M column: 20

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

Location/Qualifiers

1. .23

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0076M20"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15; DB 1; Length 23;

Best Local Similarity 78.3%; Pred. No. 3.5e+03;

Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1817 TAAGTTT TAGAATCTTTTAAATA 1839

Db |||||

23 TAAGTTT TAAAAATTTTATTATA 1

RESULT 2897

TA120E05P

LOCUS

DEFINITION

T. brucei sheared genomic DNA clone 120e05, forward sequence, genomic survey sequence.

ACCESSION

AL464555

VERSION AL464555.1 GI:11833135  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk  
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution ( 4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T\_brucei/.  
FEATURES  
source  
1. .23  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="120e05"  
Query Match 0.5%; Score 15; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2174 TTTT TTTT TTTT TTTT TTTTAA 2188  
|||||  
Db 1 TTTT TTTT TTTT TTTT TTTTAA 15  
RESULT 2898  
TA155F12Q  
LOCUS TA155F12Q 24 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 155f12, reverse sequence, genomic survey sequence.  
ACCESSION AL472698  
VERSION AL472698.1 GI:11838089  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk  
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution ( 4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T\_brucei/.  
FEATURES  
source  
1. .24  
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/mol\_type="genomic DNA"  
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/db\_xref="taxon:5691"  
/clone="155f12"  
Query Match 0.5%; Score 15; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2786 AAAAAAAAAAAAAA 2800  
|||||  
Db 1 AAAAAAAAAAAAAA 15  
RESULT 2899  
TA319G03Q/c  
LOCUS TA319G03Q 26 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 319g03, reverse sequence, genomic survey sequence.  
ACCESSION AL492820  
VERSION AL492820.1 GI:11867590  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk  
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution ( 4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T\_brucei/.  
FEATURES  
source  
1. .26  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="319g03"  
Query Match 0.5%; Score 15; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2786 AAAAAAAAAAAAAA 2800  
|||||  
Db 26 AAAAAAAAAAAAAA 12  
RESULT 2900  
AW246455/c



LOCUS AW246455 27 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2821693.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821693 3',  
mRNA sequence.  
ACCESSION AW246455  
VERSION AW246455.1 GI:6589448  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other\_ESTs: 2821693.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center.  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 10  
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 27 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: L1CM7 row: H column: 14  
High quality sequence stop: 10.  
FEATURES  
source  
1..27  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821693"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
Query Match 0.5%; Score 15; DB 1; Length 27;  
Best Local Similarity 78.3%; Pred. No. 3.3e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 2782 ATTGAAAAAATAAAAAAAAAAAAAA 2804  
||| ||||| ||||| ||||| |||||  
Db 26 ATAAAAAAAACATGAAAAAAA 4  
RESULT 2901  
TA224C08P 29 bp DNA linear GSS 13-DEC-2000  
LOCUS T. brucei sheared genomic DNA clone 224c08, forward sequence,  
genomic survey sequence.  
DEFINITION  
ACCESSION AL480654  
VERSION AL480654.1 GI:11846423  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei

ORGANISM Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.  
REFERENCE 1 (bases 1 to 29)  
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,  
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,  
Melville,S.E., Rajandream,M.A. and Barrell,B.G.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nhl@sanger.ac.uk  
COMMENT Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available  
at http://www.sanger.ac.uk/Projects/T\_brucei/.  
FEATURES  
source  
1..29  
Location/Qualifiers  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="224c08"  
Query Match 0.5%; Score 15; DB 1; Length 29;  
Best Local Similarity 78.3%; Pred. No. 3.1e+03;  
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 2779 AGAATTGAAAAAATAAAAAAAAAA 2801  
||||| | ||||| ||||| |||||  
Db 7 AGAAGGGGGGAAAAAATAAAAAAAAAA 29  
RESULT 2902  
AZ504854  
LOCUS 1M0345D16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0345D16 F, genomic survey sequence.  
ACCESSION AZ504854  
VERSION AZ504854.1 GI:10686170  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 33)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0345 row: D column: 16  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends

FEATURES  
source  
High quality sequence stop: 33.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0345D16"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 15; DB 1; Length 33;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 AAAAAAAAAAAAAA 2800  
Db 2 AAAAAAAAAAAAAA 16

RESULT 2903  
CF329020/c  
LOCUS  
DEFINITION NACL--04-D03.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-D03, mRNA sequence.  
ACCESSION CF329020  
VERSION CF329020.1 GI:33806277  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 18)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
Location/Qualifiers  
1. .18  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="NACL--04-D03"  
/tissue\_type="callus"

/dev stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAA 2802  
Db 18 GAGTAAAAAAAAAAAA 1

RESULT 2904  
AW246505  
LOCUS  
DEFINITION AW246505 18 bp mRNA linear EST 07-JAN-2000  
2821585.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821585 3', mRNA sequence.

ACCESSION AW246505  
VERSION AW246505.1 GI:6589498  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 18)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other ESTs: 2821585.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 18 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 18 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: L1CM7 row: D column: 2  
High quality sequence stop: 18.  
Location/Qualifiers  
1. .18  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:2821585"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 7"  
/note="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

FEATURES  
source

Query Match 0.5%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2166 TTTTCTTTTCTTTTCTTTT 2183  
Db 1 TTTTCTTTTCTTTTCTTTT 18

RESULT 2905  
AW246505/c  
LOCUS  
DEFINITION  
AW246505 18 bp mRNA linear EST 07-JAN-2000  
2821585.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821585 3',  
mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 18)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2821585.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 18  
contiguous PHRED high quality bases followed by vector sequence. Very  
Low Quality Sequence: Trace file contained 18 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: LCM7 row: D column: 2  
High quality sequence stop: 18.

FEATURES  
source  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821585"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 7"  
/note="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
Db 18 AAATAAAGAAAAAAAAAAAA 1

RESULT 2906  
AW247875/c  
LOCUS  
DEFINITION

AW247875 18 bp mRNA linear EST 07-JAN-2000  
2820433.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2820433 3',  
mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 18)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2820433.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 10  
contiguous PHRED high quality bases followed by vector sequence. Very  
Low Quality Sequence: Trace file contained 18 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: LLCM4 row: D column: 2  
High quality sequence stop: 10.

FEATURES  
source  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:2820433"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 7"  
/note="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 14.8; DB 1; Length 18;  
Best Local Similarity 88.9%; Pred. No. 2.6e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2778 TAGAATTGAAAAAAAAA 2795  
Db 18 TAGGCTTGAAAAAAAAA 1

RESULT 2907  
CF309858  
LOCUS  
DEFINITION  
CF309858 19 bp mRNA linear EST 15-AUG-2003  
ABF--04-D16.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--04-D16, mRNA sequence.



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ACCESSION   CF309858
VERSION     CF309858.1  GI:33681619
KEYWORDS
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source          1..19
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="ABF--04-D16"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
                     /clone_lib="ABF3-overexpressing transgenic rice plasmid
                     CDNA library (ABF)"
                     /note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

Query Match      0.5%;  Score 14.8;  DB 1;  Length 19;
Best Local Similarity 88.9%;  Pred. No. 2.9e+03;
Matches 16;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      2786  AAAAAAAAAAAAAAAAAAAAAA 2803
          |||||
Db       2  AAAAAAAAAAAAAAAAAACATA 19

RESULT 2908
AZ475079
LOCUS      AZ475079
DEFINITION 1M0293B17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0293B17 F, genomic survey sequence.
ACCESSION  AZ475079
VERSION    AZ475079.1  GI:10633204
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 19)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
```

```
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000  Std Error: 0.00
Plate: 0293  row: B  column: 17
Seg primer: CGTTGTAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0293B17"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adapted DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adapted mouse DNA was annealed to
                     adapted vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."

Query Match      0.5%;  Score 14.8;  DB 1;  Length 19;
Best Local Similarity 88.9%;  Pred. No. 2.9e+03;
Matches 16;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

QY      898  GGCTGAAGTACAGAGCG 915
          |||||
Db       2  GGCGGAAGCACAGAGCG 19

RESULT 2909
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LOCUS      AZ789309
DEFINITION 2M0036L22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0036L22 R, genomic survey sequence.
ACCESSION  AZ789309
VERSION    AZ789309.1  GI:12929974
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 19)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
```

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0036 row: L column: 22  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
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Location/Qualifiers  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0036L22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 2.9e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2165 CTTTTTTTTTTTTTTTTT 2182  
|||||  
Db 2 CTTTTTTTCTTTCT 19

RESULT 2910  
AZ789309/c  
LOCUS  
DEFINITION 2M0036L22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0036L22 R, genomic survey sequence.

ACCESSION AZ789309  
VERSION AZ789309.1 GI:12929974

KEYWORDS  
SOURCE  
ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
COMMENT Unpublished (2000)  
Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0036 row: L column: 22  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source

Location/Qualifiers  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0036L22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 2.9e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802  
|||||  
Db 18 GAAAGAAAAAAAAAAGA 1

RESULT 2911  
AZ962226/c

LOCUS  
DEFINITION 2M0231A02F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0231A02 F, genomic survey sequence.

ACCESSION AZ962226  
VERSION AZ962226.1 GI:13833453

KEYWORDS  
SOURCE  
ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
COMMENT Unpublished (2000)  
Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0231 row: A column: 02  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

FEATURES

source  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
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/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.5%; Score 14.8; DB 1; Length 19;  
Best Local Similarity 88.9%; Pred. No. 2.9e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2155 TTTTTCCTCCTTTT 2172  
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Db 18 TTTTTCCTCCTTTT 1

RESULT 2912

CF297010/c  
LOCUS CF297010 20 bp mRNA linear EST 14-AUG-2003  
DEFINITION 30DGS--07-J24.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa cDNA clone 30DGS--07-J24, mRNA sequence.

ACCESSION CF297010  
VERSION CF297010.1 GI:33666043  
KEYWORDS EST.

SOURCE

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 20)

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source  
1..20  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"

/db\_xref="taxon:4530"  
/clone="30DGS--07-J24"  
/tissue\_type="leaf"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 3.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2785 GAAAAA 2802  
|||  
Db 18 GACCAAAAAA 1

RESULT 2913

CF313751/c

LOCUS CF313751 20 bp mRNA linear EST 15-AUG-2003  
DEFINITION HD--01-P23.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--01-P23, mRNA sequence.

ACCESSION CF313751

VERSION CF313751.1 GI:33685512

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 20)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..20  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
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/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.5%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 3.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2785 GAAAAA 2802  
|||  
Db 18 GACCAAAAAA 1

RESULT 2914

CF313752



LOCUS CF313752 20 bp mRNA linear EST 15-AUG-2003  
DEFINITION HD--01-P23.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--01-P23, mRNA sequence.  
ACCESSION CF313752  
VERSION CF313752.1 GI:33685513  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source 1..20  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="HD--01-P23"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 3.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAA 2802  
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Db 3 GAGCAAAAAAAAAAAAAA 20

RESULT 2915  
AZ828826/c  
LOCUS AZ828826 20 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0106O01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0106O01 F, genomic survey sequence.  
ACCESSION AZ828826  
VERSION AZ828826.1 GI:12998734  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 1000 Std Error: 0.00  
Plate: 0106 row: 0 column: 01  
Seq primer: CGTTGTAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers 1..20  
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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source 1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.8; DB 1; Length 20;  
Best Local Similarity 88.9%; Pred. No. 3.2e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2528 TATATATACAGGGTATTA 2545  
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Db 20 TATATATAAATGGTATTA 3

RESULT 2916  
AZ625662  
LOCUS AZ625662 21 bp DNA linear GSS 13-DEC-2000  
DEFINITION 1M0465C23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0465C23 F, genomic survey sequence.  
ACCESSION AZ625662  
VERSION AZ625662.1 GI:11747852  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0465 row: C column: 23  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.

FEATURES

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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.5%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 3.4e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
|||||  
Db 2 AAAAAAAAAAAATATA 19

RESULT 2917  
AU254546/c

LOCUS

DEFINITION AU254546 3'-directed mouse cDNA library Mus musculus cDNA clone  
BED0002442 3', mRNA sequence.

ACCESSION AU254546

VERSION AU254546.1 GI:20316429

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS Kato, K. and Matoba, R.

TITLE Generation of expressed sequence tags from mouse brain

JOURNAL Unpublished (2002)

COMMENT Contact: Kikuya Kato

Graduate School of Biological Sciences

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Fax: 81-743-72-5589

Email: [kkato@bs.aist-nara.ac.jp](mailto:kkato@bs.aist-nara.ac.jp)

URL: <http://love2.aist-nara.ac.jp/BED/index.html>.

FEATURES

Location/Qualifiers

source

1. .21  
/organism="Mus musculus"  
/mol\_type="mRNA"  
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/tissue\_type="brain"  
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Query Match 0.5%; Score 14.8; DB 1; Length 21;  
Best Local Similarity 88.9%; Pred. No. 3.4e+03;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2783 TTGAAAAAAAAAAAAA 2800  
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Db 20 TTGAAAGAAAAAAAAAGA 3

RESULT 2918  
AZ331619/c

LOCUS

DEFINITION AZ331619 21 bp DNA linear GSS 29-SEP-2000  
1M0059K09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0059K09 R, genomic survey sequence.

ACCESSION AZ331619

VERSION AZ331619.1 GI:10394486

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)

Insert Length: 10000 Std Error: 0.00

Plate: 0059 row: K column: 09

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

source

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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number









JOURNAL  
COMMENT  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0034 row: H column: 14  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
1. .21  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0034H14"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 3.5e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2674 GTGTGTGGTGGTGAATGGAG 2694  
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Db 21 GTGTGTGTGTGTGAGAGAG 1

RESULT 2926  
AZ788269  
LOCUS  
DEFINITION  
2M0035D18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0035D18 F, genomic survey sequence.  
ACCESSION  
AZ788269  
VERSION  
AZ788269.1 GI:12927898  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE  
1 (bases 1 to 21)  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0035 row: D column: 18  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.  
Location/Qualifiers  
1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0035D18"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.6; DB 1; Length 21;  
Best Local Similarity 81.0%; Pred. No. 3.5e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2674 GTGTGTGGTGGTGAATGGAG 2694  
|||||||  
Db 1 GTGTGTGTGGTGTGTAGGAG 21

RESULT 2927  
AZ845735/c  
LOCUS  
DEFINITION  
2M0145J07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0145J07 R, genomic survey sequence.  
ACCESSION  
AZ845735  
VERSION  
AZ845735.1 GI:13015643  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE  
1 (bases 1 to 22)  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL  
Unpublished (2000)



## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0145 row: J column: 07  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.

## FEATURES

source

## FEATURES

source

1. .22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0145J07"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 3.6e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2779 AGAATTGAAAAA 2799  
Db 21 AAAAGCCAAAAA 1

## RESULT 2928

AZ470212

LOCUS

AZ470212 22 bp DNA linear GSS 04-OCT-2000  
1M0284L09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0284L09 F, genomic survey sequence.

ACCESSION

VERSION AZ470212.1 GI:10628337

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 22)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0284 row: L column: 09

Seq primer: CGTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 22.

## FEATURES

source

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0284L09"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 3.6e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2162 CTCCTTTT 2182  
Db 1 CTGGTTCTTTT 21

## RESULT 2929

AA888191/c

LOCUS

AA888191 22 bp mRNA linear EST 31-MAR-1998  
of82a05.s1 NCI CGAP L15 Homo sapiens cDNA clone IMAGE:1436816 3'  
similar to TR:Q33563 Q33563 EATRO 164 KINETOPLAST ;, mRNA sequence.

ACCESSION

VERSION AA888191.1 GI:3003866

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 22)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

R. Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cdNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.

FEATURES  
source

Location/Qualifiers  
1. .22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1436816"  
/tissue\_type="hepatic adenoma"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Li5"  
/note="Organ: liver; Vector: pCMV-SPORT4; Site\_1: Sali;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 0.8 kb."

Query Match 0.5%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 3.6e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2157 TTTTCTCTCTTTTCTTTTCTTTT 2177  
||| ||| ||| ||| ||| ||| ||| |||  
Db 22 TTGTTCTCTCTTTTATTTGTT 2

RESULT 2930  
AI184101/c

LOCUS AI184101 22 bp mRNA linear EST 29-OCT-1998  
DEFINITION ge24d08.x1 Soares fetal\_lung NbHL19W Homo sapiens cDNA clone  
IMAGE:1739919 3' similar to TR:000483 O00483 NADH:UBIQUINONE  
OXIDOREDUCTASE MLRQ SUBUNIT. ;, mRNA sequence.

ACCESSION AI184101  
VERSION AI184101.1 GI:3734739  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 22)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Trace considered overall poor quality  
Insert Length: 2216 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers

FEATURES  
source

1. .22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1739919"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal\_lung NbHL19W"  
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer  
[5'-TGTTACCAATCTGAAGTGGAGCGCGCAATTTTCTTTTCTTTT-3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT7T3 vector

(Pharmacia). Library went through one round of  
normalization to a Cot = 5. Library constructed by Bento  
Soares and M.Fatima Bonaldo. This library was constructed  
from the same fetus as the fetal heart library, Soares  
fetal heart NbHL19W."

Query Match 0.5%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 3.6e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2262 GCATATTATTTCAGATGTTT 2282  
||||| ||| ||| ||| ||| ||| ||| |||  
Db 21 GCATGTTCAATCCAGATGTTT 1

RESULT 2931  
BQ595200/c

LOCUS BQ595200 22 bp mRNA linear EST 06-DEC-2002  
DEFINITION E012709-024-023-E04-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
cDNA clone 024-023-E04 5-PRIME, mRNA sequence.

ACCESSION BQ595200  
VERSION BQ595200.1 GI:26124783  
KEYWORDS EST.  
SOURCE Beta vulgaris

ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 22)

REFERENCE Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)

JOURNAL MEDLINE  
PUBMED 12472698

COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: [weisshaar@mpiz-koeln.mpg.de](mailto:weisshaar@mpiz-koeln.mpg.de)  
Insert Length: 22 Std Error: 0.00  
Plate: 23 row: E column: 04  
Seq primer: SP6; CATACGATTAGGTGACACTATAG.  
Location/Qualifiers

FEATURES  
source

1. .22  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:191654"  
/db\_xref="taxon:161934"  
/clone="024-023-E04"  
/tissue\_type="developing root"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-developing root"  
/note="Vector: pCMVSPORT6; Site\_1: Sali; Site\_2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
Project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.5%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 3.6e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1775 TTTTGTGAACCCCATCTTT 1795  
Db 22 TTTTGTGAACCCCTTTT 2

RESULT 2932  
BX563723  
LOCUS  
DEFINITION BX563723 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse68e02\_plc, mRNA sequence.  
ACCESSION BX563723  
VERSION BX563723.1 GI:33430936  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 22)  
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes  
JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix g1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES  
source  
1..22  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
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/clone="Tse68e02\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected gut"  
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.5%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 3.6e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2161 TCTCCTTTTCTTTTCTTTTCTTTT 2181  
Db 2 TCTAAATATTTTCTTTTCTTTTCTTTT 22

RESULT 2933  
AZ326642/c  
LOCUS  
DEFINITION 1M0049D09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0049D09 R, genomic survey sequence.  
ACCESSION AZ326642  
VERSION AZ326642.1 GI:10384599  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AZ326642 22 bp DNA linear GSS 29-SEP-2000

REFERENCE 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0049 row: D column: 09  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.  
Location/Qualifiers  
1..22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0049D09"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 3.6e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2156 TTTTTCCTCTTTTCTTTTCTTTT 2176  
Db 22 TTGTTGCTCCATTTTCTTTTATT 2

RESULT 2934  
AZ854229/c  
LOCUS  
DEFINITION AZ854229 2M0157C14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0157C14 R, genomic survey sequence.  
ACCESSION AZ854229  
VERSION AZ854229.1 GI:13043139  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 22)

AZ854229 22 bp DNA linear GSS 21-FEB-2001



AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0157 row: C column: 14  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.  
FEATURES  
source  
1. .22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0157C14"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.5%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 3.6e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2166 TTTTCTTTCTTTCTTTCTTT 2186  
Db 22 TTTTCTTTCTTTCTTTCTTT 2

RESULT 2935  
AU267170/c  
LOCUS  
DEFINITION  
AU267170 VS Dictyostelium discoideum cDNA clone VSH269 5', mRNA  
sequence.  
ACCESSION  
AU267170  
VERSION  
AU267170.1 GI:20525968  
KEYWORDS  
EST.  
SOURCE  
Dictyostelium discoideum  
ORGANISM  
Dictyostelium discoideum  
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
REFERENCE  
1 (bases 1 to 23)  
AUTHORS  
Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,  
Takeuchi,I., Kohara,Y. and Tanaka,Y.

AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0157 row: C column: 14  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.  
FEATURES  
source  
1. .22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0157C14"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.5%; Score 14.6; DB 1; Length 22;  
Best Local Similarity 81.0%; Pred. No. 3.6e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2166 TTTTCTTTCTTTCTTTCTTT 2186  
Db 22 TTTTCTTTCTTTCTTTCTTT 2

RESULT 2935  
AU267170/c  
LOCUS  
DEFINITION  
AU267170 VS Dictyostelium discoideum cDNA clone VSH269 5', mRNA  
sequence.  
ACCESSION  
AU267170  
VERSION  
AU267170.1 GI:20525968  
KEYWORDS  
EST.  
SOURCE  
Dictyostelium discoideum  
ORGANISM  
Dictyostelium discoideum  
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
REFERENCE  
1 (bases 1 to 23)  
AUTHORS  
Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,  
Takeuchi,I., Kohara,Y. and Tanaka,Y.

TITLE  
Population analysis of cDNAs from unicellular and multicellular  
stages of Dictyostelium discoideum  
JOURNAL  
Unpublished (2002)  
COMMENT  
Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: hideko@biol.tsukuba.ac.jp.  
FEATURES  
source  
1. .23  
/organism="Dictyostelium discoideum"  
/mol\_type="mRNA"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="VSH269"  
/sex="mat A"  
/dev\_stage="vegetative"  
/clone\_lib="VS"  
Query Match 0.5%; Score 14.6; DB 1; Length 23;  
Best Local Similarity 81.0%; Pred. No. 3.6e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2166 TTTTCTTTCTTTCTTTCTTT 2186  
Db 23 TTTTCTTTCTTTCTTTCTTT 3

RESULT 2936  
AW332764/c  
LOCUS  
DEFINITION  
S12F12 AGS-1 Pneumocystis carinii cDNA 3', mRNA linear EST 31-JAN-2000  
ACCESSION  
AW332764  
VERSION  
AW332764.1 GI:6829121  
KEYWORDS  
EST.  
SOURCE  
Pneumocystis carinii  
ORGANISM  
Pneumocystis carinii  
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;  
Pneumocystidaceae; Pneumocystis.  
REFERENCE  
1 (bases 1 to 23)  
AUTHORS  
Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,  
Edman,J.C., Kovacs,J. and Cushion,M.  
TITLE  
Expressed sequence tags from Pneumocystis carinii  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Staben C  
School of Biological Sciences  
University of Kentucky  
101 Morgan Building, University of Kentucky, Lexington, KY  
40506-0225, USA  
Tel: 606 257 2161  
Fax: 606 257 1717  
Email: staben@pop.uky.edu.  
FEATURES  
source  
1. .23  
/organism="Pneumocystis carinii"  
/mol\_type="mRNA"  
/db\_xref="taxon:4754"  
/lab\_host="E. coli"  
/clone\_lib="AGS-1"  
/note="Vector: Lambda ZAP II; Site\_1: EcoRI; Site\_2: XhoI;  
P. carinii organisms (3x10e9) from a single rat (99-1-6,  
sacrificed on 3/17/99) at Cincinnati VA facilities.  
Trizol extracted RNA. Oligo dt priming, standard  
conditions described by vendor, Stratagene. Further  
details see www.uky.edu/project/Pneumocystis/"

Query Match 0.5%; Score 14.6; DB 1; Length 23;  
Best Local Similarity 81.0%; Pred. No. 3.6e+03;  
Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2170 TTTTCTTTCTTTCTTTCTTT 2190



Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source  
1. .16  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="ABF--08-G13"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid  
cDNA library (ABF)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.5%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 2.3e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2783 TTGAAAAA 2798

Db 16 TTAAAAA 1

## RESULT 2940

## CF317778

## LOCUS

DEFINITION CF317778 16 bp mRNA linear EST 15-AUG-2003  
library (HD) Oryza sativa cDNA clone HD--07-J13, mRNA sequence.

## ACCESSION

VERSION CF317778.1 GI:33689539

## KEYWORDS

## SOURCE

## ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

## AUTHORS

1 (bases 1 to 16)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

## TITLE

## JOURNAL

## COMMENT

Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

## source

1. .16  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="HD--07-J13"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.5%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 2.3e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTT 2181

Db 1 TTTG 16

## RESULT 2941

## CF317778/c

## LOCUS

DEFINITION CF317778 16 bp mRNA linear EST 15-AUG-2003  
library (HD) Oryza sativa cDNA clone HD--07-J13, mRNA sequence.

## ACCESSION

VERSION CF317778.1 GI:33689539

## KEYWORDS

## SOURCE

## ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

## AUTHORS

1 (bases 1 to 16)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

## TITLE

## JOURNAL

## COMMENT

Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

## source

1. .16  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="HD--07-J13"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

## Query Match

0.5%; Score 14.4; DB 1; Length 16;  
Best Local Similarity 93.8%; Pred. No. 2.3e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAA 2801

Db 16 AAAAAA 1

## RESULT 2942

## AW247165

## LOCUS

DEFINITION AW247165 17 bp mRNA linear EST 07-JAN-2000  
2819675.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819675 3',  
mRNA sequence.

## ACCESSION

VERSION AW247165.1 GI:6590158

## KEYWORDS

## SOURCE

## ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 17)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2819675.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: DCTD/FTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
<http://www.genome.washington.edu> Low Quality Sequence: 17  
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 17 contiguous distinct  
peaks following vector sequence.  
Plate: LLCM2 row: D column: 12  
High quality sequence stop: 17.  
Location/Qualifiers  
1. 17  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2819675"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

FEATURES  
source

Query Match 0.5%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.6e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2181  
|||||  
Db 2 TTTT TTTT TTTT TTTT 17

RESULT 2943  
AW247165/C  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AW247165 17 bp mRNA linear EST 07-JAN-2000  
2819675.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819675 3',  
mRNA sequence.  
AW247165  
AW247165.1 GI:6590158  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 17)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2819675.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: DCTD/FTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
<http://www.genome.washington.edu> Low Quality Sequence: 17  
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 17 contiguous distinct  
peaks following vector sequence.  
Plate: LLCM2 row: D column: 12  
High quality sequence stop: 17.  
Location/Qualifiers  
1. 17  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2819675"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

FEATURES  
source

Query Match 0.5%; Score 14.4; DB 1; Length 17;  
Best Local Similarity 93.8%; Pred. No. 2.6e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2801  
|||||  
Db 17 AAAAAACAAAAAAAAAAA 2

RESULT 2944  
AZ774536/C  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AZ774536 19 bp DNA linear GSS 16-FEB-2001  
2M0004P01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0004P01 F, genomic survey sequence.  
AZ774536  
AZ774536.1 GI:12900089  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0004 row: P column: 01  
Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0004P01"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.4; DB 1; Length 19;  
Best Local Similarity 93.8%; Pred. No. 3.3e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1769 GCTTTTGTGAA 1784  
|||||  
Db 19 GCTTTTGTGAA 4

RESULT 2945  
CF196152  
LOCUS 22 bp mRNA linear EST 31-JUL-2003  
DEFINITION Azvil.2.E03 AZ-VI Oryza sativa (japonica cultivar-group) cDNA clone AZ-VII.2E03 5', mRNA sequence.

ACCESSION CF196152 GI:33380809  
VERSION CF196152.1  
KEYWORDS Oryza sativa (japonica cultivar-group)  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 22)  
AUTHORS Ventelon-Debout,M., Thi-Thu Huang,N., Wissocq,A., Berger,C., Michele,L., Plegu,B., Cooke,R., Ghesquiere,A., Delseny,M. and Brugidou,C.  
TITLE Metabolism and Photosynthesis gene expression is affected in response to rice yellow mottle virus infection in Oryza sativa indica and japonica cultivars  
JOURNAL Mol. Genet. Genomics (2003) In press  
COMMENT Contact: Brugidou C

IRD  
BP 64501, 34394 Montpellier cedex 5 France  
Tel: 33 4 67 41 67 39  
Fax: 33 4 67 41 61 81  
PCR Primers  
FORWARD: 5'AATTACCCTCACTAAAGGG3'  
BACKWARD: 5'CGGGATATCACTCAGCATAATG3'  
Plate: 1.2 row: E column: 3.  
Location/Qualifiers  
1. .22

FEATURES  
source

/organism="Oryza sativa (japonica cultivar-group)"  
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/cultivar="Azucena"  
/db\_xref="taxon:39947"  
/clone="AZ-VII.2E03"  
/tissue\_type="leaves"  
/dev\_stage="3 weeks-old plants"  
/lab\_host="SOLR strain (Stratagene)"  
/clone\_lib="AZ-VI"  
/note="Vector: pBluescript SK (+/-); Site\_1: Eco RI; Site\_2: Xho I; Sample name: AZ-VI; Plant growth place: greenhouse; Soil conditions: standard; Sowing date: 28/02/2000; Harvesting date: 18/03/2000; Stress date: 15/03/2000; Cultivar: azucena; Description: AZ-RYMW inoculated leaves cDNA library; experimental condition: rymw inoculation;"

Query Match 0.5%; Score 14.4; DB 1; Length 22;  
Best Local Similarity 78.9%; Pred. No. 3.7e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2171 TTTTGTAAAC 2189  
|||||  
Db 1 TTTTGTAAAC 19

RESULT 2946  
TA120E05P/c  
LOCUS 23 bp DNA linear GSS 13-DEC-2000  
DEFINITION T. brucei sheared genomic DNA clone 120e05, forward sequence, genomic survey sequence.

ACCESSION AL464555 GI:11833135  
VERSION AL464555.1  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE 1 (bases 1 to 23)  
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.  
TITLE Direct Submission  
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T\_brucei/.

FEATURES  
source  
1. .23  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="120e05"

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Best Local Similarity 93.8%; Pred. No. 3.7e+03;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2783 TTGAAAAA 2798  
|||||





TITLE  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0564 row: H column: 19  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0564H19"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 3.4e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
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Db 1 AAAAAAAAAAAAAAAAAATGGAA 19

RESULT 2950  
AZ962226  
LOCUS  
DEFINITION  
2M0231A02F Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0231A02 F, genomic survey sequence.  
ACCESSION  
AZ962226  
VERSION  
AZ962226.1 GI:13833453  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 19)  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0231 row: A column: 02  
Seq primer: CGTTGTAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0231A02"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 19;  
Best Local Similarity 84.2%; Pred. No. 3.4e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAATGGAAAAAAAAAA 19

RESULT 2951  
AI364573  
LOCUS  
DEFINITION  
AI364573 19 bp mRNA linear EST 15-FEB-1999  
qw37g03.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:1993300 3,  
similar to TR:Q39835 Q39835 EXTENSIN. ; mRNA sequence.  
ACCESSION  
AI364573  
VERSION  
AI364573.1 GI:4124262  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 19)  
AUTHORS  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL  
Unpublished (1997)  
COMMENT  
Contact: Robert Strausberg, Ph.D.







Db

19 TTTTAAAAAATTTT 1

RESULT 2956

AZ775624

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1 ACACACAAAAAAAAAAAA 19

19 bp DNA linear GSS 16-FEB-2001

Mus musculus genomic clone UUGC2M0008E01 R, genomic survey sequence.

GI:12902356

Mus musculus (house mouse)

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0008 row: E column: 01

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. .19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0008E01"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity

Matches

Score

DB

Length

0.5%;

84.2%;

16;

Conservative

0;

Mismatches

3;

Indels

0;

Gaps

0;

QY

2786 AAAAAAAAAAAAAAAAAA 2804

2166 TTTTTTTTTTTTTTTT 2184

|||||||

Db

19 TTTTAAAAAATTTT 1

Db

1 ACACACAAAAAAAAAAAA 19

RESULT 2957

AZ775624/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1 ACACACAAAAAAAAAAAA 19

19 bp DNA linear GSS 16-FEB-2001

Mus musculus genomic clone UUGC2M0008E01 R, genomic survey sequence.

GI:12902356

Mus musculus (house mouse)

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0008 row: E column: 01

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0008E01"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match

Best Local Similarity

Matches

Score

DB

Length

0.5%;

84.2%;

16;

Conservative

0;

Mismatches

3;

Indels

0;

Gaps

0;

QY

2786 AAAAAAAAAAAAAAAAAA 2804

2166 TTTTTTTTTTTTTTTT 2184

|||||||

Db

19 TTTTAAAAAATTTT 1



Query Match 0.5%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2159 TTTCTCCTTTT TTTT TTTT 2177  
Db 2 TTTCCAGTTT TTTT TTTT 20

RESULT 2961  
AU257221

LOCUS AU257221 20 bp mRNA linear EST 25-APR-2002  
DEFINITION AU257221 3'-directed mouse cDNA library Mus musculus cDNA clone  
ACCESSION BED0010046 3', mRNA sequence.  
VERSION AU257221 GI:20321628  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Kato,K. and Matoba,R.  
TITLE Generation of expressed sequence tags from mouse brain  
JOURNAL Unpublished (2002)  
COMMENT Contact: Kikuya Kato  
Graduate School of Biological Sciences  
Nara Institute of Science and Technology  
8916-5 Takayama, Ikoma, Nara 630-0101, Japan  
Tel: 81-743-72-5581  
Fax: 81-743-72-5589  
Email: kkato@bs.aist-nara.ac.jp,  
URL:http://love2.aist-nara.ac.jp/BED/index.html.

FEATURES  
source  
1. .20  
/organism="Mus musculus"  
/mol\_type="mRNA"  
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/clone\_lib="3'-directed mouse cDNA library"

Query Match 0.5%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2460 GATCCAATTTTAAATATA 2478  
Db 1 GATCCAATTTGATTATCAA 19

RESULT 2962  
CF339443

LOCUS CF339443 20 bp mRNA linear EST 18-AUG-2003  
DEFINITION RCL1--04-003.g1 Regenerated callus lambda phage cDNA library (RCL1)  
ORyza sativa cDNA clone RCL1--04-003, mRNA sequence.  
ACCESSION CF339443  
VERSION CF339443 GI:33827271  
KEYWORDS EST.  
SOURCE ORyza sativa  
ORGANISM ORyza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1. .20  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="RCL1--04-003"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli SOLR"  
/clone\_lib="Regenerated callus lambda phage cDNA library (RCL1)"  
/note="Vector: pBluescript SK(+); Site 1: SstI; Site\_2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5' end with SstI and 3' end with XhoI site. Callus was induced on 2N6 media for 30 days and cultured for 36hrs on regenerated media"

Query Match 0.5%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 51 GCGGCGGGGCGGCGGCAG 69  
Db 1 GCGGCGGAGCGGCGGCGG 19

RESULT 2963  
AZ304038/c

LOCUS AZ304038 20 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0003L08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0003L08 R, genomic survey sequence.  
ACCESSION AZ304038 GI:10339611  
VERSION AZ304038.1  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0003 row: L column: 08  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source  
1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0003L08"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"



/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2785 GAAAAAATAAAGAAAAA 2803  
||||| | |||| | |||| |  
Db 19 GAAAAAATAAAGAAAAA 1

RESULT 2964  
AZ308410/c  
LOCUS  
DEFINITION  
AZ308410  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AZ308410 20 bp DNA linear GSS 29-SEP-2000  
1M0011A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0011A24 F, genomic survey sequence.

ACCESSION  
AZ308410 GI:10348378  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0011 row: A column: 24  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0011A24"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.

FEATURES  
source

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 290 CCCGCGCCACCCCTCTCCC 308  
||||| | |||| | |||| |  
Db 20 CCCGCGCCCCCGCCCGCC 2

RESULT 2965  
AZ345646/c  
LOCUS  
DEFINITION  
AZ345646  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AZ345646 20 bp DNA linear GSS 29-SEP-2000  
1M0080K20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0080K20 F, genomic survey sequence.

ACCESSION  
AZ345646 GI:10424883  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0080 row: K column: 20  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0080K20"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson

FEATURES  
source

Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2175 TTTT TTTT TTTT TTTT AACTTTG 2193  
|||||  
Db 20 TTTT TTTT TTTT TAATGTTG 2

RESULT 2966  
AZ346143/c  
LOCUS AZ346143 20 bp DNA linear GSS 29-SEP-2000  
DEFINITION IM0081P11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0081P11 F, genomic survey sequence.  
ACCESSION AZ346143  
VERSION AZ346143.1 GI:10425380  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
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JOURNAL Unpublished (2000)  
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Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0081 row: P column: 11  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0081P11"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2165 CTTT TTTT TTTT TTTT TTTT 2183  
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Db 19 CTTT TTTT TTTT TTTT TTTT 1

RESULT 2967  
AZ426873/c  
LOCUS AZ426873 20 bp DNA linear GSS 03-OCT-2000  
DEFINITION IM0208L05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0208L05 R, genomic survey sequence.  
ACCESSION AZ426873  
VERSION AZ426873.1 GI:10550886  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
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Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0208 row: L column: 05  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0208L05"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 20;  
Best Local Similarity 84.2%; Pred. No. 3.6e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2160 TTCTCCTTTT TTTT TTTT TTTT 2178  
| | | | | | | | | | | | | | | | | | | | | |  
Db 19 TACATCTTTT TTTT TTTT TTTT 1

RESULT 2968  
AZ345540/c  
LOCUS AZ345540 21 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0080P05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080P05 F, genomic survey sequence.  
ACCESSION AZ345540  
VERSION AZ345540.1 GI:10424777  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

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JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
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University of Utah  
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Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0080 row: P column: 05  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.

FEATURES  
source  
1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0080P05"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 21;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
| | | | | | | | | | | | | | | | | | | | | |  
Db 21 AAAGAAGAAAAAAGAAAA 3

RESULT 2969  
AZ346717/c  
LOCUS AZ346717 21 bp DNA linear GSS 29-SEP-2000  
DEFINITION 1M0082O02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0082O02 F, genomic survey sequence.  
ACCESSION AZ346717  
VERSION AZ346717.1 GI:10425954  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0082 row: O column: 02  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0082O02"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA



was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 21;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 21 AAAAAAAAAAGAAAGAA 3

RESULT 2970  
AZ339966/c  
LOCUS  
DEFINITION 1M0071L11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0071L11 R, genomic survey sequence.

ACCESSION AZ339966  
VERSION AZ339966.1 GI:10414760  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0071 row: L column: 11  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.

Location/Qualifiers  
1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0071L11"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

FEATURES  
source

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 21;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 19 AAGAAGAAAAAAAAAGAAA 1

RESULT 2971  
AW248826  
LOCUS  
DEFINITION 2821056.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821056 3', mRNA sequence.

ACCESSION AW248826  
VERSION AW248826.1 GI:6591819  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 21)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2821056.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 21 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 21 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LLCM5 row: N column: 1  
High quality sequence stop: 21.  
Location/Qualifiers  
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/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="IMAGE:2821056"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC 7"  
/note="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5'

FEATURES  
source

adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 14.2; DB 1; Length 21;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1771 TTTT TTTT TTTT TTTT GAACCCCA 1789  
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Db 1 TTTT TTTT TTTT TTTT GGACCCCTA 19

RESULT 2972

AZ331046

LOCUS

DEFINITION

21 bp DNA linear GSS 29-SEP-2000

1M0056K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0056K08 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Muscle whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0056 row: K column: 08

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0056K08"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 21;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2517 GGT TTTATTTCATATATA 2535  
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Db 2 GGTATTATACATACATATA 20

RESULT 2973

AZ629111

LOCUS

DEFINITION

21 bp DNA linear GSS 13-DEC-2000

1M0481D22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0481D22 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

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Unpublished (2000)

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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0481 row: D column: 22

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 21.

Location/Qualifiers

1. .21

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/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0481D22"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and

FEATURES

source

adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 21;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2674 GTGTGTGGTGAATGG 2692  
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Db 2 GTGTGTGTGTGAAGG 20

RESULT 2974  
AZ471736 22 bp DNA linear GSS 04-OCT-2000  
LOCUS  
DEFINITION  
1M0286112R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0286112 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS  
1 (bases 1 to 22)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0286 row: I column: 12  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 22.

FEATURES  
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/sex="Male"  
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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 22;  
Best Local Similarity 84.2%; Pred. No. 3.8e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAA 2804  
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Db 3 AAAAAAAAAACATAAAAAA 21

RESULT 2975  
AZ468097/c 23 bp DNA linear GSS 04-OCT-2000  
LOCUS  
DEFINITION  
1M0279K22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0279K22 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS  
1 (bases 1 to 23)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0279 row: K column: 22  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 23.

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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells



and selected for ampicillin resistance."

Query Match 0.5%; Score 14.2; DB 1; Length 23;  
Best Local Similarity 84.2%; Pred. No. 3.8e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
||||| ||| ||| ||| ||| |||  
Db 22 AAAAAACAACAACAAAAA 4

RESULT 2976  
AW245956/c  
LOCUS  
DEFINITION  
2823002.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2823002 3',  
mRNA sequence.  
ACCESSION  
AW245956  
VERSION  
AW245956.1 GI:6588949  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 23)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
AUTHORS  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL  
Unpublished (1999)  
COMMENT  
Other ESTs: 2823002.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project  
Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
<http://www.genome.washington.edu/LowQuality> Sequence: 9 contiguous  
PHRED high quality bases following vector sequence. Very Low  
Quality Sequence: Trace file contained 23 contiguous distinct peaks  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: L1CM10 row: 0 column: 3  
High quality sequence stop: 9.  
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/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 14.2; DB 1; Length 23;  
Best Local Similarity 84.2%; Pred. No. 3.8e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
||||| ||| ||| ||| ||| |||  
Db 22 AAAAAACAACAACAAAAA 4

Query Match 0.5%; Score 14.2; DB 1; Length 23;  
Best Local Similarity 84.2%; Pred. No. 3.8e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
||||| ||| ||| ||| ||| |||

Db 20 AAAAAATAAGAAAAAGAAA 2

RESULT 2977  
AZ308225/c

LOCUS  
DEFINITION  
24 bp DNA linear GSS 29-SEP-2000  
1M0011E06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0011E06 F, genomic survey sequence.

ACCESSION  
AZ308225  
VERSION  
AZ308225.1 GI:10348004  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1 (bases 1 to 24)

AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
Unpublished (2000)

COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0011 row: E column: 06

Seq primer: CGTGTAAACGACGGCCAGT  
Class: plasmid ends

High quality sequence stop: 24.  
Location/Qualifiers  
1. .24

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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

source

Query Match 0.5%; Score 14.2; DB 1; Length 24;  
Best Local Similarity 84.2%; Pred. No. 3.7e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
||||| ||| ||| ||| ||| |||

Db 21 AAACAACAACAACAAAAA 3

RESULT 2978  
AU265714  
LOCUS  
DEFINITION AU265714 VS Dictyostelium discoideum cDNA clone VSF741 5', mRNA linear EST 10-MAY-2002  
sequence.  
ACCESSION AU265714  
VERSION AU265714.1 GI:20524512  
KEYWORDS EST.  
SOURCE Dictyostelium discoideum  
ORGANISM Dictyostelium discoideum  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.  
TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum  
JOURNAL Unpublished (2002)  
COMMENT Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: hideko@biol.tsukuba.ac.jp.  
Location/Qualifiers  
1..26  
/organism="Dictyostelium discoideum"  
/mol\_type="mRNA"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="VSF741"  
/sex="mat A"  
/dev\_stage="vegetative"  
/clone\_lib="VS"  
Query Match 0.5%; Score 14.2; DB 1; Length 26;  
Best Local Similarity 84.2%; Pred. No. 3.5e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 2 AAAAAAAAAAGGAAAAAAAA 20  
RESULT 2979  
AZ808163/c  
LOCUS  
DEFINITION AZ808163 30 bp DNA linear GSS 20-FEB-2001  
clone UUGC2M0071N08 R, genomic survey sequence.  
ACCESSION AZ808163  
VERSION AZ808163.1 GI:12973424  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

RESULT 2978  
AU265714  
LOCUS  
DEFINITION AU265714 VS Dictyostelium discoideum cDNA clone VSF741 5', mRNA linear EST 10-MAY-2002  
sequence.  
ACCESSION AU265714  
VERSION AU265714.1 GI:20524512  
KEYWORDS EST.  
SOURCE Dictyostelium discoideum  
ORGANISM Dictyostelium discoideum  
REFERENCE 1 (bases 1 to 26)  
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.  
TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum  
JOURNAL Unpublished (2002)  
COMMENT Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: hideko@biol.tsukuba.ac.jp.  
Location/Qualifiers  
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/organism="Dictyostelium discoideum"  
/mol\_type="mRNA"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="VSF741"  
/sex="mat A"  
/dev\_stage="vegetative"  
/clone\_lib="VS"  
Query Match 0.5%; Score 14.2; DB 1; Length 26;  
Best Local Similarity 84.2%; Pred. No. 3.5e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 2 AAAAAAAAAAGGAAAAAAAA 20  
RESULT 2979  
AZ808163/c  
LOCUS  
DEFINITION AZ808163 30 bp DNA linear GSS 20-FEB-2001  
clone UUGC2M0071N08 R, genomic survey sequence.  
ACCESSION AZ808163  
VERSION AZ808163.1 GI:12973424  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0071 row: N column: 08  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 30.  
Location/Qualifiers  
1..30  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."  
Query Match 0.5%; Score 14.2; DB 1; Length 30;  
Best Local Similarity 84.2%; Pred. No. 3e+03;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 28 AAACAAACAAACAAAAAAAA 10  
RESULT 2980  
BQ586422  
LOCUS  
DEFINITION BQ586422 14 bp mRNA linear EST 06-DEC-2002  
024-013-002 3-PRIME, mRNA sequence.  
ACCESSION BQ586422  
VERSION BQ586422.1 GI:26116004  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 14 Std Error: 0.00  
Plate: 13 row: 0 column: 02  
Seq primer: T7; GTAATACGACTCACTATAGGCG.  
Location/Qualifiers  
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/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:186441"  
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/clone="024-013-002"  
/tissue\_type="leaf"  
/lab\_host="EMDH10B"  
/clone\_lib="MPIZ-ADIS-024-leaf"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2179  
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DB 1 TTTT TTTT TTTT TTTT TTTT 14

RESULT 2981  
BQ586422/c  
LOCUS  
DEFINITION S013307-024-013-002-T7 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone  
204-013-002 3-PRIME, mRNA sequence.  
ACCESSION BQ586422  
VERSION BQ586422.1 GI:26116004  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@piz-koeln.mpg.de  
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024-009-B02 3-PRIME, mRNA sequence.  
ACCESSION BQ587890  
VERSION BQ587890.1 GI:26117472  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
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Fax: 00492215062851  
Email: weisshaar@piz-koeln.mpg.de  
Insert Length: 14 Std Error: 0.00  
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FEATURES  
source



SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database:http://gabi.rzpd.de"

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LOCUS BQ587890 14 bp mRNA linear EST 06-DEC-2002  
DEFINITION S013302-024-009-B02-T7 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
024-009-B02 3-PRIME, mRNA sequence.

ACCESSION BQ587890  
VERSION BQ587890.1 GI:26117472  
KEYWORDS EST.

SOURCE

Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE

AUTHORS 1 (bases 1 to 14)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL

MEDLINE Plant J. 32 (5), 845-857 (2002)

PUBMED

22362189

COMMENT

12472698

Contact: Weisshaar B

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Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 14 Std Error: 0.00

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Location/Qualifiers

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cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and

orientation:

SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2984

BQ589191

LOCUS BQ589191 14 bp mRNA linear EST 06-DEC-2002

DEFINITION S014009-024-015-I20-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
cDNA clone 024-015-I20 3-PRIME, mRNA sequence.

ACCESSION BQ589191  
VERSION BQ589191.1 GI:26118774  
KEYWORDS EST.

SOURCE

Beta vulgaris

ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 14)

AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189

PUBMED 12472698

COMMENT

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Max-Planck-Institute for Plant Breeding Research

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Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 14 Std Error: 0.00

Plate: 15 row: I column: 20

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Location/Qualifiers

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Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and

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SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: http://gabi.rzpd.de"

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Db 1 TTTT TTTT TTTT TTTT 14

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LOCUS BQ589191 14 bp mRNA linear EST 06-DEC-2002

DEFINITION S014009-024-015-I20-T7 MP1Z-ADIS-024-storage root Beta vulgaris

cDNA clone 024-015-I20 3-PRIME, mRNA sequence.

ACCESSION BQ589191  
VERSION BQ589191.1 GI:26118774  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
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AUTHORS Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
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JOURNAL Plant J. 32 (5), 845-857 (2002)  
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COMMENT Contact: Weissshaar B  
ADIS DNA core facility at MPiZ  
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Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaampiz-koeln.mpg.de  
Insert Length: 14 Std Error: 0.00  
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SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"  
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Db 14 AAAAAAAAAAAAAA 1  
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LOCUS Beta vulgaris  
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CDNA clone 024-019-E16 5-PRIME, mRNA sequence.  
ACCESSION BQ590242  
VERSION BQ590242.1 GI:26119825  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 14)  
AUTHORS Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
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JOURNAL Plant J. 32 (5), 845-857 (2002)  
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ADIS DNA core facility at MPiZ  
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Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaampiz-koeln.mpg.de  
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Db 14 AAAAAAAAAAAAAA 1  
RESULT 2986  
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LOCUS Beta vulgaris  
DEFINITION E012840-024-019-E16-SP6 MPIZ-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-019-E16 5-PRIME, mRNA sequence.  
ACCESSION BQ590242  
VERSION BQ590242.1 GI:26119825  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
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AUTHORS Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
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Fax: 00492215062851  
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SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
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Fax: 00492215062851  
Email: weissshaampiz-koeln.mpg.de  
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SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"  
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Db 1 TTTTTTTTTTTTTT 14  
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DEFINITION E012840-024-019-E16-SP6 MPIZ-ADIS-024-storage root Beta vulgaris  
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ACCESSION BQ590242  
VERSION BQ590242.1 GI:26119825  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 14)  
AUTHORS Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
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Fax: 00492215062851  
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Fax: 00492215062851  
Email: weissshaampiz-koeln.mpg.de  
Insert Length: 14 Std Error: 0.00  
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Location/Qualifiers

FEATURES

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SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 14; DB 1; Length 14;  
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RESULT 2988

BQ590261

LOCUS

DEFINITION

E012844-024-019-K14-T7 MPIZ-ADIS-024-storage root Beta vulgaris

CDNA clone 024-019-K14 3-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Beta vulgaris

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 14)

Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

and Radelof,U.

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22362189

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COMMENT

Contact: Weissshaar B

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Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weissshaampiz-koeln.mpg.de

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Seq primer: T7; GTAATACGACTCACTATAGGCG.

Location/Qualifiers

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SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTTTTTTTTTTTT 14

RESULT 2989

BQ590261/c

LOCUS

DEFINITION

E012844-024-019-K14-T7 MPIZ-ADIS-024-storage root Beta vulgaris

CDNA clone 024-019-K14 3-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Beta vulgaris

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 14)

Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

22362189

12472698

COMMENT

Contact: Weissshaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weissshaampiz-koeln.mpg.de

Insert Length: 14 Std Error: 0.00

Plate: 19 row: K column: 14

Seq primer: T7; GTAATACGACTCACTATAGGCG.

Location/Qualifiers

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/organism="Beta vulgaris"

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/cultivar="KWS2320 (double haploid, monogerm breeding line)"

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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS



Kleinwanzlebener Saatzeit AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.5%; Score 14; DB 1; Length 14;  
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Db 14 AAAAAAAAAAAAAA 1

RESULT 2990  
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LOCUS  
DEFINITION BQ5911168 14 bp mRNA linear EST 06-DEC-2002  
CDNA clone 024-017-H18-T7 MPIZ-ADIS-024-storage root Beta vulgaris

ACCESSION BQ5911168  
VERSION BQ5911168.1 GI:26120751  
KEYWORDS EST.  
SOURCE Beta vulgaris

ORGANISM

Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE

AUTHORS Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

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cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatzeit AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites Sali-NotI, primer sites and

orientation:

SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:

Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.5%; Score 14; DB 1; Length 14;

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2166 TTTTTTTTTTTTTT 2179  
Db 1 TTTTTTTTTTTTTT 14

RESULT 2991

BQ5911168/c

LOCUS

DEFINITION BQ5911168 14 bp mRNA linear EST 06-DEC-2002  
CDNA clone 024-017-H18 3-PRIME, mRNA sequence.

ACCESSION

BQ5911168

VERSION

BQ5911168.1 GI:26120751

KEYWORDS

EST.

SOURCE

Beta vulgaris

ORGANISM

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 14)

Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

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fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

Insert Length: 14 Std Error: 0.00

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Location/Qualifiers

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cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatzeit AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites Sali-NotI, primer sites and

orientation:

SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:

Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.5%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2799

Db 14 AAAAAAAAAAAAAA 1

RESULT 2992

BQ5911176

LOCUS BQ5911176 14 bp mRNA linear EST 06-DEC-2002  
DEFINITION E012715-024-017-N20-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-017-N20 3-PRIME, mRNA sequence.  
ACCESSION BQ5911176  
VERSION BQ5911176.1 GI:26120759  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weissshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaampiz-koeln.mpg.de  
Insert Length: 14 Std Error: 0.00  
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cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

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Db 1 TTTT TTTT TTTT TTTT TTTT 14

RESULT 2993  
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LOCUS BQ5911176 14 bp mRNA linear EST 06-DEC-2002  
DEFINITION E012715-024-017-N20-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-017-N20 3-PRIME, mRNA sequence.  
ACCESSION BQ5911176  
VERSION BQ5911176.1 GI:26120759  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE BQ5911176 14 bp mRNA linear EST 06-DEC-2002  
AUTHORS Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weissshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaampiz-koeln.mpg.de  
Insert Length: 14 Std Error: 0.00  
Plate: 17 row: N column: 20  
Seq primer: T7; GTAATACGACTCACTATAGGCG.  
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Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 AAAAAAAAAAAAAA 1

RESULT 2994  
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LOCUS BQ591207 14 bp mRNA linear EST 06-DEC-2002  
DEFINITION E012715-024-017-B04-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
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ACCESSION BQ591207  
VERSION BQ591207.1 GI:26120790  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698

COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaampiz-koeln.mpg.de  
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SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 14; DB 1; Length 14;  
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Db 1 TTTT TTTT TTTT TTTT 14

RESULT 2995  
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DEFINITION E012715-024-017-B04-T7 MPIZ-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-017-B04 3-PRIME, mRNA sequence.  
ACCESSION BQ591207  
VERSION BQ591207.1 GI:26120790  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaampiz-koeln.mpg.de  
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SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

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SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

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Db 14 AAAAAA AAAAAA 1

RESULT 2996  
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DEFINITION E012714-024-017-B15-T7 MPIZ-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-017-B15 3-PRIME, mRNA sequence.  
ACCESSION BQ591380  
VERSION BQ591380.1 GI:26120963  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
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JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaampiz-koeln.mpg.de  
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cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTT TTTT TTTT TTTT TTTT 14

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VERSION BQ591380.1 GI:26120963  
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SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE  
AUTHORS 1 (bases 1 to 14)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698

COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851

Email: weisshaa@mpiz-koeln.mpg.de  
Insert Length: 14 Std Error: 0.00  
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Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 14; DB 1; Length 14;  
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RESULT 2998  
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DEFINITION E012713-024-017-M04-T7 MPIZ-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-017-M04 3-PRIME, mRNA sequence.

ACCESSION BQ591482  
VERSION BQ591482.1 GI:26121065  
KEYWORDS EST.  
SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE  
AUTHORS 1 (bases 1 to 14)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698

COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851

Email: weisshaa@mpiz-koeln.mpg.de  
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Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 14; DB 1; Length 14;  
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RESULT 2999  
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ACCESSION BQ591482  
VERSION BQ591482.1 GI:26121065  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weissshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaampiz-koeln.mpg.de  
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Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"  
Query Match 0.5%; Score 14; DB 1; Length 14;  
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Db 14 AAAAAAAAAAAAAA 1  
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CDNA clone 024-028-C03 5-PRIME, mRNA sequence.  
ACCESSION BQ593052  
VERSION BQ593052.1 GI:26122635  
KEYWORDS EST.  
SOURCE Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weissshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaampiz-koeln.mpg.de  
Insert Length: 14 Std Error: 0.00  
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Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"  
Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT 2179  
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Db 1 TTTT TTTT TTTT TTTT 14  
RESULT 3001  
BQ593052/c  
LOCUS  
DEFINITION E012375-024-028-C03-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
CDNA clone 024-028-C03 5-PRIME, mRNA sequence.  
ACCESSION BQ593052  
VERSION BQ593052.1 GI:26122635  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Herwig,R., Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698  
Contact: Weisshaar B  
ADIS DNA core facility at MPiZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 14 Std Error: 0.00  
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SP6-SalI-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

## Query Match

Best Local Similarity 0.5%; Score 14; DB 1; Length 14;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2799

Db 14 AAAAAAAAAAAAAA 1

## RESULT 3002

CF277935

LOCUS

DEFINITION 14ETL--03-K11.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa cDNA clone 14ETL--03-K11, mRNA sequence.

ACCESSION

VERSION CF277935.1 GI:33655321

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

COMMENT

Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2179

Db 1 TTTT TTTT TTTT TTTT TTTT 14

## RESULT 3003

CF277935/c

LOCUS

DEFINITION

14ETL--03-K11.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa cDNA clone 14ETL--03-K11, mRNA sequence.

ACCESSION

VERSION CF277935.1 GI:33655321

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

COMMENT

Unpublished (2003)  
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2799

Db 14 AAAAAAAAAAAAAA 1

## RESULT 3004

CF278001



LOCUS CF278001 14 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ETL--03-L21.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa cDNA clone 14ETL--03-L21, mRNA sequence.  
ACCESSION CF278001  
VERSION CF278001.1 GI:33655387  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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QY 2166 TTTT TTTT TTTT TTTT 2179  
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Db 1 TTTT TTTT TTTT TTTT 14

RESULT 3005  
LOCUS CF278001/c 14 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ETL--03-L21.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa cDNA clone 14ETL--03-L21, mRNA sequence.  
ACCESSION CF278001  
VERSION CF278001.1 GI:33655387  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 AAAAAA AAAAAA 1

RESULT 3006  
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DEFINITION 14ETL--04-F22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa cDNA clone 14ETL--04-F22, mRNA sequence.  
ACCESSION CF278452  
VERSION CF278452.1 GI:33655838  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source

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/lab\_host="E.coli DH10B"  
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Query Match 0.5%; Score 14; DB 1; Length 14;  
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Db 1 TTTT TTTT TTTT TTTT 14

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CF278452/c
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14ETL--04-F22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--04-F22, mRNA sequence.
ACCESSION
CF278452
VERSION
CF278452.1 GI:33655838
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
REFERENCE
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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QY 2786 AAAAAAAAAAAAAA 2799
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Db 14 AAAAAAAAAAAAAA 1

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LOCUS
DEFINITION
14ETL--05-M14.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--05-M14, mRNA sequence.
ACCESSION
CF279473
VERSION
CF279473.1 GI:33656859
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 AAAAAAAAAAAAAA 1

RESULT 3009
CF279473/c
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DEFINITION
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Oryza sativa cDNA clone 14ETL--05-M14, mRNA sequence.
ACCESSION
CF279473
VERSION
CF279473.1 GI:33656859
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTT 2179
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Db 1 TTTTTTTTTTTTTT 14
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTT 2179
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Db 1 TTTTTTTTTTTTTT 14

RESULT 3009
CF279473/c
LOCUS
DEFINITION
14ETL--05-M14.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--05-M14, mRNA sequence.
ACCESSION
CF279473
VERSION
CF279473.1 GI:33656859
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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QY 2166 TTTTTTTTTTTTTT 2179
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Db 1 TTTTTTTTTTTTTT 14
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Db      14 AAAAAAAAAAAAAA 1

RESULT 3010
CF279992
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DEFINITION 14ETL--06-I01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--06-I01, mRNA sequence.
ACCESSION  CF279992
VERSION     CF279992.1 GI:33657378
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RESULT 3011
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DEFINITION 14ETL--06-I01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--06-I01, mRNA sequence.
ACCESSION  CF279992
VERSION     CF279992.1 GI:33657378
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
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JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db      14 AAAAAAAAAAAAAA 1

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DEFINITION 14ETL--09-D24.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--09-D24, mRNA sequence.
ACCESSION  CF281958
VERSION     CF281958.1 GI:33659345
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
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Db 1 TTTT TTTT TTTT TTTT TTTT 14

RESULT 3013
CF281958/c
LOCUS
DEFINITION 14ETL--09-D24.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--09-D24, mRNA sequence.
ACCESSION CF281958
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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Db 14 AAAAAA AAAAAA AAAAAA 1

RESULT 3014
CF282350
LOCUS
DEFINITION 14ETL--09-N05.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--09-N05, mRNA sequence.
ACCESSION CF282350
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTT TTTT TTTT TTTT TTTT 14

RESULT 3015
CF282350/c
LOCUS
DEFINITION 14ETL--09-N05.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--09-N05, mRNA sequence.
ACCESSION CF282350
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzaceae; Oryza.
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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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with oligoribonucleotides and then used as templates for
RT-PCR."

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 1 (bases 1 to 14)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

Query Match 0.5%; Score 14; DB 1; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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 Db 14 AAAAAAAAAAAAAA 1

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 DEFINITION sativa cDNA clone 30DGS--03-P15, mRNA sequence.  
 ACCESSION CF294449  
 VERSION CF294449.1 GI:33663482  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 14)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
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Query Match 0.5%; Score 14; DB 1; Length 14;  
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 DEFINITION sativa cDNA clone 30DGS--03-P15, mRNA sequence.  
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 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
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 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
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RESULT 3017  
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 DEFINITION sativa cDNA clone 30DGS--03-P15, mRNA sequence.  
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 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
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 CF294449/c  
 LOCUS 30DGS--03-P15.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
 DEFINITION sativa cDNA clone 30DGS--03-P15, mRNA sequence.  
 ACCESSION CF294449  
 VERSION CF294449.1 GI:33663482  
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 SOURCE Oryza sativa  
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RESULT 3017  
 CF294449/c  
 LOCUS 30DGS--03-P15.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
 DEFINITION sativa cDNA clone 30DGS--03-P15, mRNA sequence.  
 ACCESSION CF294449  
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 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 14)  
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Query Match 0.5%; Score 14; DB 1; Length 14;  
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 DEFINITION sativa cDNA clone 30DGS--03-P15, mRNA sequence.  
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 VERSION CF294449.1 GI:33663482  
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 ORGANISM Oryza sativa  
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 1 (bases 1 to 14)  
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 Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

Query Match 0.5%; Score 14; DB 1; Length 14;  
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 Db 1 TTTT TTTT TTTT TTTT 14

RESULT 3017  
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 LOCUS 30DGS--03-P15.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
 DEFINITION sativa cDNA clone 30DGS--03-P15, mRNA sequence.  
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 VERSION CF294449.1 GI:33663482  
 KEYWORDS EST.  
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 ORGANISM Oryza sativa  
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Db 14 AAAAAAAAAAAAAA 1

## RESULT 3022

CF297969

LOCUS  
DEFINITION 7LEAF--01-C16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--01-C16, mRNA sequence.

ACCESSION  
VERSION CF297969.1 GI:33669730  
KEYWORDS  
SOURCE EST.

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

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/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTT 2179

Db 1 TTTTTTTTTTTTTT 14

## RESULT 3023

CF297969/c

LOCUS

DEFINITION 7LEAF--01-C16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--01-C16, mRNA sequence.

ACCESSION

VERSION CF297969

KEYWORDS

CF297969.1 GI:33669730

EST.

## SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

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QY 2786 AAAAAAAAAAAAAA 2799

Db 14 AAAAAAAAAAAAAA 1

## RESULT 3024

CF298109

LOCUS

DEFINITION 7LEAF--01-F19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--01-F19, mRNA sequence.

ACCESSION

VERSION CF298109

KEYWORDS

EST.

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

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DB      14 AAAAAAAAAAAAAA 1

RESULT 3028
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LOCUS      7LEAF--05-B01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION      sativa cDNA clone 7LEAF--05-B01, mRNA sequence.
ACCESSION      CF300542
VERSION      CF300542.1 GI:33672303
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 14)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RESULT 3029
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LOCUS      7LEAF--05-B01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION      sativa cDNA clone 7LEAF--05-B01, mRNA sequence.
ACCESSION      CF300542
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CF300542.1 GI:33672303
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SOURCE      Oryza sativa
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 14)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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JOURNAL      Unpublished (2003)
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DB      14 AAAAAAAAAAAAAA 1

RESULT 3030
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DEFINITION      sativa cDNA clone 7LEAF--05-L10, mRNA sequence.
ACCESSION      CF301020
VERSION      CF301020.1 GI:33672781
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 14)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RESULT 3030
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DEFINITION      sativa cDNA clone 7LEAF--05-L10, mRNA sequence.
ACCESSION      CF301020
VERSION      CF301020.1 GI:33672781
KEYWORDS      EST.
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Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE      1 (bases 1 to 14)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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JOURNAL      Unpublished (2003)
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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                /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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                with oligoribonucleotides and then used as templates for
                RT-PCR."

Query Match      0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTTTTTTTTTTTT 2179
DB      1 TTTTTTTTTTTTTT 14

RESULT 3029
CF300542/c
LOCUS      7LEAF--05-B01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION      sativa cDNA clone 7LEAF--05-B01, mRNA sequence.
ACCESSION      CF300542
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2179
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Db 1 TTTT TTTT TTTT TTTT TTTT 14

RESULT 3031
CF301020/c
LOCUS      CF301020      14 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION 7LEAF--05-L10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-L10, mRNA sequence.
ACCESSION  CF301020
VERSION     CF301020.1 GI:33672781
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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   /lab_host="E.coli DH10B"
   /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
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RT-PCR."

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2179
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Db 1 TTTT TTTT TTTT TTTT TTTT 14

RESULT 3032
CF301020/c
LOCUS      CF301020      14 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION 7LEAF--05-M19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-M19, mRNA sequence.
ACCESSION  CF301020
VERSION     CF301020.1 GI:33672781
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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with oligoribonucleotides and then used as templates for
RT-PCR."

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Db 14 AAAAAA AAAAAA AAAAAA 1

RESULT 3032
CF301083/c
LOCUS      CF301083      14 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION 7LEAF--05-M19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-M19, mRNA sequence.
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CF301083
CF301083.1 GI:33672844
EST.
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2179
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Db 1 TTTT TTTT TTTT TTTT TTTT 14

RESULT 3033
CF301083/c
LOCUS      CF301083      14 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION 7LEAF--05-M19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-M19, mRNA sequence.
ACCESSION  CF301083
VERSION     CF301083.1 GI:33672844
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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/cultivar="Nackdong"
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2799
Db      14 AAAAAAAAAAAAAA 1

RESULT 3034
CF301380
LOCUS      7LEAF--06-D16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION      sativa cDNA clone 7LEAF--06-D16, mRNA sequence.
ACCESSION      CF301380
VERSION      CF301380.1 GI:33673141
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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RT-PCR."

Query Match      0.5%; Score 14; DB 1; Length 14;
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTTTTTTTTTTTT 2179
Db      1 TTTTTTTTTTTTTT 14

RESULT 3035
CF301380/c
LOCUS      7LEAF--06-D16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION      14 bp mRNA linear EST 15-AUG-2003

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sativa cDNA clone 7LEAF--06-D16, mRNA sequence.
CF301380
VERSION      CF301380.1 GI:33673141
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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with oligoribonucleotides and then used as templates for
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Query Match      0.5%; Score 14; DB 1; Length 14;
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2799
Db      14 AAAAAAAAAAAAAA 1

RESULT 3036
CF302675
LOCUS      7LEAF--08-G18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION      sativa cDNA clone 7LEAF--08-G18, mRNA sequence.
ACCESSION      CF302675
VERSION      CF302675.1 GI:33674436
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .14
/organism="Oryza sativa"

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RT-PCR."
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Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2799  
Db 14 AAAAAAAAAAAAAA 1

RESULT 3040  
CF308006 14 bp mRNA linear EST 15-AUG-2003  
LOCUS  
DEFINITION  
ABF--01-K10.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--01-K10, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2179  
Db 1 TTTT TTTT TTTT TTTT 14

RESULT 3041  
CF308006/c  
LOCUS  
DEFINITION  
ABF--01-K10.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--01-K10, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Contact: Nahm B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2799  
Db 14 AAAAAAAAAAAAAA 1

RESULT 3042  
CF308220  
LOCUS  
DEFINITION  
ABF--01-P06.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--01-P06, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

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1. .14  
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/lab\_host="E.coli DH10B"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid  
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for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2179  
Db 1 TTTT TTTT TTTT TTTT 14

RESULT 3043  
CF308220/c

LOCUS  
DEFINITION  
ABF--01-P06.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--01-P06, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CF308220 14 bp mRNA linear EST 15-AUG-2003  
ABF--01-P06.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--01-P06, mRNA sequence.  
EST.  
CF308220.1 GI:33679981  
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Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

TITLE  
JOURNAL  
COMMENT

FEATURES

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1. .14  
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then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

line."

Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA 2799  
Db 14 AAAAAA AAAAAA 1

RESULT 3044  
CF308445

LOCUS  
DEFINITION  
ABF--02-E10.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--02-E10, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CF308445 14 bp mRNA linear EST 15-AUG-2003  
ABF--02-E10.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--02-E10, mRNA sequence.  
EST.  
CF308445.1 GI:33680206  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

TITLE

JOURNAL

COMMENT

FEATURES

source

1. .14  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="ABF--02-E10"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid  
cDNA library (ABF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2179  
Db 1 TTTT TTTT TTTT TTTT 14

RESULT 3045  
CF308445/c

LOCUS  
DEFINITION  
ABF--02-E10.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--02-E10, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CF308445 14 bp mRNA linear EST 15-AUG-2003  
ABF--02-E10.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--02-E10, mRNA sequence.  
EST.  
CF308445.1 GI:33680206  
Oryza sativa  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source

Location/Qualifiers

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/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="ABF--02-E10"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid

cdna library (ABF)"

/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2799

Db 14 AAAAAAAAAAAAAA 1

RESULT 3046

CF308918  
LOCUS 14 bp mRNA linear EST 15-AUG-2003  
DEFINITION ABF--02-O16.b1 ABF3-overexpressing transgenic rice plasmid cdna library (ABF) Oryza sativa cdna clone ABF--02-O16, mRNA sequence.

ACCESSION CF308918  
VERSION CF308918.1 GI:33680679  
KEYWORDS EST.

SOURCE

Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source

Location/Qualifiers

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/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

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/clone\_lib="ABF3-overexpressing transgenic rice plasmid

cdna library (ABF)"

/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2179

Db 1 TTTT TTTT TTTT TTTT 14

RESULT 3047

CF308918/c

LOCUS

DEFINITION ABF--02-O16.b1 ABF3-overexpressing transgenic rice plasmid cdna library (ABF) Oryza sativa cdna clone ABF--02-O16, mRNA sequence.

ACCESSION CF308918

VERSION CF308918.1 GI:33680679

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

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/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

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/clone="ABF--02-O16"

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/clone\_lib="ABF3-overexpressing transgenic rice plasmid

cdna library (ABF)"

/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2799

Db 14 AAAAAAAAAAAAAA 1





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Query Match      0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT 2179
Db      1 TTTT TTTT TTTT TTTT 14

RESULT 3051
CF3111201/c
LOCUS      CF3111201      14 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION ABF--06-F09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--06-F09, mRNA sequence.
ACCESSION  CF3111201
VERSION     CF3111201.1 GI:33682962
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 14)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES             source
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                /clone_lib="ABF3-overexpressing transgenic rice plasmid
                cDNA library (ABF)"
                /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
                for 2hrs. Oligo-capped mRNA was reverse transcribed and
                then used for PCR. mRNA was prepared from ABA-responsive
                element binding transcription factor 3 overexpression
                line."

Query Match      0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2799
Db      14 AAAAAAAAAAAAAA 1

RESULT 3052
CF3111813
LOCUS      CF3111813      14 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION ABF--07-D22.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--07-D22, mRNA sequence.
ACCESSION  CF3111813
VERSION     CF3111813.1 GI:33683574
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES             source
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                for 2hrs. Oligo-capped mRNA was reverse transcribed and
                then used for PCR. mRNA was prepared from ABA-responsive
                element binding transcription factor 3 overexpression
                line."

Query Match      0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT 2179
Db      1 TTTT TTTT TTTT TTTT 14

RESULT 3053
CF3111813/c
LOCUS      CF3111813      14 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION ABF--07-D22.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--07-D22, mRNA sequence.
ACCESSION  CF3111813
VERSION     CF3111813.1 GI:33683574
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES             source
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                element binding transcription factor 3 overexpression
                line."

Query Match      0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2799
Db      14 AAAAAAAAAAAAAA 1

RESULT 3052
CF3111813
LOCUS      CF3111813      14 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION ABF--07-D22.g1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--07-D22, mRNA sequence.
ACCESSION  CF3111813
VERSION     CF3111813.1 GI:33683574
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
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cdna_library (ABF)"
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for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2799
Db      14 AAAAAAAAAAAAAA 1

RESULT 3054
CF318323
LOCUS
DEFINITION
HD--08-G13.b1 OSHDAC1-overexpressing transgenic rice plasmid
library (HD) Oryza sativa cdna clone HD--08-G13, mRNA sequence.
CF318323
ACCESSION
CF318323.1 GI:33690084
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..14
/organism="Oryza sativa"
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/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cdna_library (HD)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT 2179
Db      1 TTTT TTTT TTTT TTTT 14

RESULT 3055
CF318323
LOCUS
DEFINITION
HD--08-G13.b1 OSHDAC1-overexpressing transgenic rice plasmid
library (HD) Oryza sativa cdna clone HD--08-G13, mRNA sequence.
CF318323
ACCESSION
CF318323.1 GI:33690084
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cdna_library (HD)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2799
Db      14 AAAAAAAAAAAAAA 1

RESULT 3056
CF318450
LOCUS
DEFINITION
HD--08-J08.b1 OSHDAC1-overexpressing transgenic rice plasmid
library (HD) Oryza sativa cdna clone HD--08-J08, mRNA sequence.
CF318450
ACCESSION
CF318450.1 GI:33690211
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
```

```
CF318323/c
LOCUS
DEFINITION
HD--08-G13.b1 OSHDAC1-overexpressing transgenic rice plasmid cdna
library (HD) Oryza sativa cdna clone HD--08-G13, mRNA sequence.
CF318323
ACCESSION
CF318323.1 GI:33690084
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..14
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--08-G13"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cdna_library (HD)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2799
Db      14 AAAAAAAAAAAAAA 1

RESULT 3056
CF318450
LOCUS
DEFINITION
HD--08-J08.b1 OSHDAC1-overexpressing transgenic rice plasmid
library (HD) Oryza sativa cdna clone HD--08-J08, mRNA sequence.
CF318450
ACCESSION
CF318450.1 GI:33690211
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
```



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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers

1. .14  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
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cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2179

Db 1 TTTT TTTT TTTT TTTT 14

RESULT 3057

CF318450/c

LOCUS

DEFINITION HD--08-J08.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--08-J08, mRNA sequence.

ACCESSION CF318450.1 GI:33690211

VERSION EST.

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

TITLE

JOURNAL

COMMENT

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Fax: 82 31 321 6355

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FEATURES

source

Location/Qualifiers

1. .14  
/organism="Oryza sativa"  
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
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QY 2786 AAAAAA AAAAAA 2799

Db 14 AAAAAA AAAAAA 1

RESULT 3058

CF319826

LOCUS

DEFINITION HD--10-H16.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--10-H16, mRNA sequence.

ACCESSION CF319826

VERSION EST.

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

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FEATURES

source

Location/Qualifiers

1. .14  
/organism="Oryza sativa"

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/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was

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reverse transcribed and then used for PCR. mRNA was

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line."

Query Match 0.5%; Score 14; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

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QY 2166 TTTT TTTT TTTT TTTT 2179

Db 1 TTTT TTTT TTTT TTTT 14

RESULT 3059

CF319826/c

LOCUS

DEFINITION HD--10-H16.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--10-H16, mRNA sequence.

ACCESSION CF319826

VERSION EST.

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE  
AUTHORS Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
Location/Qualifiers

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cDNA library (HD)"  
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derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2799

Db 14 AAAAAAAAAAAAAA 1

RESULT 3060

CF321246

LOCUS  
DEFINITION HD--12-G24.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--12-G24, mRNA sequence.

ACCESSION CF321246

VERSION CF321246.1 GI:33693007

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT

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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..14

/organism="Oryza sativa"

/mol\_type="mRNA"

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/db\_xref="taxon:4530"

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/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
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reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTTTT 2179

Db 1 TTTTTTTTTTTTTT 14

RESULT 3061

CF321246/c

LOCUS

DEFINITION

HD--12-G24.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa cDNA clone HD--12-G24, mRNA sequence.

ACCESSION CF321246

VERSION CF321246.1 GI:33693007

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

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/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="HD--12-G24"

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/lab\_host="E.coli DH10B"

/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid

cDNA library (HD)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was

treated with ABA(20um) for 1hr. Oligo-capped mRNA was

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derived from rice Histone Deacetylase overexpression

line."

QY 2786 AAAAAAAAAAAAAA 2799

Db 14 AAAAAAAAAAAAAA 1

RESULT 3062

CF327097





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CF327119/c
LOCUS      CF327119              14 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--01-H14.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION  CF327119
VERSION    CF327119.1  GI:33802493
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
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                     RT-PCR."

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QY      2166 TTTT-----TTT 2179
Db      1 TTTT-----TTT 14

RESULT 3067
CF327445/c
LOCUS      CF327445              14 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--01-O24.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION  CF327445
VERSION    CF327445.1  GI:33803149
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
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                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

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QY      2786 AAAAAAAAAAAAAA 2799
Db      14 AAAAAAAAAAAAAA 1

RESULT 3066
CF327445/c
LOCUS      CF327445              14 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--01-O24.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION  CF327445
VERSION    CF327445.1  GI:33803149
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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FEATURES             Location/Qualifiers
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                     RT-PCR."

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QY      2166 TTTT-----TTT 2179
Db      1 TTTT-----TTT 14

RESULT 3067
CF327445/c
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DEFINITION NACL--01-O24.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION  CF327445
VERSION    CF327445.1  GI:33803149
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
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            of Bioscience and Bioinformatics, Myongji University
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            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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QY      2786 AAAAAAAAAAAAAA 2799
Db      14 AAAAAAAAAAAAAA 1
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RESULT 3068
CF328490
LOCUS
DEFINITION NACL--03-G21.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-G21, mRNA sequence.
ACCESSION CF328490
VERSION CF328490.1 GI:33805226
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2179
Db 1 TTTT TTTT TTTT TTTT TTTT 14

RESULT 3069
CF328490/c
LOCUS
DEFINITION NACL--03-G21.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-G21, mRNA sequence.
ACCESSION CF328490
VERSION CF328490.1 GI:33805226
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

FEATURES
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.5%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2179
Db 1 TTTT TTTT TTTT TTTT TTTT 14
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 14 AAAAAA AAAAAA AAAAAA 1

RESULT 3070
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DEFINITION NACL--03-H24.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-H24, mRNA sequence.
ACCESSION CF328540
VERSION CF328540.1 GI:33805324
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 1 TTTT TTTT TTTT TTTT TTTT 14
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LOCUS
DEFINITION NACL--03-H24.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-H24, mRNA sequence.
ACCESSION CF328540
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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COMMENT Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 AAAAAAAAAAAAAA 1

RESULT 3072
CF328669
LOCUS
DEFINITION NACL--03-K23.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-K23, mRNA sequence.
ACCESSION CF328669
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 14 AAAAAAAAAAAAAA 1

RESULT 3073
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LOCUS
DEFINITION NACL--03-K23.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-K23, mRNA sequence.
ACCESSION CF328669
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
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AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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QY 2786 AAAAAAAAAAAAAA 2799
Db 14 AAAAAAAAAAAAAA 1
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTT TTTT TTTT TTTT TTTT 14

RESULT 3073
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LOCUS
DEFINITION NACL--03-K23.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-K23, mRNA sequence.
ACCESSION CF328669
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 14)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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QY 2786 AAAAAAAAAAAAAA 2799
Db 14 AAAAAAAAAAAAAA 1
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## RESULT 3074

CF328994  
LOCUS  
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ACCESSION CF328994  
VERSION CF328994.1 GI:33806228  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

## FEATURES

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QY 2166 TTTT TTTT TTTT TTTT 2179

Db 1 TTTT TTTT TTTT TTTT 14

## RESULT 3075

CF328994/c  
LOCUS  
DEFINITION NACL--04-C11.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa CDNA clone NACL--04-C11, mRNA sequence.  
ACCESSION CF328994  
VERSION CF328994.1 GI:33806228  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

## FEATURES

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QY 2786 AAAAAAAAAAAAAA 2799

Db 14 AAAAAAAAAAAAAA 1

## RESULT 3076

## CF329217

LOCUS  
DEFINITION NACL--04-H10.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa CDNA clone NACL--04-H10, mRNA sequence.  
ACCESSION CF329217  
VERSION CF329217.1 GI:33806672  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

## FEATURES

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QY 2166 TTTT TTTT TTTT TTTT 2179

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Db      1 TTTT TTTT TTTT TTTT 14

RESULT 3077
CF329217/c
LOCUS
DEFINITION   NACL--04-H10.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 AAAAAAAAAAAAAA 14

RESULT 3078
CF329990
LOCUS
DEFINITION   NACL--05-I11.g1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RESULT 3079
CF329990
LOCUS
DEFINITION   NACL--05-I11.g1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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1 (bases 1 to 14)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Best Local Similarity 100.0%; Pred.No. 1.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2799
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Db      14 AAAAAAAAAAAAAA 1

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Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

#### FEATURES

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QY 2786 AAAAAAAAAAAAAA 2799  
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 Db 1 AAAAAAAAAAAAAA 14

#### RESULT 3079

CF329990/c  
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 ACCESSION  
 VERSION  
 KEYWORDS  
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 ORGANISM  
 Oryza sativa  
 Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 14)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, MyongJi University  
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 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

#### FEATURES

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Query Match 0.5%; Score 14; DB 1; Length 14;  
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 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2179

of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Db 14 TTTT TTTT TTTT TTTT 1

RESULT 3080

CF330784

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CF330784 14 bp mRNA linear EST 18-AUG-2003  
NACL--06-K10.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--06-K10, mRNA sequence.

CF330784  
CF330784.1 GI:33809790  
EST.  
Oryza sativa  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)  
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FEATURES

source

Location/Qualifiers

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/organism="Oryza sativa"

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/cultivar="Nackdong"

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/tissue\_type="callus"

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/lab\_host="E.coli DH10B"

/clone\_lib="Rice callus plasmid cDNA library (NACL)"

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RT-PCR."

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QY 2166 TTTT TTTT TTTT TTTT 2179

Db 1 TTTT TTTT TTTT TTTT 14

RESULT 3081

CF330784/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CF330784 14 bp mRNA linear EST 18-AUG-2003  
NACL--06-K10.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--06-K10, mRNA sequence.

CF330784  
CF330784.1 GI:33809790  
EST.  
Oryza sativa  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

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FEATURES

source

Location/Qualifiers

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/organism="Oryza sativa"

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/cultivar="Nackdong"

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0; Mismatches

0; Indels

0; Gaps

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QY 2786 AAAAAA AAAAAA 2799

Db 14 AAAAAA AAAAAA 1

RESULT 3082

CF331272

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CF331272 14 bp mRNA linear EST 18-AUG-2003  
NACL--07-F09.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--07-F09, mRNA sequence.

CF331272  
CF331272.1 GI:33810755  
EST.  
Oryza sativa  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
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FEATURES

source

Location/Qualifiers

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/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match

Best Local Similarity

Matches

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0; Mismatches

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0.5%; Score 14; DB 1; Length 14;  
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0; Mismatches 0; Indels 0; Gaps 0;



QY 2166 TTTT TTTT TTTT TTTT 2179  
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Db 1 TTTT TTTT TTTT TTTT 14

RESULT 3083  
CF331272/c

LOCUS CF331272 14 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--07-F09.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--07-F09, mRNA sequence.

ACCESSION CF331272  
VERSION CF331272.1 GI:33810755  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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JOURNAL Unpublished (2003)

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Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

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/organism="Oryza sativa"

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Db 14 AAAAAAAAAAAAAA 1

RESULT 3084

CF331861

LOCUS CF331861 14 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--08-C10.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--08-C10, mRNA sequence.

ACCESSION CF331861

VERSION CF331861.1 GI:33811945

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Query Match

Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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FEATURES

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/organism="Oryza sativa"

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2179

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Db 1 TTTT TTTT TTTT TTTT 14

RESULT 3085

CF331861/c

LOCUS CF331861 14 bp mRNA linear EST 18-AUG-2003

DEFINITION NACL--08-C10.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--08-C10, mRNA sequence.

ACCESSION CF331861

VERSION CF331861.1 GI:33811945

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

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FEATURES

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Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
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QY 2786 AAAAAAAAAAAAAA 2799  
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Db 1 AAAAAAAAAAAAAA 14

RESULT 3089  
CF333215/c  
LOCUS  
DEFINITION JMT--02-A10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
ACCESSION CF333215  
VERSION CF333215.1 GI:33814709  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 14)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
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FEATURES  
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Query Match 0.5%; Score 14; DB 1; Length 14;  
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Db 14 TTTT TTTT TTTT TTTT 1

RESULT 3090  
CF333399  
LOCUS  
DEFINITION JMT--02-E12.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
ACCESSION CF333399  
VERSION CF333399.1 GI:33815074  
KEYWORDS EST.  
SOURCE Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 14)  
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FEATURES  
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/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
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Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTT TTTT TTTT TTTT 14

RESULT 3091  
CF333399/c  
LOCUS  
DEFINITION JMT--02-E12.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
ACCESSION CF333399  
VERSION CF333399.1 GI:33815074  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 14)  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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1..14  
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prepared from Arabidopsis Jasmonate Carboxyl  
methyltransferase overexpression line."

Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2799  
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Db 14 AAAAAAAAAAAAAA 1

## RESULT 3092

CF334202 14 bp mRNA linear EST 18-AUG-2003  
LOCUS JMT--03-G11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (JMT) Oryza sativa cDNA clone JMT--03-G11, mRNA sequence.

ACCESSION CF334202.1 GI:33816736  
VERSION  
KEYWORDS EST.

## SOURCE

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

1 (bases 1 to 14)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
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Unpublished (2003)

## JOURNAL

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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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was reverse transcribed and then used for PCR. mRNA was  
prepared from Arabidopsis Jasmonate Carboxyl  
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QY 2166 TTTTTTTTTTTTTT 2179  
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Db 1 TTTTTTTTTTTTTT 14

## RESULT 3093

CF334202/c

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

1 (bases 1 to 14)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

## JOURNAL

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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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QY 2786 AAAAAAAAAAAAAA 2799  
|||||  
Db 14 AAAAAAAAAAAAAA 1

## RESULT 3094

CF334281

LOCUS  
DEFINITION

CF334281 14 bp mRNA linear EST 18-AUG-2003  
JMT--03-I05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--03-I05, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

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Fax: 82 31 321 6355

Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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Db 1 TTTT TTTT TTTT TTTT 14

RESULT 3095

CF334281/c

LOCUS

DEFINITION JMT--03-I05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--03-I05, mRNA sequence.

ACCESSION CF334281

VERSION CF334281.1 GI:33816894

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs

TITLE

JOURNAL

COMMENT

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Fax: 82 31 321 6355  
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FEATURES

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prepared from Arabidopsis Jasmonate Carboxyl  
methyltransferase overexpression line."

Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.8e+03;  
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QY 2786 AAAAAAAAAAAAAA 2799

Db 14 AAAAAAAAAAAAAA 1

RESULT 3096

CF334290

LOCUS

DEFINITION JMT--03-I11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--03-I11, mRNA sequence.

ACCESSION CF334290

VERSION CF334290.1 GI:33816914

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs

TITLE

JOURNAL

COMMENT

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Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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Query Match 0.5%; Score 14; DB 1; Length 14;  
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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2179

Db 1 TTTT TTTT TTTT TTTT 14

RESULT 3097

CF334290/c

LOCUS

DEFINITION JMT--03-I11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--03-I11, mRNA sequence.

ACCESSION CF334290

VERSION CF334290.1 GI:33816914

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs

TITLE

JOURNAL Unpublished (2003)  
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Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2799  
Db 14 AAAAAAAAAAAAAA 1

## RESULT 3098

CF335781  
LOCUS 14 bp mRNA linear EST 18-AUG-2003  
DEFINITION JMT--05-J13.b1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--05-J13, mRNA sequence.  
CF335781

ACCESSION CF335781.1 GI:33819936  
VERSION  
KEYWORDS  
SOURCE

## ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

## COMMENT

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Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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QY 2166 TTTT TTTT TTTT TTTT 2179  
Db 1 TTTT TTTT TTTT TTTT 14

## RESULT 3099

CF335781/c  
LOCUS 14 bp mRNA linear EST 18-AUG-2003  
DEFINITION JMT--05-J13.b1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--05-J13, mRNA sequence.  
CF335781

ACCESSION CF335781.1 GI:33819936  
VERSION  
KEYWORDS  
SOURCE

## ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

## COMMENT

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FEATURES  
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QY 2786 AAAAAAAAAAAAAA 2799  
Db 14 AAAAAAAAAAAAAA 1

## RESULT 3100

CF336094  
LOCUS 14 bp mRNA linear EST 18-AUG-2003  
DEFINITION JMT--06-A10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--06-A10, mRNA sequence.  
CF336094

ACCESSION CF336094.1 GI:33820566  
VERSION  
KEYWORDS  
SOURCE

## ORGANISM

Oryza sativa  
Oryza sativa





DEFINITION JMT--06-A17.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--06-A17, mRNA sequence.

ACCESSION CF336106

VERSION CF336106.1 GI:33820590

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

AUTHORS 1 (bases 1 to 14)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

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FEATURES  
source

Location/Qualifiers

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QY 2786 AAAAAAAAAAAAAA 2799

Db 14 AAAAAAAAAAAAAA 1

RESULT 3104

CF336287

LOCUS

DEFINITION JMT--06-E15.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--06-E15, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source

Location/Qualifiers

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Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred.No. 1.8e+03;  
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QY 2166 TTTT TTTT TTTT TTTT 2179

Db 1 TTTT TTTT TTTT TTTT 14

RESULT 3105

CF336287/c

LOCUS

DEFINITION

JMT--06-E15.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--06-E15, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 14)

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Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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FEATURES  
source

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Query Match 0.5%; Score 14; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred.No. 1.8e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2799





Query Match 0.5%; Score 14; DB 1; Length 15;  
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QY 2786 AAAAAAAAAAAAAA 2799  
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Db 14 AAAAAAAAAAAAAA 1

RESULT 3109  
CF296652  
LOCUS 15 bp mRNA linear EST 14-AUG-2003  
DEFINITION 30DGS--07-C02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa cDNA clone 30DGS--07-C02, mRNA sequence.  
ACCESSION CF296652  
VERSION CF296652.1 GI:33665685  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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QY 2166 TTTT TTTT TTTT TTTT 2179  
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Db 1 TTTT TTTT TTTT TTTT 14

RESULT 3110  
CF296652/c  
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DEFINITION 30DGS--07-C02.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
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ACCESSION CF296652  
VERSION CF296652.1 GI:33665685  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1. .15  
/organism="Oryza sativa"  
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with oligoribonucleotides and then used as templates for  
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Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2799  
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Db 14 AAAAAAAAAAAAAA 1

RESULT 3111  
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LOCUS 15 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--04-K23.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--04-K23, mRNA sequence.  
ACCESSION CF329379  
VERSION CF329379.1 GI:33806995  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 14; DB 1; Length 15;  
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Qy 2166 TTTT TTTT TTTT TTTT TTTT 2179  
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RESULT 3112  
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LOCUS CF329379 15 bp mRNA linear EST 18-AUG-2003  
 DEFINITION NACL--04-K23.g1 Rice callus plasmid cDNA library (NACL) Oryza  
 sativa cDNA clone NACL--04-K23, mRNA sequence.

ACCESSION CF329379  
 VERSION CF329379.1 GI:33806995  
 KEYWORDS EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 15)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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1..15  
 /organism="Oryza sativa"  
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 /clone="NACL--04-K23"  
 /tissue\_type="callus"  
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 /clone\_lib="Rice callus plasmid cDNA library (NACL)"  
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 RT-PCR."

Query Match 0.5%; Score 14; DB 1; Length 15;  
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 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2799  
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 Db 15 AAAAAAAAAAAAAA 2

RESULT 3113  
 CF291803/c

LOCUS CF291803 16 bp mRNA linear EST 14-AUG-2003  
 DEFINITION 14ROOT--02-G05.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
 sativa cDNA clone 14ROOT--02-G05, mRNA sequence.

ACCESSION CF291803  
 VERSION CF291803.1 GI:33660836  
 KEYWORDS EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 16)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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 with oligoribonucleotides and then used as templates for  
 RT-PCR."

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 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT TTTT 2179  
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 Db 16 TTTT TTTT TTTT TTTT TTTT 3

RESULT 3114  
 AW250784

LOCUS AW250784 17 bp mRNA linear EST 07-JAN-2000  
 DEFINITION 2822335.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2822335 3',  
 mRNA sequence.

ACCESSION AW250784  
 VERSION AW250784.1 GI:6593777  
 KEYWORDS EST.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 17)

AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)

COMMENT Other ESTs: 2822335.5prime  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-re@mail.nih.gov

Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling  
 Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
 Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
 project Clone distribution: MGC clone distribution information can  
 be found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
 Scores: PHRED from University of Washington Genome Center. Vector  
 Trimming: cross match from University of Washington Genome Center  
 PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
 Drosophila Genome Project. University of Washington Genome Center:  
 http://www.genome.washington.edu/low Quality Sequence: 0 contiguous  
 PHRED high quality bases following vector sequence. Very Low  
 Quality Sequence: Trace file contained 17 contiguous distinct peaks  
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 Location/Qualifiers

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 /mol\_type="mRNA"

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/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Query Match 0.5%; Score 14; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 3e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2166 TTTTNTTTT 2182  
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Db 1 TTNNTTTT 17

RESULT 3115  
AW250784/c

LOCUS AW250784 17 bp mRNA linear EST 07-JAN-2000  
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mRNA sequence.  
ACCESSION AW250784  
VERSION AW250784.1 GI:6593777  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2822335.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling  
Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
<http://www.genome.washington.edu> Low Quality Sequence: 0 contiguous  
PHRED high quality bases following vector sequence. Very Low  
Quality Sequence: Trace file contained 17 contiguous distinct peaks  
following vector sequence.  
Plate: LLCM9 row: C column: 8.

FEATURES  
source  
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/note="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 14; DB 1; Length 17;  
Best Local Similarity 82.4%; Pred. No. 3e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2802  
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Db 17 AAAAAAAAAAANNNA 1

RESULT 3116  
BG673623/c

LOCUS BG673623 17 bp mRNA linear EST 30-APR-2001  
DEFINITION DRNAQC09 Rat DRG Library Rattus norvegicus cDNA clone DRNAQC09  
5', mRNA sequence.  
ACCESSION BG673623  
VERSION BG673623.1 GI:13895722  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 17)  
Xiao, H.S., Huang, Q.H., Zhang, F.X., Bao, L., Lu, Y.J., Guo, C.,  
Yang, L., Huang, W.J., Fu, G., Xu, S.H., Cheng, X.P., Yan, Q., Zhu, Z.D.,  
Zhang, X., Chen, Z., Han, Z.G. and Zhang, X.  
Identification of gene expression profile of dorsal root ganglion  
in the rat peripheral axotomy model of neuropathic pain  
Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)

REFERENCE 1  
AUTHORS Xiao, H.S., Huang, Q.H., Zhang, F.X., Bao, L., Lu, Y.J., Guo, C.,  
Yang, L., Huang, W.J., Fu, G., Xu, S.H., Cheng, X.P., Yan, Q., Zhu, Z.D.,  
Zhang, X., Chen, Z., Han, Z.G. and Zhang, X.  
TITLE Identification of gene expression profile of dorsal root ganglion  
in the rat peripheral axotomy model of neuropathic pain  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)  
MEDLINE 22056133  
PUBMED 12060780  
COMMENT Contact: Zhang Xu  
Laboratory of Sensory System  
Institute of Neuroscience  
320 Yue Yang Road, Shanghai 200031, P.R.China  
Tel: 86-21-64748700-121  
Fax: 86-21-64713446  
Email: [xu.zhang@ion.ac.cn](mailto:xu.zhang@ion.ac.cn)  
This clone is also available at Chinese National Human Genome  
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,  
Pudong New Area, P.R.China. Please contact with Zhang Xu  
([xu.zhang@ion.ac.cn](mailto:xu.zhang@ion.ac.cn)) or Han Zeguang ([hanzg@chgc.sh.cn](mailto:hanzg@chgc.sh.cn))  
PCR Primers  
FORWARD: T3  
BACKWARD: T7  
Seq primer: T3  
POLYA=NO.

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2175 TTTTNTTTT 2188  
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Db 17 TTTTNTTTT 4

RESULT 3117



AZ465954/c  
LOCUS  
DEFINITION  
AZ465954  
1M0276E16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0276E16 F, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0276 row: E column: 16  
Seq primer: CGTTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.5%; Score 14; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
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Qy 2786 AAAAAAAAAAAAAA 2799  
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Db 19 AAAAAAAAAAAAAA 6  
RESULT 3118  
AZ856873

AZ856873  
LOCUS  
DEFINITION  
AZ856873  
2M0161O19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0161O19 F, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
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High quality sequence stop: 19.  
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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.5%; Score 14; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2166 TTTTTTTTTTTTTT 2179  
|||||  
Db 1 TTTTTTTTTTTTTT 14  
RESULT 3119  
AZ950028/c  
LOCUS  
AZ950028

DEFINITION 2M0213L19R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0213L19 R, genomic survey sequence.

ACCESSION AZ950028

VERSION AZ950028.1 GI:13821255

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0213 row: L column: 19  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

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/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 14; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2179

Db 19 TTTT TTTT TTTT TTTT TTTT 6

RESULT 3120

CF332005/C

LOCUS

DEFINITION NACL--08-F13.b1 Rice callus plasmid cDNA library (NACL) Oryza

sativa cDNA clone NACL--08-F13, mRNA sequence.

CF332005

VERSION CF332005.1 GI:33812230

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 19)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source Location/Qualifiers  
1..19  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="NACL--08-F13"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.Coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 14; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAA AAAAAA AAAAA 2798  
|||||

Db 14 GAAAAA AAAAAA AAAAA 1

RESULT 3121

CF313751

LOCUS

DEFINITION HD--01-P23.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--01-P23, mRNA sequence.

ACCESSION CF313751

VERSION CF313751.1 GI:33685512

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE 1 (bases 1 to 20)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source Location/Qualifiers  
1..20  
/organism="Oryza sativa"

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/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--01-P23"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAc1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

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Query Match          0.5%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	2166	TTTTTTTTTTTTTT	2179
Db	1	TTTTTTTTTTTTTT	14

RESULT 3122	CF313752/c	CF313752	20 bp	mRNA	linear	EST 15-AUG-2003
LOCUS						
DEFINITION						HD--01-P23.g1 OSHDACL-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--01-P23, mRNA sequence.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

AUTHORS	Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr

```
Query Match          0.5%; Score 14; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2166 TTTTTTTTTTTTTT 2179

```

Db                20 TTTTTTTTTTTTTT 7

RESULT 3123
AZ785791
LOCUS              AZ785791          21 bp      DNA      linear      GSS 16-FEB-2001
DEFINITION        IM0030019F Mouse 10kb plasmid UUGClM library Mus musculus genomic
                   clone UUGClM0030019 F, genomic survey sequence.

```

REFERENCE  
1 (bases 1 to 21)

Query Match 0.5%; Score 14; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	2166	TTTTTTTTTTTTTTTT	2179
Db	1	TTTTTTTTTTTTTTTT	14



RESULT 3124	AZ375417	22 bp	DNA	linear	GSS 02-OCT-2000
LOCUS	1M0128E13R	Mouse 10kb plasmid	UUGC1M	library	Mus musculus genomic
DEFINITION	clone UUGC1M0128E13 R,	genomic survey	sequence.		
ACCESSION	AZ375417				
VERSION	AZ375417.1	GI:10489117			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 22)				
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0128 row: E column: 13 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 22.				
FEATURES	Location/Qualifiers				
source	1. .22				
	/organism="Mus musculus"				
	/mol_type="genomic DNA"				
	/strain="CS7BL/6J"				
	/db_xref="taxon:10090"				
	/clone="UUGC1M0128E13"				
	/sex="Male"				
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"				
	/clone_lib="Mouse 10kb plasmid UUGC1M library"				
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."				
Query Match	0.5%;	Score 14;	DB 1;	Length 22;	
Best Local Similarity	100.0%;	Pred. No. 3.9e+03;			
Matches	14;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	2786	AAAAAAAAAAAAA	2799		
Db	7	AAAAAAAAAAAAA	20		
RESULT 3125	AZ854229	22 bp	DNA	linear	GSS 21-FEB-2001
LOCUS	2M0157C14R	Mouse 10kb plasmid	UUGC1M	library	Mus musculus genomic
DEFINITION	clone UUGC2M0157C14 R,	genomic survey	sequence.		
ACCESSION	AZ854229				
VERSION	AZ854229.1	GI:13043139			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 22)				
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0157 row: C column: 14 Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 22.				
FEATURES	Location/Qualifiers				
source	1. .22				
	/organism="Mus musculus"				
	/mol_type="genomic DNA"				
	/strain="CS7BL/6J"				
	/db_xref="taxon:10090"				
	/clone="UUGC2M0157C14"				
	/sex="Male"				
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"				
	/clone_lib="Mouse 10kb plasmid UUGC1M library"				
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."				
Query Match	0.5%;	Score 14;	DB 1;	Length 22;	
Best Local Similarity	77.3%;	Pred. No. 3.9e+03;			
Matches	17;	Conservative 0;	Mismatches 5;	Indels 0;	Gaps 0;
Qy	2779	AGATTGAAAAAAAAA	2800		
Db	1	AAAGAGAGAGAAAGAAAAA	22		



QY 2786 AAAAAAAAAAAAAA 2799  
Db 24 AAAAAAAAAAAAAA 11

RESULT 3129  
CNS00HLD/c  
LOCUS  
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC:  
BACR35D24 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.  
ACCESSION AL073529  
VERSION AL073529.1 GI:4953410  
KEYWORDS GSS.  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
COMMENT Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

FEATURES  
source  
1. .24  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACR35D24"  
/clone\_lib="RPCI-98"  
/note="end : T7"

Query Match 0.5%; Score 14; DB 1; Length 24;  
Best Local Similarity 78.9%; Pred. No. 3.7e+03;  
Matches 15; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2804  
Db 23 AAAAAAAAAHBAAACAAA 5

RESULT 3130  
AU012885  
LOCUS  
DEFINITION AU012885 Schizosaccharomyces pombe late log phase cDNA  
Schizosaccharomyces pombe cDNA clone spc07426, mRNA sequence.  
ACCESSION AU012885  
VERSION AU012885.1 GI:3357794  
KEYWORDS EST.  
SOURCE Schizosaccharomyces pombe (fission yeast)  
ORGANISM Schizosaccharomyces pombe  
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomycetes.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Morimyo,M. and Mita,K.

TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe  
JOURNAL Unpublished (1998)  
COMMENT Contact: Mitsuoki Morimyo  
Genome Research Group  
National Institute of Radiological Sciences  
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan  
Email: morimyo@nirs.go.jp.  
FEATURES  
source  
1. .25  
/organism="Schizosaccharomyces pombe"  
/mol\_type="mRNA"  
/strain="972"  
/db\_xref="taxon:4896"  
/clone="spc07426"  
/sex="h minus"  
/clone\_lib="Schizosaccharomyces pombe late log phase cDNA"  
/note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, <http://www.nirs.go.jp>)"

Query Match 0.5%; Score 14; DB 1; Length 25;  
Best Local Similarity 77.3%; Pred. No. 3.6e+03;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAA 2802  
Db 4 AACTCAAAGCTAAAAAAAAA 25

RESULT 3131  
AZ510128  
LOCUS  
DEFINITION 1M0354L23F Mouse 10kb plasmid UUGClM library Mus musculus genomic clone UUGClM0354L23 F, genomic survey sequence.  
ACCESSION AZ510128  
VERSION AZ510128.1 GI:10691444  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb Plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [rdunn@genetics.utah.edu](mailto:rdunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0354 row: L column: 23  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 25.  
FEATURES  
source  
1. .25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="CS7BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGClM0354L23"



/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

```
Query Match          0.5%; Score 14; DB 1; Length 25;  
Best Local Similarity 77.3%; Pred. NO. 3.6e+03;  
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

QY 2783 TTGAAAAAAAAAAAAAAAAAAAAA 2804  
||| ||||||| | |  
db 1 TTAACAAAAAAAAAAACCATACA 22

RESULT	3132
AZ997733	
LOCUS	AZ997733          25 bp        DNA         linear         GSS 27-APR-2001
DEFINITION	2M0284E22F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0284E22 F, genomic survey sequence.

SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 25)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb

```

FEATURES
source
1. .25
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0284E22"
/sex="Female"

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/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match	0.5%;	Score 14;	DB 1;	Length 25;
Best Local Similarity	100.0%;	Pred. No. 3.6e+03;		
Matches 14;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	2786	AAAAAAAAAAAAAAAA	2799	
Db	1	AAAAAAAAAAAAAAAA	14	

RESULT 3133  
AW246446  
LOCUS  
DEFINITION  
AW246446  
2821601.3prime NIH\_MGC\_7 Homo sapiens CDNA clone IMAGE:2821601 3',  
17 bp mRNA linear  
mRNA sequence. EST 07-JAN-2000

REFERENCE  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other ESRs: 2821601.5prime

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FEATURES
  source
    1. .17
      /organism="Homo sapiens"
      /mol_type="mrna"
      /db_xref="taxon:9606"

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/clone="IMAGE:2821601"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Query Match 0.5%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 3.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1922 TTTTTCAGTGTAA 1938  
Db 1 TTTTTCAGTGTAA 17

RESULT 3134  
AW247949  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AW247949 17 bp mRNA linear EST 07-JAN-2000  
2820605.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2820605 3',  
mRNA sequence.  
AW247949  
AW247949.1 GI:6591037  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2820605.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center.  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 0 contiguous  
PHRED high quality bases following vector sequence. Very Low  
Quality Sequence: Trace file contained 17 contiguous distinct peaks  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LLCM4 row: K column: 6.  
Location/Qualifiers  
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/cell\_line="MGC3"  
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/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average

Query Match 0.5%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 3.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1922 TTTTTCAGTGTAA 1938  
Db 1 TTTTTCAGTGTAA 17

RESULT 3134  
AW247949  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AW247949 17 bp mRNA linear EST 07-JAN-2000  
2820605.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2820605 3',  
mRNA sequence.  
AW247949  
AW247949.1 GI:6591037  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2820605.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center.  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 0 contiguous  
PHRED high quality bases following vector sequence. Very Low  
Quality Sequence: Trace file contained 17 contiguous distinct peaks  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LLCM4 row: K column: 6.  
Location/Qualifiers  
1. .17  
/organism="Homo sapiens"  
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/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 3.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2166 TTTTTCAGTGTAA 2182  
Db 1 TTTTTCAGTGTAA 17

RESULT 3135  
AW247949/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AW247949 17 bp mRNA linear EST 07-JAN-2000  
2820605.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2820605 3',  
mRNA sequence.  
AW247949  
AW247949.1 GI:6591037  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2820605.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center.  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 0 contiguous  
PHRED high quality bases following vector sequence. Very Low  
Quality Sequence: Trace file contained 17 contiguous distinct peaks  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LLCM4 row: K column: 6.  
Location/Qualifiers  
1. .17  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2820605"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 3.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      17 AAAAACTAAAAAAAAAAAA 1

RESULT 3136
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LOCUS
DEFINITION
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  2820717.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820717 3',
  mRNA sequence.
ACCESSION
  AW247976
  2820717.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820717 3',
  mRNA sequence.
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 17)
REFERENCE
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Other ESTs: 2820717.5prime
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
  Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
  Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
  project Clone distribution: MGC clone distribution information can
  be found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
  Scores: PHRED from University of Washington Genome Center. Vector
  Trimming: cross match from University of Washington Genome Center
  PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
  Drosophila Genome Project. University of Washington Genome Center:
  http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
  PHRED high quality bases following vector sequence. Very Low
  Quality Sequence: Trace file contained 17 contiguous distinct peaks
  following vector sequence. Polyadenylation: Based upon the presence
  of a XhoI site followed by a run of 14 or more T residues at the
  beginning of the sequence, this cDNA insert was polyadenylated.
  Plate: LLC4 row: 0 column: 22.
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  /cell_line="MGC3"
  /lab_host="DH10B (phage-resistant)"
  /clone_lib="NIH MGC 7"
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  EcoRI; cDNA made by oligo-dT priming. Directionally
  cloned into EcoRI/XhoI sites using the following 5'
  adaptor: GGCACGAG(G). Size-selected >500bp for average
  insert size 1.8kb. Library constructed by Ling Hong in
  the laboratory of Gerald M. Rubin (University of
  California, Berkeley) using ZAP-cDNA synthesis kit
  (Stratagene) and Superscript II RT (Life Technologies)."
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Query Match      0.5%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.2e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2177 TTTTNTTTTAACTTTG 2193
Db      1 TTTTNTTTTAAATG 17

RESULT 3137
AW248779/c
LOCUS
DEFINITION
  AW248779
  2821015.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821015 3',
  mRNA sequence.
ACCESSION
  AW248779
  2821015.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821015 3',
  mRNA sequence.
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 17)
REFERENCE
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Other ESTs: 2820717.5prime
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
  Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
  Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
  project Clone distribution: MGC clone distribution information can
  be found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
  Scores: PHRED from University of Washington Genome Center. Vector
  Trimming: cross match from University of Washington Genome Center
  PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
  Drosophila Genome Project. University of Washington Genome Center:
  http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
  PHRED high quality bases following vector sequence. Very Low
  Quality Sequence: Trace file contained 17 contiguous distinct peaks
  following vector sequence. Polyadenylation: Based upon the presence
  of a XhoI site followed by a run of 14 or more T residues at the
  beginning of the sequence, this cDNA insert was polyadenylated.
  Plate: LLC4 row: 0 column: 22.
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  /cell_line="MGC3"
  /lab_host="DH10B (phage-resistant)"
  /clone_lib="NIH MGC 7"
  /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
  EcoRI; cDNA made by oligo-dT priming. Directionally
  cloned into EcoRI/XhoI sites using the following 5'
  adaptor: GGCACGAG(G). Size-selected >500bp for average
  insert size 1.8kb. Library constructed by Ling Hong in
  the laboratory of Gerald M. Rubin (University of
  California, Berkeley) using ZAP-cDNA synthesis kit
  (Stratagene) and Superscript II RT (Life Technologies)."
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QY      2778 TAGAATTGAAAAAAAA 2794
Db      17 TAGCTTGAAAAAAAA 1

RESULT 3138
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LOCUS
DEFINITION
  BQ797972
  EST 6910 Ripening Grape berries Lambda Zap II Library Vitis
  vinifera cDNA clone RT092F02 3', mRNA sequence.
ACCESSION
  BQ797972
  BQ797972.1 GI:22012938
  EST.
SOURCE
  Vitis vinifera
  Vitis vinifera
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  rosids; Vitaceae; Vitis.

mRNA sequence.
AW248779
AW248779.1 GI:6591772
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 17)
REFERENCE
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Other ESTs: 2821015.5prime
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
  Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
  Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
  project Clone distribution: MGC clone distribution information can
  be found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
  Scores: PHRED from University of Washington Genome Center. Vector
  Trimming: cross match from University of Washington Genome Center
  PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
  Drosophila Genome Project. University of Washington Genome Center:
  http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
  PHRED high quality bases following vector sequence. Very Low
  Quality Sequence: Trace file contained 17 contiguous distinct peaks
  following vector sequence. Polyadenylation: Based upon the presence
  of a XhoI site followed by a run of 14 or more T residues at the
  beginning of the sequence, this cDNA insert was polyadenylated.
  Plate: LLC5 row: L column: 8.
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  EcoRI; cDNA made by oligo-dT priming. Directionally
  cloned into EcoRI/XhoI sites using the following 5'
  adaptor: GGCACGAG(G). Size-selected >500bp for average
  insert size 1.8kb. Library constructed by Ling Hong in
  the laboratory of Gerald M. Rubin (University of
  California, Berkeley) using ZAP-cDNA synthesis kit
  (Stratagene) and Superscript II RT (Life Technologies)."
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REFERENCE 1 (bases 1 to 17)  
AUTHORS Abbal,P., Agasse,A., Ageorges,A., Atanassova,R., Barrieu,F., Couture,C., Dedaldechamp,F., Delrot,S., Glissant,D., Grimplet,J., Hamdi,S., Romieu,C. and Terrier,N.  
TITLE Generation of Expressed Sequence Tag from Grape Berry (skin, pulp or seeds) at Various Developmental Stages  
JOURNAL Unpublished (2002)  
COMMENT Contact: Romieu C.  
Unite de Recherche des Produits de la Vigne  
Institut National de la Recherche Agronomique  
2, place Viala, 34 060 Montpellier Cedex 01, France  
Tel: 00-33-(0)4-99-61-28-62  
Fax: 00-33-(0)4-99-61-28-57  
Email: romieu@ensam.inra.fr  
Seq primer: T7.

FEATURES Location/Qualifiers  
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/note="Organ: Fruit; Vector: Lambda Zap II; Site\_1: Eco RI; Site\_2: XhoI; Oriented library, construction described in Generation of ESTs from grape Berry (skin, pulp or seeds) at various developmental stages by Terrier,N., Ageorges,A., Abbal,P., Romieu,C. in J. Plant Physiol. 158 (12): 1575-83 2001"

Query Match 0.5%; Score 13.8; DB 1; Length 17;  
Best Local Similarity 88.2%; Pred. No. 3.2e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1129 TGAAGCCGAATTCCTA 1145  
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RESULT 3139  
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LOCUS AW249856 18 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2821566.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821566 3', mRNA sequence.  
ACCESSION AW249856  
VERSION AW249856.1 GI:6592849  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other\_ESTs: 2821566.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project  
Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 9 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 18 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence

of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated. Plate: LLCM7 row: C column: 7  
High quality sequence stop: 9.

FEATURES Location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="IMAGE:2821566"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 13.8; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2166 TTTTNTTTTNTTTT 2183  
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Db 1 TTTTNTTTTNTTTCCT 18

RESULT 3140  
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LOCUS AW249856 18 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2821566.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821566 3', mRNA sequence.

ACCESSION AW249856  
VERSION AW249856.1 GI:6592849  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other\_ESTs: 2821566.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project  
Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 9 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 18 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated. Plate: LLCM7 row: C column: 7  
High quality sequence stop: 9.

FEATURES Location/Qualifiers  
source 1..18  
/organism="Homo sapiens"  
/mol\_type="mRNA"



Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 19)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers  
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/clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 88.2%; Pred. No. 3.7e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2784 TGAATAAAAAAAAAAAAAA 2800  
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Db 17 TGTATAAAAAAAAAAAAAA 1

RESULT 3144  
AZ323986 19 bp DNA linear GSS 29-SEP-2000  
LOCUS 1M0045P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0045P09 R, genomic survey sequence.  
ACCESSION AZ323986  
VERSION AZ323986.1 GI:10379252  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0045 row: P column: 09  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. .19

FEATURES  
source

/organism="Mus musculus"  
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/db\_xref="taxon:10090"  
/clone="UUGC1M0045P09"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.5%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 88.2%; Pred. No. 3.7e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2164 CCTTTTCTTTTCTTTTCTTTT 2180  
||||| ||||| |||||  
Db 3 CCTTTTCTTTTCTTTTCTTTT 19

RESULT 3145  
AZ854647/c 19 bp DNA linear GSS 21-FEB-2001  
LOCUS 2M0158P15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0158P15 F, genomic survey sequence.  
ACCESSION AZ854647  
VERSION AZ854647.1 GI:13043971  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
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plasmid inserts  
Unpublished (2000)  
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University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0158 row: P column: 15  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
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/organism="Mus musculus"

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source



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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.5%; Score 13.8; DB 1; Length 19;  
Best Local Similarity 88.2%; Pred. No. 3.7e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 51 GCGGCGGGGGCGGGCGGC 67  
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Db 17 GGGGCGGGGGCGGGGGGC 1

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RESULT 3146
AZ304038
LOCUS AZ304038 20 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0003L08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0003L08 R, genomic survey sequence.
ACCESSION AZ304038
VERSION AZ304038.1 GI:10339611
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0003 row: L column: 08
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
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/mol_type="genomic DNA"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.5%; Score 13.8; DB 1; Length 20;  
Best Local Similarity 88.2%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2176 TTTT TTTT TTTT TTAAC TTT 2192  
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Db 1 TTTT TCTTTT TATC TTT 17

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RESULT 3147
AZ469472
LOCUS AZ469472 20 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0283A06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0283A06 F, genomic survey sequence.
ACCESSION AZ469472
VERSION AZ469472.1 GI:10627597
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0283 row: A column: 06
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
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Location/Qualifiers
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

```
Query Match      0.5%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2161 TCTCCTTTTGTGTTTTT 2177
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Db      4 TCTGCTTTTGTGTTTTT 20
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RESULT 3148
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LOCUS      20 bp      DNA      linear      GSS 05-OCT-2000
DEFINITION      1M0357J21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0357J21 R, genomic survey sequence.
ACCESSION      AZ512414
VERSION      AZ512414.1 GI:10693730
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0357 row: J column: 21
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
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10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

```
Query Match      0.5%; Score 13.8; DB 1; Length 20;
Best Local Similarity 88.2%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      49 GCGCGCGGGGGCGGCG 65
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RESULT 3149
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LOCUS      21 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION      1M0059K09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0059K09 R, genomic survey sequence.
ACCESSION      AZ331619
VERSION      AZ331619.1 GI:10394486
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE      1 (bases 1 to 21)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0059 row: K column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
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/clone="UUGC1M0059K09"
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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.8; DB 1; Length 21;  
Best Local Similarity 88.2%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2783 TTGAAAAA 2799  
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Db 5 TTTAAAAA 21

RESULT 3150  
AZ788269/c  
LOCUS  
DEFINITION  
2M0035D18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0035D18 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0035 row: D column: 18  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.

FEATURES  
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/sex="Male"

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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.8; DB 1; Length 21;  
Best Local Similarity 88.2%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1851 CCAACAGACCCACAC 1867  
|||  
Db 19 CCTACACCCACAC 3

RESULT 3151  
AZ386904/c

LOCUS  
DEFINITION  
1M0146C12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0146C12 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0146 row: C column: 12  
Seq primer: CGTTGTAACGACGCCAGT  
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High quality sequence stop: 21.

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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"



/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.5%; Score 13.8; DB 1; Length 21;  
Best Local Similarity 88.2%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1941 TAATGGTTGGTTTGT 1957  
Db 17 TCATGGTTGGTTGTGT 1

RESULT 3152  
AW249550/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 23)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2821204.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 9 contiguous  
PHRED high quality bases following vector sequence. Very low  
Quality Sequence: Trace file contained 23 contiguous distinct peaks  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: L1CM6 row: D column: 5  
High quality sequence stop: 9.  
Location/Qualifiers  
1. .23  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821204"

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 9 contiguous  
PHRED high quality bases following vector sequence. Very low  
Quality Sequence: Trace file contained 23 contiguous distinct peaks  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: L1CM6 row: D column: 5  
High quality sequence stop: 9.  
Location/Qualifiers  
1. .23  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821204"

FEATURES  
source  
1. .23  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821204"

/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 13.8; DB 1; Length 23;  
Best Local Similarity 88.2%; Pred. No. 3.8e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2781 AATTGAAAAA 2797  
Db 17 AATTGTTAAAAA 1

RESULT 3153  
AI560179  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 25)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .25  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2213137"  
/tissue\_type="well-differentiated endometrial  
adenocarcinoma, 7 pooled tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI-CGAP\_Utl1"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.75 kb. Life Technologies catalog #:  
11538-014"

FEATURES  
source  
1. .25  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2213137"  
/tissue\_type="well-differentiated endometrial  
adenocarcinoma, 7 pooled tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI-CGAP\_Utl1"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.75 kb. Life Technologies catalog #:  
11538-014"

Query Match 0.5%; Score 13.8; DB 1; Length 25;  
Best Local Similarity 88.2%; Pred. No. 3.6e+03;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802  
Db 1 AAAAAAAGAAAAAA 17

RESULT 3154  
AZ426873  
LOCUS  
DEFINITION 1M0208L05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0208L05 R, genomic survey sequence.  
ACCESSION AZ426873  
VERSION AZ426873.1 GI:10550886  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0208 row: L column: 05  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0208L05"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1979 AAAAAAAAAAGTGTAT 1998  
Db 1 AAAAAAAAAAGATGAT 20

RESULT 3155  
AZ303903/c  
LOCUS  
DEFINITION AZ303903 20 bp DNA linear GSS 29-SEP-2000  
1M0003B18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0003B18 R, genomic survey sequence.  
ACCESSION AZ303903  
VERSION AZ303903.1 GI:10339339  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0003 row: B column: 18  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0003B18"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;





RESULT 3158  
AZ645269  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source  
1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0510B10"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 289 CCGCGCGCCACCCCTCTCCC 308  
|||||  
1 CCCCCCCCCCCCCCTCCCC 20

Db

RESULT 3159  
AZ786781  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source  
1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0032C05"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2161 TCTCCTTTTCTTTTCTTTTCTTTT 2180  
|||||  
1 TCCCATATATATTTTCTTTT 20

Db

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RESULT 3160
AU267211/c
LOCUS
DEFINITION AU267211 VS Dictyostelium discoideum cDNA clone VSH291 5', mRNA
sequence.
ACCESSION AU267211 23 bp mRNA linear EST 10-MAY-2002
VERSION AU267211.1 GI:20526009
KEYWORDS
SOURCE
ORGANISM Dictyostelium discoideum
REFERENCE Dictyostelium discoideum
AUTHORS Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 23)
TITLE Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M.,
Takeuchi,I., Kohara,Y. and Tanaka,Y.
POPULATION ANALYSIS Population analysis of cDNAs from unicellular and multicellular
STAGES OF Dictyostelium discoideum
UNPUBLISHED Unpublished (2002)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.
FEATURES
source
Location/Qualifiers
1..23
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSH291"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

Query Match 0.5%; Score 13.6; DB 1; Length 23;
Best Local Similarity 80.0%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1772 TTTT TTTT TTTT GAACCCCAT 1791
Db 23 TTTT TTTT TTTT GTATACATT 4

RESULT 3161
CK277017/c
LOCUS
DEFINITION CK277017 potato abiotic stress cDNA library Solanum tuberosum cDNA
clone POADX19 3' end, mRNA sequence.
ACCESSION CK277017
VERSION CK277017.1 GI:398333995
KEYWORDS
SOURCE
ORGANISM Solanum tuberosum (potato)
REFERENCE Solanum tuberosum
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
JOURNAL asterids; lamids; Solanales; Solanaceae; Solanum.
COMMENT 1 (bases 1 to 23)
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
Generation of ESTs from abiotic stressed potato tissue
UNPUBLISHED (2003)
Other_ESTs: EST723094
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.
FEATURES
source
Location/Qualifiers
1..23
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"

RESULT 3162
CF290849
LOCUS
DEFINITION CF290849 15 bp mRNA linear EST 14-AUG-2003
14ROOT--01-A17.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-A17, mRNA sequence.
ACCESSION CF290849
VERSION CF290849.1 GI:33659882
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--01-A17"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
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/db_xref="taxon:4113"
/clone="POADX19"
/tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="potato abiotic stress cDNA library"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
application. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots:3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."

Query Match 0.5%; Score 13.6; DB 1; Length 23;
Best Local Similarity 80.0%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2783 TTGA AAAAAA AAAAAA AAAAAA 2802
Db 21 TTAAGAAA AAAAAA AAGAAATAA 2

RESULT 3162
CF290849
LOCUS
DEFINITION CF290849 15 bp mRNA linear EST 14-AUG-2003
14ROOT--01-A17.g1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-A17, mRNA sequence.
ACCESSION CF290849
VERSION CF290849.1 GI:33659882
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
Location/Qualifiers
1..15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ROOT--01-A17"
/tissue_type="root"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
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/clone_lib="Rice root plasmid cDNA library (14ROOT)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.5%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2800
      ||||| ||||| |||||
Db      1 AAAAAATAAAAAAAA 15

RESULT 3163
CF290849/c
LOCUS      14ROOT--01-A17.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION      sativa cDNA clone 14ROOT--01-A17, mRNA sequence.
ACCESSION      CF290849
VERSION      CF290849.1 GI:33659882
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 15)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES      source
      1..15
      /organism="Oryza sativa"
      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:4530"
      /clone="14ROOT--01-A17"
      /tissue_type="root"
      /dev_stage="14 days after germination"
      /lab_host="E.coli DH10B"
      /clone_lib="Rice root plasmid cDNA library (14ROOT)"
      /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
      with oligoribonucleotides and then used as templates for
      RT-PCR."

REFERENCE      1 (bases 1 to 15)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES      source
      1..15
      /organism="Oryza sativa"
      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:4530"
      /clone="14ROOT--01-A17"
      /tissue_type="root"
      /dev_stage="14 days after germination"
      /lab_host="E.coli DH10B"
      /clone_lib="Rice root plasmid cDNA library (14ROOT)"
      /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
      with oligoribonucleotides and then used as templates for
      RT-PCR."

Query Match      0.5%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2166 TTTTTTTTTTTTTT 2180
      ||||| ||||| |||||
Db      15 TTTTTTTTATTTT 1

RESULT 3164
CF291030
LOCUS      14ROOT--01-E19.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION      sativa cDNA clone 14ROOT--01-E19, mRNA sequence.
ACCESSION      CF291030
VERSION      CF291030.1 GI:33660063
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 15)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES      source
      1..15
      /organism="Oryza sativa"
      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:4530"
      /clone="14ROOT--01-E19"
      /tissue_type="root"
      /dev_stage="14 days after germination"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 15)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES      source
      1..15
      /organism="Oryza sativa"
      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:4530"
      /clone="14ROOT--01-E19"
      /tissue_type="root"
      /dev_stage="14 days after germination"
      /lab_host="E.coli DH10B"
      /clone_lib="Rice root plasmid cDNA library (14ROOT)"
      /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
      with oligoribonucleotides and then used as templates for
      RT-PCR."

Query Match      0.5%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.8e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2800
      ||||| ||||| |||||
Db      1 AAAAAATAAAAAAAA 15

RESULT 3165
CF291030/c
LOCUS      14ROOT--01-E19.g1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION      sativa cDNA clone 14ROOT--01-E19, mRNA sequence.
ACCESSION      CF291030
VERSION      CF291030.1 GI:33660063
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 15)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES      source
      1..15
      /organism="Oryza sativa"
      /mol_type="mRNA"
      /cultivar="Nackdong"
      /db_xref="taxon:4530"
      /clone="14ROOT--01-E19"
      /tissue_type="root"
      /dev_stage="14 days after germination"
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/lab\_host="E.coli DH10B"  
/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2.8e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTATTTTATTTT 2180  
| | | | | | | | | |  
Db 15 TTTTATTTTATTTT 1

RESULT 3166  
CF301470 15 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--06-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--06-F15, mRNA sequence.

ACCESSION CF301470  
VERSION CF301470.1 GI:33673231  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 15)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

1..15  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--06-F15"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2.8e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTATTTTATTTT 2180  
| | | | | | | | | |  
Db 1 TGTATTTTATTTT 15

RESULT 3167  
CF301470/c 15 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--06-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--06-F15, mRNA sequence.

ACCESSION CF301470  
VERSION CF301470.1 GI:33673231  
KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 15)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..15  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2.8e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800  
| | | | | | | | | |  
Db 15 AAAAAAAAAAAAAA 1

RESULT 3168

CF330669/c

LOCUS

DEFINITION

NACL--06-H16.g1 Rice callus plasmid cDNA library (NACL) Oryza

sativa cDNA clone NACL--06-H16, mRNA sequence.

ACCESSION CF330669

VERSION CF330669.1 GI:33809573

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 15)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

1..15  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
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/clone="NACL--06-H16"  
/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2.8e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2178 TTTTCTTTTAACTTT 2192  
|||||  
Db 15 TTTTCTTTTAAATTT 1

RESULT 3169  
CF543203/c  
LOCUS 15 bp mRNA linear EST 22-SEP-2003  
DEFINITION S014679-024-030-D05-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone  
024-030-D05 5-PRIME, mRNA sequence.

ACCESSION CF543203.1 GI:34891643  
VERSION  
KEYWORDS  
SOURCE

ORGANISM

Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 15)  
AUTHORS Herwig,R.; Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED

COMMENT

Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851  
Email: weisssha@mpiz-koeln.mpg.de  
Insert Length: 15 Std Error: 0.00  
Plate: 30 row: D column: 05  
Seq primer: SP6.

FEATURES

source

Location/Qualifiers  
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/organism="Beta vulgaris"  
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line)"

/db\_xref="GABI:936579"  
/db\_xref="taxon:161934"  
/clone="024-030-D05"  
/tissue\_type="leaf"  
/lab\_host="EMDH10B"

/clone\_lib="MPIZ-ADIS-024-leaf"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and

orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.5%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2.8e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2175 TTTTCTTTTAAAC 2189  
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Db 15 TTTTCTTTTTCAC 1

RESULT 3170

BQ583458/c

LOCUS

DEFINITION

BQ583458 16 bp mRNA linear EST 06-DEC-2002  
E011979-024-005-J11-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris  
cDNA clone 024-005-J11 5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 16)

AUTHORS

Herwig,R.; Schulz,B., Weissshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189

PUBMED 12472698

COMMENT

Contact: Weisshaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weisssha@mpiz-koeln.mpg.de

Insert Length: 16 Std Error: 0.00

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Seq primer: SP6; CATACGATTAGGTGACACTATAG.

Location/Qualifiers

1..16

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line)"

/db\_xref="GABI:183240"

/db\_xref="taxon:161934"

/clone="024-005-J11"

/tissue\_type="inflorescence"

/lab\_host="EMDH10B"

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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and

orientation:

SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:

Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match

0.5%; Score 13.4; DB 1; Length 16;

Best Local Similarity 93.3%; Pred. No. 3.2e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2162 CTCCTTTTCTTTT 2176

|||||

Db 15 CCCCTTTTCTTTT 1

RESULT 3171

CF319827/c

LOCUS

DEFINITION

HD--10-H16.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
16 bp mRNA linear EST 15-AUG-2003





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/clone="UUGC2M0064M15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

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Query Match      0.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      2625 CTTTGTCTCGTTCCT 2639
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Db      2 CTTTGCCTCGTTCCT 16
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RESULT 3174
AZ810717
LOCUS      AZ810717      19 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION 2M0076N24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0076N24 F, genomic survey sequence.
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ACCESSION  AZ810717
VERSION     AZ810717.1  GI:12978242
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
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```
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0076 row: N column: 24
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0076N24"
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FEATURES
      source
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

```
Query Match      0.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      2783 TTGAAAAAATAAAAA 2797
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Db      5 TTGAAAAAATAAAAA 19
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RESULT 3175
AZ387816/c
LOCUS      AZ387816      20 bp      DNA      linear      GSS 02-OCT-2000
DEFINITION 1M0147B22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0147B22 R, genomic survey sequence.
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ACCESSION  AZ387816
VERSION     AZ387816.1  GI:10501524
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
```

```
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0147 row: B column: 22
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0147B22"
/sex="Male"
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FEATURES
      source
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/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 4.1e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1492 GGAGAAATGGAGAA 1506  
|||||  
Db 17 GGAGAAATGGAGTA 3

RESULT 3176  
AZ772074  
LOCUS  
DEFINITION  
1M0574M10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0574M10 R, genomic survey sequence.  
AZ772074  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0574 row: M column: 10  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0574M10"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

FEATURES  
source  
1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0574M10"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 4.1e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2672 CAGTGTGTGTGGTG 2686  
|||||  
Db 3 CAGTGTGTGTGTG 17

RESULT 3177  
AZ836069  
LOCUS  
DEFINITION  
2M0130J11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0130J11 R, genomic survey sequence.  
AZ836069  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0130 row: J column: 11  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0130J11"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

FEATURES  
source  
1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0130J11"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 4.1e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1299 TCGCCCCCAGTCTTGG 1313  
|||||||  
Db 6 TCGCCCCCATCTTGG 20

RESULT 3178

AZ957966  
LOCUS AZ957966 20 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0225I01F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0225I01 F, genomic survey sequence.

ACCESSION AZ957966  
VERSION AZ957966.1 GI:13829193  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0225 row: 1 column: 01

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

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/db\_xref="taxon:10090"

/clone="UUGC2M0225I01"

/sex="Female"

/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC2M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 4.1e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2162 CTCCTTTT TTTT TTTT 2176  
|||||||  
Db 6 CCGCTTTT TTTT TTTT 20

RESULT 3179

BX563723/c

LOCUS BX563723 22 bp mRNA linear EST 10-OCT-2003

DEFINITION BX563723 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse68e02\_plc, mRNA sequence.

ACCESSION BX563723

VERSION BX563723.1 GI:33430936

KEYWORDS EST.

SOURCE Glossina morsitans morsitans

ORGANISM Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Hippoboscoidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 22)

AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,

Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.

Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune

response genes

Genome Biol. 4 (10), R63 (2003)

22881942

14519198

COMMENT Contact: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J.Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix qlc are reverse primer reads starting at 5'

end of the cDNA all plc reads are from

the 3' end.

FEATURES

source

1..22 Location/Qualifiers

/organism="Glossina morsitans morsitans"

/mol\_type="mRNA"

/sub\_species="morsitans"

/db\_xref="taxon:37546"

/clone="Tse68e02\_plc"

/tissue\_type="adult infected gut"

/clone\_lib="Glossina morsitans morsitans adult infected gut"

/note="country: Zimbabwe; EST from adult gut infected with







Query Match 0.5%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 4e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2782 ATTGAAAAAATAAAAAA 2799  
||| | ||||| |||||  
Db 18 ATTAGTAAAAAATAAAAA 1

RESULT 3185  
CF332005  
LOCUS  
DEFINITION  
NACL--08-F13.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--08-F13, mRNA sequence.  
CF332005  
ACCESSION  
VERSION  
CF332005.1 GI:33812230  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
1 (bases 1 to 19)  
AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE  
Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1..19  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="NACL--08-F13"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13.2; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 4.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1771 TTTT TTTT TTTT GAACCC 1788  
||||| |||||  
Db 1 TTTT TTTT TTTT TTTT CCCC 18

RESULT 3186  
AA878744/c  
LOCUS  
DEFINITION  
AA878744  
of85a08.s1 NCI CGAP Li5 Homo sapiens cDNA clone IMAGE:1437110 3'  
similar to TR:Q67633 Q67633 ECO Q PROTEIN. [1]; contains TAR1.t2  
TAR1 repetitive element ;, mRNA sequence.  
AA878744  
AA878744.1 GI:2987709  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 19)  
AUTHORS  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL  
Unpublished (1997)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
unknown library type  
Trace considered overall poor quality  
Seq primer: -40m13 fwd. Et from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1..19  
source  
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/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Li5"  
/note="Organ: liver; Vector: pCMV-SPORT4; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 0.8 kb."

Query Match 0.5%; Score 13.2; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 4.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 53 GCGGGGGCGGGCGGCAGA 70  
||| ||||| |||||  
Db 19 GGGGGGGGGGGGGGCAGA 2

RESULT 3187  
AI476315/c  
LOCUS  
DEFINITION  
AI476315  
tal5c09.x1 NCI CGAP Lym5 Homo sapiens cDNA clone IMAGE:2044144 3'  
similar to TR:Q61431 Q61431 PROCOLLAGEN TYPE V ALPHA 2. ;contains  
OPR.b3 MSRI repetitive element ;, mRNA sequence.

ACCESSION  
VERSION  
AI476315.1 GI:4329360  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 19)  
AUTHORS  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL  
COMMENT  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Mark Raffeld, M.D.  
cDNA Library Preparation: Stratagene, Inc.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1..19  
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/mol\_type="mRNA"  
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/tissue\_type="follicular lymphoma"  
/lab\_host="SOLR (Stratagene, kanamycin resistant)"  
/clone\_lib="NCI CGAP\_Lym5"  
/note="Organ: lymph node; Vector: pBluescript SK-; Site 1:  
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:



Oligo dT. Average insert size 1.2 kb. Non-amplified library. ~5' adaptor sequence: 5' GAATTCGGCAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3"

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Query Match          0.5%;   Score 13.2;   DB 1;   Length 19;
Best Local Similarity 83.3%;   Pred. NO. 4.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 481 CCGCCAGAGCCAGGAGGG 498  
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Db 18 CCCCCAGGCCAGGGGG 1

[illegible]

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FEATURES
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Location/Qualifiers
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/clone="IMAGE:2820669"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

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Query Match 0.5%; Score 13.2; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 4.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1771 TTTT TTTT TTTT GAACCC 1788

Db 2 TTTT TTTTAGGAACCTC 19

RESULT	3189
AW248167/c	
LOCUS	AW248167
DEFINITION	2819811.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819811 5', mRNA sequence.
ACCESSION	AW248167
VERSION	AW248167.1 GI:6591160
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Other_ESTS: 2819811.3prime Contact: Robert Strausberg, Ph.D.

```

FEATURES
  source
    Location/Qualifiers
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        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="IMAGE:2819811"
        /tissue_type="small cell carcinoma"
        /cell_line="MGC3"
        /lab_host="DH10B (phage-resistant)"
        /clone_lib="NIH_MGC_7"
        /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
        EcoRI; cDNA made by oligo-dT priming. Directionally
        cloned into EcoRI/XhoI sites using the following 5'
        adaptor: GGCACGAG(G). Size-selected >500bp for average
        insert size 1.8kb. Library constructed by Ling Hong in
        the laboratory of Gerald M. Rubin (University of
        California, Berkeley) using ZAP-cDNA synthesis kit
        (Stratagene) and Superscript II RT (Life Technologies)."
```

```

Query Match          0.5%;   Score 13.2;   DB 1;   Length 19;
Best Local Similarity 83.3%;   Pred. NO. 4.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy 2782 ATTGAAAAAATAAAAAA 2799

18 ATCGGAAGAAAAAAA 1

QV 1771 TTTTTTTTTTGAACCCC 1788  
1771 TTTTTTTTTTGAACCCC 1788  
18 AAAAAAAAAAAAAAAAAA 1  
18 AAAAAAAAAAAAAAAAAA 1



TITLE  
JOURNAL  
COMMENT  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2822502.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-re@mail.nih.gov  
Tissue Procurement: DCTD/DTp cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clome distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross-match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 19  
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 19 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: L1CM9 row: J column: 7  
High quality sequence stop: 19.  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2822502"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 13.2; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 4.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1772 TTTT TTTT TTTT GAACCCCA 1789  
|||||  
Db 1 TTTT TTTT TTTT GGCCCA 18

RESULT 3193  
BQ588375 19 bp mRNA linear EST 06-DEC-2002  
LOCUS  
DEFINITION  
E012307-024-008-P19-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
024-008-P19 5-PRIME, mRNA sequence.  
BQ588375  
BQ588375.1 GI:26117958  
EST.  
Beta vulgaris  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 19)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 19 Std Error: 0.00  
Plate: 8 row: P column: 19  
Seq primer: SP6; CATACGATTAGGTGACACTATAG.

12472698  
Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 19 Std Error: 0.00  
Plate: 8 row: P column: 19  
Seq primer: SP6; CATACGATTAGGTGACACTATAG.  
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/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"  
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/clone="024-008-P19"  
/tissue\_type="leaf"  
/lab\_host="EMDH10B"  
/clone\_lib="MPIZ-ADIS-024-leaf"  
/note="Vector: pCMVSPORT6; Site 1: SalI; Site\_2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.5%; Score 13.2; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 4.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
|||  
Db 1 AACAAAAAAAAATCAAAAA 18

RESULT 3194  
BQ588375/c  
LOCUS  
DEFINITION  
BQ588375 19 bp mRNA linear EST 06-DEC-2002  
E012307-024-008-P19-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
024-008-P19 5-PRIME, mRNA sequence.  
BQ588375  
BQ588375.1 GI:26117958  
EST.  
Beta vulgaris  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 19)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698  
Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 19 Std Error: 0.00  
Plate: 8 row: P column: 19  
Seq primer: SP6; CATACGATTAGGTGACACTATAG.



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Location/Qualifiers
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/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:184440"
/db_xref="taxon:161934"
/clone="024-008-P19"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

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Query Match	0.5%;	Score 13.2;	DB 1;	Length 19;
Best Local Similarity	83.3%;	Pred. No. 4.2e+03;		
Matches 15;	Conservative	0;	Mismatches 3;	Indels 0;
Gaps 0;				
Qy	2166	TTTTTTTTTTTTTTTTTT	2183	
db	18	TTTTTTGATTTTTTGT	1	

RESULT 3195  
AZ447864  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

AZ447864  
1M0245A14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0245A14 F, genomic survey sequence.  
AZ447864  
AZ447864.1 GI:10600087  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0245 row: A column: 14  
Seq primer: CGTTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

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Query Match          0.5%;   Score 13.2;   DB 1;   Length 19;
Best Local Similarity 83.3%;   Pred. No. 4.2e+03;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      2467  TTTTAAATATTAACTTTTA 2484
      ||||| ||||| |||||
db      1  TTTTATATTCAATTTTA 18

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RESULT 3196	AZ514792	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT												
	AZ514792		1M0361B17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0361B17 R, genomic survey sequence.	AZ514792	AZ514792.1 GI:10696108	GSS.	Mus musculus (house mouse)	Mus musculus	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	1 (bases 1 to 19)	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	Unpublished (2000)	Contact: Robert B. Weiss	University of Utah Genome Center	University of Utah	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA	Tel: 801 585 5606	Fax: 801 585 7177	Email: ddunn@genetics.utah.edu	Insert Length: 10000 Std Error: 0.00	Plate: 0361 row: B column: 17	Seq primer: CACACAGGAACAGCTATGACC	Class: plasmid ends	High quality sequence stop: 19.

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FEATURES
  source
    Location/Qualifiers
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        /mol_type="genomic DNA"
        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC1M0361B17"
        /sex="Male"
        /lab host="E. Coli strain XL10-Gold, T1-resistant, F-"

```



musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.2; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 4.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2670 TACAGTGTGTGGGTGA 2687  
| | | | | | | | | | | | | | | | | |  
Db 19 TTCAGTTGTGTGGGTCA 2

RESULT 3199

AZ648404 19 bp DNA linear GSS 14-DEC-2000  
LOCUS 1M0517123F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC1M0517123 F, genomic survey sequence.

ACCESSION AZ648404  
VERSION AZ648404.1 GI:11780837  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0517 row: I column: 23

Seq primer: CGTTGTAACACGCGGCAGT

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

Location/Qualifiers

1..19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0517123"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.2; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 4.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1900 AGATCAACAGATCAACAA 1917  
| | | | | | | | | | | | | | | | | |  
Db 2 ACAACAACAGAACAA 19

RESULT 3200

AZ841555/c

LOCUS

DEFINITION

AZ841555 19 bp DNA linear GSS 20-FEB-2001  
2M0139P06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0139P06 R, genomic survey sequence.

ACCESSION AZ841555

VERSION AZ841555.1 GI:13011463

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 19)

REFERENCE

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0139 row: P column: 06

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

FEATURES

source

Location/Qualifiers

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/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource





0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 4.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803  
||| | ||||| |||||  
Db 3 AACATTAAAAAAAAAAAA 20

RESULT 3203  
AZ346143  
LOCUS  
DEFINITION  
1M0081P11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0081P11 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0081 row: P column: 11  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 4.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2803  
||| | ||||| |||||  
Db 1 AACACAAAGAAAAAAAAA 18

RESULT 3204  
AZ387841

LOCUS  
DEFINITION  
1M0147H24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0147H24 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0147 row: H column: 24  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

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/mol\_type="genomic DNA"  
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/clone="UUGC1M0147H24"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 4.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2165 CTTTTTTTTTTTTTTT 2182  
Db 2 CTTTTTCATTTCTTTT 19

RESULT 3205  
AU264645/c  
LOCUS  
DEFINITION AU264645 VS Dictyostelium discoideum cDNA clone VSD846 5', mRNA sequence.  
ACCESSION AU264645  
VERSION AU264645.1 GI:20523443  
KEYWORDS EST.  
SOURCE Dictyostelium discoideum  
ORGANISM Dictyostelium discoideum

REFERENCE Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
AUTHORS 1 (bases 1 to 20)  
Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.  
TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum

JOURNAL Unpublished (2002)  
COMMENT Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: hideko@biol.tsukuba.ac.jp.

FEATURES  
source  
1. .20  
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Best Local Similarity 83.3%; Pred. No. 4.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2175 TTTTTTTTTTTTAACTTT 2192  
Db 20 TTTTTTTTTTAAAAATTT 3

RESULT 3206  
AU267884/c  
LOCUS  
DEFINITION AU267884 VS Dictyostelium discoideum cDNA clone VSH730 3', mRNA sequence.  
ACCESSION AU267884  
VERSION AU267884.1 GI:20526682

KEYWORDS EST.  
SOURCE Dictyostelium discoideum  
ORGANISM Dictyostelium discoideum  
REFERENCE Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
AUTHORS 1 (bases 1 to 20)  
Urushihara,H., Morio,T., Saito,T., Koriki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.  
TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum  
JOURNAL Unpublished (2002)  
COMMENT Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: hideko@biol.tsukuba.ac.jp.

FEATURES  
source  
1. .20  
/organism="Dictyostelium discoideum"  
/mol\_type="mRNA"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="VSH730"  
/sex="mat A"  
/dev\_stage="vegetative"  
/clone\_lib="VS"

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 4.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2785 GAAAAAAGCAAAAAA 2802  
Db 19 GAGAAAAAGCAAAAAA 2

RESULT 3207  
AW249928  
LOCUS  
DEFINITION AW249928 20 bp mRNA linear EST 07-JAN-2000  
2821805.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821805 3', mRNA sequence.  
ACCESSION AW249928  
VERSION AW249928.1 GI:6592921  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS 1 (bases 1 to 20)  
TITLE NIH-MGC http://mgc.nci.nih.gov/.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Other ESTs: 2821805.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
Project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 9 contiguous  
PHRED high quality bases following vector sequence. Very low  
Quality Sequence: Trace file contained 20 contiguous distinct peaks  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LLCM7 row: M column: 6



RESULT 3209	
CF302574	
LOCUS	CF302574 20 bp mRNA linear EST 15-AUG-2003
DEFINITION	7LEAF--08-E02.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--08-E02, mRNA sequence.
ACCESSION	CF302574
VERSION	CF302574.1 GI:33674335
KEYWORDS	EST.
SOURCE	Oryza sativa
ORGANISM	Oryza sativa
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
AUTHORS	Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
CONTACT	Contact: Nahm B.H.
FEATURES	Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
	Yongin, Kyeonggi, Korea
	Tel: 82 31 330 6193
	Fax: 82 31 321 6355
	Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
	Location/Qualifiers

```

/organism="Oryza sativa"
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/dev_stage="7 days after germination"
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.5%;   Score 13.2;   DB 1;   Length 20;
Best Local Similarity 83.3%;   Pred. No. 4.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2798
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Db 3 ACTTCGAAAAA 20

RESULT 3210
CF302574/c
LOCUS CF302574 linear mRNA EST 15-AUG-2003

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CF302574.1 GI:33674335  
7LEAF--08-E02.g1 Rice leaf plasmid CDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--08-E02, mRNA sequence.  
CF302574  
EST.  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 20)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea

Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers  
1. .20  
/organism="Oryza sativa"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 4.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2173 TTTTCTTTTCTTTTAACT 2190  
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Db 20 TTTTCTTTTCTTTTGAAGT 3

RESULT 3211

CF302637

LOCUS

DEFINITION 7LEAF--08-F12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--08-F12, mRNA sequence.

ACCESSION CF302637

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 20)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

Location/Qualifiers  
1. .20  
/organism="Oryza sativa"  
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 4.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1767 AAGCTTTTCTTTTGA 1784  
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Db 1 AAAATTTTCTTTTAAA 18

RESULT 3212

CF322590

LOCUS

DEFINITION

CF322590 20 bp mRNA linear EST 18-AUG-2003  
HDN--01-I03.g1 OshDAC1-overexpressing transgenic rice lambda phage  
cDNA library II (HDN) Oryza sativa cDNA clone HDN--01-I03, mRNA  
sequence.

ACCESSION CF322590

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 20)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .20

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="HDN--01-I03"

/tissue\_type="callus"

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/lab\_host="E.coli SOLR"

/clone\_lib="OshDAC1-overexpressing transgenic rice lambda

phage cDNA library II (HDN)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:

XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at

5' end with EcoRI and 3' end with XhoI site. mRNA was

derived from rice Histone Deacetylase overexpression

line."

Query Match 0.5%; Score 13.2; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 4.2e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1771 TTTTCTTTTCTTTGAACCCC 1788

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Db 1 TTTTCTTTTCTTTCCCCCCC 18

RESULT 3213

AZ764505/c

LOCUS

DEFINITION

AZ764505 20 bp DNA linear GSS 16-FEB-2001

1M0560M06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0560M06 R, genomic survey sequence.

ACCESSION AZ764505

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhauser,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL  
COMMENT

plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0560 row: M column: 06  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES

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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 4.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 43 GCCCGCGCGCGCGGGG 60  
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RESULT 3214

AZ789280/c

LOCUS

DEFINITION

AZ789280 20 bp DNA linear GSS 16-FEB-2001  
2M0037A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0037A08 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

REFERENCE

AUTHORS

1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE

JOURNAL

COMMENT

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0037 row: A column: 08  
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Class: plasmid ends  
High quality sequence stop: 20.

FEATURES

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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 4.2e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 3215

AU254546

LOCUS

DEFINITION

AU254546 21 bp mRNA linear EST 25-APR-2002  
BED0002442 3', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)  
Kato,K. and Matoba,R.  
Generation of expressed sequence tags from mouse brain Unpublished (2002)  
Contact: Kikuya Kato  
Graduate School of Biological Sciences  
Nara Institute of Science and Technology  
8916-5 Takayama, Ikoma, Nara 630-0101, Japan







Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaampiz-koeln.mpg.de  
Insert Length: 13 Std Error: 0.00  
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Location/Qualifiers

FEATURES

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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2798

Db 1 AAAAAAAAAAAAAA 13

RESULT 3221

BQ583549/c

LOCUS

DEFINITION

BQ583549 13 bp mRNA linear EST 06-DEC-2002

E011978-024-005-C14-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris

cDNA clone 024-005-C14 5-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Beta vulgaris

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 13)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

22362189

12472698

Contact: Weisshaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weissshaampiz-koeln.mpg.de

Insert Length: 13 Std Error: 0.00

Plate: 5 row: C column: 14

Seq primer: SP6; CATACGATTGAGTGACACTATAG.

Location/Qualifiers

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/db\_xref="GABI:183152"

/db\_xref="taxon:161934"

/clone="024-005-C14"

/tissue\_type="inflorescence"

/lab\_host="EMDH10B"

/clone\_lib="MPIZ-ADIS-024-inflorescence"

/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

/mol\_type="mRNA"  
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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTT 2178

Db 13 TTTTTTTTTTTT 1

RESULT 3222

BQ589180

LOCUS

DEFINITION

BQ589180 13 bp mRNA linear EST 06-DEC-2002

S014009-024-015-I22-T7 MPIZ-ADIS-024-storage root Beta vulgaris

cDNA clone 024-015-I22 3-PRIME, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Beta vulgaris

Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (bases 1 to 13)

Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,

Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

22362189

12472698

Contact: Weisshaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weissshaampiz-koeln.mpg.de

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Location/Qualifiers

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cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

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S014009-024-015-I22-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
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ACCESSION BQ589180  
VERSION BQ589180.1 GI:26118763  
KEYWORDS EST.

SOURCE Beta vulgaris  
ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

AUTHORS 1 (bases 1 to 13)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PubMed 12472698

COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
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SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

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Db 1 AAAAAAAAAAAAAA 13

RESULT 3225

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Db 13 AAAAAAAAAAAAAA 1

RESULT 3224

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ACCESSION BQ590337  
VERSION BQ590337.1 GI:26119920  
KEYWORDS EST.

SOURCE Beta vulgaris  
ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

AUTHORS 1 (bases 1 to 13)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PubMed 12472698

COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
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SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798
Db 13 AAAAAAAAAAAAAA 1

RESULT 3228
CF280420
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DEFINITION
14ETL--07-B11.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--07-B11, mRNA sequence.
ACCESSION
CF280420
VERSION
CF280420.1 GI:33657806
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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Oryza sativa cDNA clone 14ETL--07-B11, mRNA sequence.
ACCESSION
CF280420
VERSION
CF280420.1 GI:33657806
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KEYWORDS
SOURCE
EST.
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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Db 13 AAAAAAAAAAAAAA 1

RESULT 3230
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14ETL--07-H19.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--07-H19, mRNA sequence.
ACCESSION
CF280707
VERSION
CF280707.1 GI:33658093
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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Db 1 TTTT TTTT TTTT TTTT 13  
  
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LOCUS  
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Oryza sativa cDNA clone 14ETL--07-H19, mRNA sequence.  
ACCESSION CF280707  
VERSION CF280707.1 GI:33658093  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
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LOCUS  
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Oryza sativa cDNA clone 14ETL--07-I21, mRNA sequence.  
ACCESSION CF280757  
VERSION CF280757.1 GI:33658143  
KEYWORDS EST.  
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
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DEFINITION 14ETL--07-I21.b1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa cDNA clone 14ETL--07-I21, mRNA sequence.  
ACCESSION CF280757  
VERSION CF280757.1 GI:33658143  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
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LOCUS  
DEFINITION 14ETL--07-I21.b1 13 bp mRNA linear EST 14-AUG-2003  
Oryza sativa cDNA clone 14ETL--07-I21, mRNA sequence.  
ACCESSION CF280757  
VERSION CF280757.1 GI:33658143  
KEYWORDS EST.  
SOURCE Oryza sativa  
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers  
1. .13  
/organism="Oryza sativa"  
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RESULT 3234
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2798
Db      13 AAAAAAAAAAAAAA 1

RESULT 3235
CF282369/c
LOCUS
DEFINITION
Oryza sativa cDNA clone 14ETL--09-N16, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="14ETL--09-N16"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2798
Db      13 AAAAAAAAAAAAAA 1

RESULT 3236
CF290970
LOCUS
DEFINITION
Oryza sativa cDNA clone 14ROOT--01-D13, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
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/tissue_type="leaf"
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/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTTITTTTTTTTT 2178
Db      1 TTTTITTTTTTTTT 13
```

Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source  
Location/Qualifiers  
1. .13  
/organism="Oryza sativa"  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT 2178

Db 1 TTTT TTTT TTTT 13

## RESULT 3237

CF290970/c  
LOCUS  
DEFINITION 14ROOT--01-D13.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-D13, mRNA sequence.

ACCESSION CF290970

VERSION CF290970.1 GI:33660003

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source  
Location/Qualifiers  
1. .13  
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/tissue\_type="root"  
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/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA 2798

|||||

Db 13 AAAAAA AAAAAA 1

## RESULT 3238

CF290971  
LOCUS  
DEFINITION 14ROOT--01-D13.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-D13, mRNA sequence.

ACCESSION CF290971

VERSION CF290971.1 GI:33660004

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source  
Location/Qualifiers  
1. .13  
/organism="Oryza sativa"  
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/clone="14ROOT--01-D13"  
/tissue\_type="root"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA 2798

|||||

Db 1 AAAAAA AAAAAA 13

## RESULT 3239

CF290971/c  
LOCUS  
DEFINITION 14ROOT--01-D13.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-D13, mRNA sequence.

ACCESSION CF290971

VERSION CF290971.1 GI:33660004

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Fax: 82 31 321 6355  
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

source

Location/Qualifiers  
1. .13  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
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/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT 2178

Db 13 TTTT TTTT TTTT TTTT 1

## RESULT 3240

CF291011

LOCUS CF291011 13 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--01-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-E10, mRNA sequence.

ACCESSION CF291011

VERSION CF291011.1 GI:33660044

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

COMMENT

Unpublished (2003)  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

source

Location/Qualifiers  
1. .13  
/organism="Oryza sativa"  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT 2178

Db 1 TTTT TTTT TTTT TTTT 13

## RESULT 3241

CF291011/c

LOCUS

DEFINITION 14ROOT--01-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-E10, mRNA sequence.

ACCESSION CF291011

VERSION CF291011.1 GI:33660044

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

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JOURNAL

COMMENT

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Contact: Nahm B.H.  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

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Location/Qualifiers  
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/tissue\_type="root"  
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/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2798

Db 13 AAAAAAAAAAAAAA 1

## RESULT 3242

CF291060

LOCUS

DEFINITION 14ROOT--01-F11.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-F11, mRNA sequence.

ACCESSION CF291060

VERSION CF291060.1 GI:33660093

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

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COMMENT

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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

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1. .13  
/organism="Oryza sativa"  
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RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178  
Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3243

CF291060/c  
LOCUS  
DEFINITION 14ROOT--01-F11.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-F11, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source  
1. .13  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
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/tissue\_type="root"  
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
Db 13 AAAAAAAAAAAAAA 1

RESULT 3244

CF291061  
LOCUS  
DEFINITION 14ROOT--01-F11.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-F11, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES

source  
1. .13  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
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/tissue\_type="root"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
Db 1 AAAAAAAAAAAAAA 13

RESULT 3245

CF291061/c  
LOCUS  
DEFINITION 14ROOT--01-F11.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-F11, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

source

Location/Qualifiers  
1. .13  
/organism="Oryza sativa"  
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/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="14ROOT--01-F11"  
/tissue\_type="root"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178

Db 13 TTTT TTTT TTTT TTTT 1

## RESULT 3246

CF291167

LOCUS

DEFINITION CF291167 13 bp mRNA linear EST 14-AUG-2003  
sativa cDNA clone 14ROOT--01-H20, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

COMMENT

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Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

source

Location/Qualifiers  
1. .13  
/organism="Oryza sativa"  
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/clone="14ROOT--01-H20"  
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/lab\_host="E.coli DH10B"  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178

Db 1 TTTT TTTT TTTT TTTT 13

## RESULT 3247

CF291167/c

LOCUS

DEFINITION CF291167 13 bp mRNA linear EST 14-AUG-2003  
sativa cDNA clone 14ROOT--01-H20, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

COMMENT

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Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

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Location/Qualifiers  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798

Db 13 AAAAAAAAAAAAAA 1

## RESULT 3248

CF291214

LOCUS

DEFINITION CF291214 13 bp mRNA linear EST 14-AUG-2003  
sativa cDNA clone 14ROOT--01-I22, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
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JOURNAL

Unpublished (2003)



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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Qy 2166 TTTT TTTT TTTT TTTT 2178  
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Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3249  
CF291214/c  
LOCUS CF291214 13 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--01-I22.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-I22, mRNA sequence.  
ACCESSION CF291214  
VERSION CF291214.1 GI:33660247  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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/organism="Oryza sativa"  
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Qy 2166 TTTT TTTT TTTT TTTT 2178  
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Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3249  
CF291214/c  
LOCUS CF291214 13 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--01-I22.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-I22, mRNA sequence.  
ACCESSION CF291214  
VERSION CF291214.1 GI:33660247  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Tel: 82 31 330 6193  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAA AAAAAA 2798  
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Db 13 AAAAAA AAAAAA 1

RESULT 3250  
CF291427  
LOCUS CF291427 13 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--01-N14.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-N14, mRNA sequence.  
ACCESSION CF291427  
VERSION CF291427.1 GI:33660460  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source  
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1. .13  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTT TTTT TTTT TTTT 2178  
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Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3251  
CF291427/c  
LOCUS CF291427 13 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--01-N14.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-N14, mRNA sequence.  
ACCESSION CF291427  
VERSION CF291427.1 GI:33660460  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)  
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## FEATURES

source Location/Qualifiers  
1.13  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
|||||  
Db 13 AAAAAAAAAAAAAA 1

## RESULT 3252

CF291469  
LOCUS 14ROOT--01-012.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
DEFINITION sativa cDNA clone 14ROOT--01-012, mRNA sequence.

ACCESSION CF291469  
VERSION CF291469.1 GI:33660502  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Unpublished (2003)

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## FEATURES

source Location/Qualifiers  
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RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178  
|||||  
Db 1 TTTT TTTT TTTT TTTT 13

## RESULT 3253

CF291469/c  
LOCUS 14ROOT--01-012.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
DEFINITION sativa cDNA clone 14ROOT--01-012, mRNA sequence.

ACCESSION CF291469  
VERSION CF291469.1 GI:33660502  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Unpublished (2003)

CONTACT: Nahm B.H.

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source Location/Qualifiers  
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RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
|||||  
Db 13 AAAAAAAAAAAAAA 1

## RESULT 3254

CF291479  
LOCUS 14ROOT--01-017.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
DEFINITION sativa cDNA clone 14ROOT--01-017, mRNA sequence.

ACCESSION CF291479  
VERSION CF291479.1 GI:33660512  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

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of Bioscience and Bioinformatics, Myongji University  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTNTTTTTTTT 2178  
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Db 1 TTTTNTTTTTTTT 13

## RESULT 3255

CF291479/c  
LOCUS CF291479 13 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--01-O17.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-O17, mRNA sequence.

ACCESSION CF291479  
VERSION CF291479.1 GI:33660512  
KEYWORDS EST.

## SOURCE

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAA 2798  
|||||  
Db 13 AAAAAAAAAAAA 1

## RESULT 3256

CF291514  
LOCUS CF291514 13 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--01-P13.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-P13, mRNA sequence.

ACCESSION CF291514  
VERSION CF291514.1 GI:33660547

## KEYWORDS

EST.

## SOURCE

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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1. .13  
/organism="Oryza sativa"  
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Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTNTTTTTTTT 2178  
|||||  
Db 1 TTTTNTTTTTTTT 13

## RESULT 3257

CF291514/c  
LOCUS CF291514 13 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--01-P13.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-P13, mRNA sequence.

ACCESSION CF291514  
VERSION CF291514.1 GI:33660547

## KEYWORDS

EST.

## SOURCE

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,



TITLE  
JOURNAL  
COMMENT

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Unpublished (2003)  
Contact: Nahm B.H.  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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/organism="Oryza sativa"  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798

Db 13 AAAAAAAAAAAAAA 1

## RESULT 3258

CF291515

LOCUS

DEFINITION  
14ROOT--01-P13.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-P13, mRNA sequence.

ACCESSION

VERSION CF291515.1 GI:33660548

KEYWORDS

SOURCE EST.

ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)

## REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE

JOURNAL

COMMENT

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Fax: 82 31 321 6355  
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## FEATURES

source

Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
Db 1 AAAAAAAAAAAAAA 13

## RESULT 3259

CF291515/c

LOCUS

DEFINITION  
14ROOT--01-P13.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-P13, mRNA sequence.

ACCESSION

VERSION CF291515

KEYWORDS

SOURCE EST.

ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)

## REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

JOURNAL

COMMENT

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Contact: Nahm B.H.  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

Location/Qualifiers  
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QY 2166 TTTTTTTTTTTT 2178

Db 13 TTTTTTTTTTTT 1

## RESULT 3260

CF291596

LOCUS

DEFINITION  
14ROOT--02-B12.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--02-B12, mRNA sequence.

ACCESSION

VERSION CF291596

KEYWORDS

SOURCE EST.

ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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1. .13  
/organism="Oryza sativa"  
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Query Match 0.5%; Score 13; DB 1; Length 13;  
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QY 2166 TTTT TTTT TTTT TTTT 2178

Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3261

CF291596/c

LOCUS

DEFINITION 14ROOT--02-B12.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--02-B12, mRNA sequence.

ACCESSION CF291596

VERSION CF291596.1 GI:33660629

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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Query Match 0.5%; Score 13; DB 1; Length 13;  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798

Db 13 AAAAAAAAAAAAAA 1

RESULT 3262

CF291597

LOCUS

DEFINITION 14ROOT--02-B12.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--02-B12, mRNA sequence.

ACCESSION CF291597

VERSION CF291597.1 GI:33660630

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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/clone\_lib="Rice root plasmid cDNA library (14ROOT)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
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RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798

Db 1 AAAAAAAAAAAAAA 13

RESULT 3263

CF291597/c

LOCUS

DEFINITION 14ROOT--02-B12.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--02-B12, mRNA sequence.

ACCESSION CF291597

VERSION CF291597.1 GI:33660630

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS 1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
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with oligoribonucleotides and then used as templates for  
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Query Match 0.5%; Score 13; DB 1; Length 13;  
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QY 2166 TTTT TTTT TTTT TTTT 2178  
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Db 13 TTTT TTTT TTTT TTTT 1

RESULT 3264  
CF291726 13 bp mRNA linear EST 14-AUG-2003  
LOCUS 14ROOT--02-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
DEFINITION sativa cDNA clone 14ROOT--02-E10, mRNA sequence.

ACCESSION CF291726.1 GI:33660759  
VERSION  
KEYWORDS  
SOURCE

ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS 1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178  
|||||  
Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3265  
CF291726/c

LOCUS 13 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--02-E10.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--02-E10, mRNA sequence.

ACCESSION CF291726  
VERSION CF291726.1 GI:33660759  
KEYWORDS  
SOURCE

ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS 1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
|||||  
Db 13 AAAAAAAAAAAAAA 1

RESULT 3266  
CF291903

LOCUS 13 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--02-I10.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--02-I10, mRNA sequence.

ACCESSION CF291903  
VERSION CF291903.1 GI:33660936  
KEYWORDS  
SOURCE

ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;



REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

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RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
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QY 2786 AAAAAAAAAAAAAA 2798

Db 1 AAAAAAAAAAAAAA 13

## RESULT 3267

CF291903/c  
LOCUS 14ROOT--02-I10.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
DEFINITION sativa cDNA clone 14ROOT--02-I10, mRNA sequence.

ACCESSION CF291903.1 GI:33660936

VERSION EST.

KEYWORDS Oryza sativa

SOURCE Oryza sativa

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

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## FEATURES

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Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178

Db 13 TTTT TTTT TTTT TTTT 1

## RESULT 3268

CF298590

LOCUS

DEFINITION 7LEAF--02-A19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--02-A19, mRNA sequence.

ACCESSION CF298590

VERSION EST.

KEYWORDS Oryza sativa

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS

TITLE

JOURNAL

COMMENT

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Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

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1..13  
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with oligoribonucleotides and then used as templates for  
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## Query Match

0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178

Db 1 TTTT TTTT TTTT TTTT 13

## RESULT 3269

CF298590/c

LOCUS

DEFINITION 7LEAF--02-A19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--02-A19, mRNA sequence.

ACCESSION CF298590

VERSION EST.

KEYWORDS Oryza sativa

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2798

Db 13 AAAAAAAAAAAAAA 1

## RESULT 3270

CF298592

LOCUS  
DEFINITION  
7LEAF--02-A21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--02-A21, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

## FEATURES

source

1. .13  
/organism="Oryza sativa"  
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Qy 2166 TTTT TTTT TTTT 2178

Db 1 TTTT TTTT TTTT 13

## RESULT 3271

CF298592/c

LOCUS

DEFINITION  
7LEAF--02-A21.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--02-A21, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

## FEATURES

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1. .13  
/organism="Oryza sativa"  
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with oligoribonucleotides and then used as templates for  
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Qy 2786 AAAAAAAAAAAAAA 2798

Db 13 AAAAAAAAAAAAAA 1

## RESULT 3272

CF298736

LOCUS

DEFINITION  
7LEAF--02-E22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--02-E22, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

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REFERENCE
AUTHORS      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
              1 (bases 1 to 13)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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              Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, MyongJi University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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QY      2166 TTTT-TTTT-TTTT-TTTT 2178
Db      1 TTTT-TTTT-TTTT-TTTT 13

RESULT 3273
CF298736/c
LOCUS      CF298736      13 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION      7LEAF--02-E22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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ACCESSION      CF298736
VERSION      CF298736.1 GI:33670497
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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/organism="Oryza sativa"
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RT-PCR."

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT-TTTT-TTTT-TTTT 2178
Db      1 TTTT-TTTT-TTTT-TTTT 13

RESULT 3273
CF298736/c
LOCUS      CF298736      13 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION      7LEAF--02-E22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
              sativa cDNA clone 7LEAF--02-E22, mRNA sequence.
ACCESSION      CF298736
VERSION      CF298736.1 GI:33670497
KEYWORDS
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ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa"
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Db      1 TTTT-TTTT-TTTT-TTTT 13

RESULT 3275
CF298764/c
LOCUS      CF298764      13 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION      7LEAF--02-F20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
              sativa cDNA clone 7LEAF--02-F20, mRNA sequence.
ACCESSION      CF298764
VERSION      CF298764.1 GI:33670525
KEYWORDS
SOURCE
Oryza sativa
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      13 AAAAAAAAAAAAAA 1

RESULT 3274
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LOCUS      CF298764      13 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION      7LEAF--02-F20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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ACCESSION      CF298764
VERSION      CF298764.1 GI:33670525
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Db      1 TTTT-TTTT-TTTT-TTTT 13

RESULT 3275
CF298764/c
LOCUS      CF298764      13 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION      7LEAF--02-F20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
              sativa cDNA clone 7LEAF--02-F20, mRNA sequence.
ACCESSION      CF298764
VERSION      CF298764.1 GI:33670525
KEYWORDS
SOURCE
Oryza sativa
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ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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RESULT 3276  
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DEFINITION 7LEAF--02-G14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--02-G14, mRNA sequence.  
ACCESSION CF298795  
VERSION CF298795.1 GI:33670556  
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SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RESULT 3277  
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DEFINITION 7LEAF--02-G14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--02-G14, mRNA sequence.  
ACCESSION CF298795  
VERSION CF298795.1 GI:33670556  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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QY 2786 AAAAAAAAAAAAAA 2798  
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Db 13 AAAAAAAAAAAAAA 1

RESULT 3278  
CF298908  
LOCUS 13 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--02-K03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--02-K03, mRNA sequence.  
ACCESSION CF298908  
VERSION CF298908.1 GI:33670669  
KEYWORDS EST.

SOURCE  
ORGANISM  
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Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
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1 (bases 1 to 13)  
AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE  
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JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Nahm B.H.  
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RESULT 3279  
CF298908/c  
LOCUS  
DEFINITION  
7LEAF--02-K03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
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ACCESSION  
CF298908  
VERSION  
CF298908.1 GI:33670669  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
1 (bases 1 to 13)  
AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE  
Large-scale Sequencing Analysis of Rice ESTs  
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Unpublished (2003)  
COMMENT  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
Location/Qualifiers  
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Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3279  
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LOCUS  
DEFINITION  
7LEAF--02-K03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
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ACCESSION  
CF298908  
VERSION  
CF298908.1 GI:33670669  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
1 (bases 1 to 13)  
AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE  
Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
Location/Qualifiers  
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/organism="Oryza sativa"  
/mol\_type="mRNA"  
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/db\_xref="taxon:4530"  
/clone="7LEAF--02-K03"

/tissue\_type="leaf"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA 2798  
|||||  
Db 13 AAAAAA AAAAAA 1

RESULT 3280  
CF299133  
LOCUS  
DEFINITION  
7LEAF--03-A06.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--03-A06, mRNA sequence.  
ACCESSION  
CF299133  
VERSION  
CF299133.1 GI:33670894  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
1 (bases 1 to 13)  
AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
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QY 2166 TTTT TTTT TTTT TTTT 2178  
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Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3281  
CF299133/c  
LOCUS  
DEFINITION  
7LEAF--03-A06.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--03-A06, mRNA sequence.  
ACCESSION  
CF299133  
VERSION  
CF299133.1 GI:33670894

KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
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FEATURES  
source Location/Qualifiers

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 13 AAAAAAAAAAAAAA 1

RESULT 3282  
CF299359  
LOCUS 13 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--03-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--03-F15, mRNA sequence.

ACCESSION CF299359  
VERSION CF299359.1 GI:33671120  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
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FEATURES  
source Location/Qualifiers

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3283  
CF299359/c

LOCUS 13 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--03-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--03-F15, mRNA sequence.

ACCESSION CF299359  
VERSION CF299359.1 GI:33671120  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
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FEATURES  
source Location/Qualifiers

1. .13  
/organism="Oryza sativa"  
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Query Match 0.5%; Score 13; DB 1; Length 13;  
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Db 13 AAAAAAAAAAAAAA 1

RESULT 3284  
CF299937

LOCUS 13 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--04-C12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--04-C12, mRNA sequence.

ACCESSION CF299937





ACCESSION CF300118  
 VERSION CF300118.1 GI:33671879  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
 REFERENCE 1 (bases 1 to 13)  
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
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# FEATURES

source

1. .13  
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/organism="Oryza sativa"  
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 Db 13 AAAAAAAAAAAAAA 1

# RESULT 3288

CF300587  
 LOCUS 7LEAF--05-C01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 DEFINITION sativa cDNA clone 7LEAF--05-C01, mRNA sequence.

ACCESSION CF300587  
 VERSION CF300587.1 GI:33672348  
 KEYWORDS EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)  
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source

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 Db 13 AAAAAAAAAAAAAA 1

RESULT 3290  
 CF300658  
 LOCUS 7LEAF--05-D14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

DEFINITION sativa cDNA clone 7LEAF--05-D14, mRNA sequence.

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QY 2166 TTTT TTTT TTTT TTTT 2178  
 Db 1 TTTT TTTT TTTT TTTT 13

# RESULT 3289

CF300587/c  
 LOCUS 7LEAF--05-C01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 DEFINITION sativa cDNA clone 7LEAF--05-C01, mRNA sequence.

ACCESSION CF300587  
 VERSION CF300587.1 GI:33672348  
 KEYWORDS EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)  
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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FEATURES  
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QY 2786 AAAAAAAAAAAAAA 2798  
 Db 13 AAAAAAAAAAAAAA 1

RESULT 3290  
 CF300658  
 LOCUS 7LEAF--05-D14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

DEFINITION sativa cDNA clone 7LEAF--05-D14, mRNA sequence.

sativa cDNA clone 7LEAF--05-D14, mRNA sequence.

ACCESSION CF300658  
VERSION CF300658.1 GI:33672419  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
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FEATURES Location/Qualifiers

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/organism="Oryza sativa"  
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QY 2166 TTTT TTTT TTTT TTTT 2178

Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3291

CF300658/c

LOCUS

DEFINITION 7LEAF--05-D14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--05-D14, mRNA sequence.

ACCESSION CF300658

VERSION CF300658.1 GI:33672419

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

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/organism="Oryza sativa"

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Db 13 AAAAAAAAAAAAAA 1

RESULT 3292

CF300929

LOCUS

DEFINITION 7LEAF--05-J11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--05-J11, mRNA sequence.

ACCESSION CF300929

VERSION CF300929.1 GI:33672690

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

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Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

source

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RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178

Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3293

CF300929/c

LOCUS

CF300929 13 bp mRNA linear EST 15-AUG-2003



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DEFINITION 7LEAF--05-J11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION sativa cDNA clone 7LEAF--05-J11, mRNA sequence.
VERSION CF300929.1 GI:33672690
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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with oligoribonucleotides and then used as templates for
RT-PCR."

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 13 AAAAAAAAAAAAAA 1

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LOCUS 7LEAF--06-A15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--06-A15, mRNA sequence.
ACCESSION CF301247
VERSION CF301247.1 GI:33673008
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798
Db 13 AAAAAAAAAAAAAA 1

RESULT 3294
CF301247
LOCUS 7LEAF--06-A15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--06-A15, mRNA sequence.
ACCESSION CF301247
VERSION CF301247.1 GI:33673008
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
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Query Match 0.5%; Score 13; DB 1; Length 13;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3294
CF301247
LOCUS 7LEAF--06-A15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--06-A15, mRNA sequence.
ACCESSION CF301247
VERSION CF301247.1 GI:33673008
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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QY 2786 AAAAAAAAAAAAAA 2798
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RESULT 3294
CF301247
LOCUS 7LEAF--06-A15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--06-A15, mRNA sequence.
ACCESSION CF301247
VERSION CF301247.1 GI:33673008
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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Best Local Similarity 100.0%; Pred. No. 2.2e+03;
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Db 13 AAAAAAAAAAAAAA 1

RESULT 3296
CF301286
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QY 2166 TTTT TTTT TTTT TTTT 2178
Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3295
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LOCUS 7LEAF--06-A15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sativa cDNA clone 7LEAF--06-A15, mRNA sequence.
ACCESSION CF301247
VERSION CF301247.1 GI:33673008
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798
Db 13 AAAAAAAAAAAAAA 1

RESULT 3296
CF301286
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LOCUS CF301286 13 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--06-B15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--06-B15, mRNA sequence.  
ACCESSION CF301286  
VERSION CF301286.1 GI:33673047  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3297  
CF301286/c  
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DEFINITION 7LEAF--06-B15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--06-B15, mRNA sequence.  
ACCESSION CF301286  
VERSION CF301286.1 GI:33673047  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
Location/Qualifiers

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QY 2786 AAAAAAAAAAAAAA 2798  
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Db 13 AAAAAAAAAAAAAA 1

RESULT 3298  
CF302158  
LOCUS  
DEFINITION 7LEAF--07-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--07-G20, mRNA sequence.  
ACCESSION CF302158  
VERSION CF302158.1 GI:33673919  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

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QY 2166 TTTT TTTT TTTT TTTT 2178  
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Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3299

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CF302158/c
LOCUS       CF302158               13 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--07-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF302158
VERSION     CF302158.1  GI:33673919
KEYWORDS    EST.
SOURCE      Oryza sativa
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REFERENCE   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      13 AAAAAAAAAAAAAA 1

RESULT 3300
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DEFINITION   7LEAF--08-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF302830
VERSION     CF302830.1  GI:33674591
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
REFERENCE   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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QY      2786 AAAAAAAAAAAAAA 2798
Db      13 AAAAAAAAAAAAAA 1

RESULT 3300
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DEFINITION   7LEAF--08-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF302830
VERSION     CF302830.1  GI:33674591
KEYWORDS    EST.
SOURCE      Oryza sativa
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REFERENCE   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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RESULT 3301
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DEFINITION   7LEAF--08-L16.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION   CF302830
VERSION     CF302830.1  GI:33674591
KEYWORDS    EST.
SOURCE      Oryza sativa
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REFERENCE   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Ehrhartoideae; Oryzeae; Oryza.
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.2e+03;
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QY      2786 AAAAAAAAAAAAAA 2798
Db      13 AAAAAAAAAAAAAA 1
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RESULT 3302
CF302898      13 bp      mRNA      linear      EST 15-AUG-2003
LOCUS      7LEAF--08-N08.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION      sativa cDNA clone 7LEAF--08-N08, mRNA sequence.
ACCESSION      CF302898
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT 2178
Db      1 TTTT TTTT TTTT TTTT 13

RESULT 3303
CF302898/c
LOCUS      CF302898      13 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION      7LEAF--08-N08.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--08-N08, mRNA sequence.
ACCESSION      CF302898
VERSION
KEYWORDS
SOURCE
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355

```

```

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES      source
1. .13
Location/Qualifiers
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with oligoribonucleotides and then used as templates for
RT-PCR."

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2798
Db      13 AAAAAAAAAAAAAA 1

RESULT 3304
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LOCUS      CF310516      13 bp      mRNA      linear      EST 15-AUG-2003
DEFINITION      ABF--05-D09.b1 ABF3-overexpressing transgenic rice plasmid cDNA
library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.
ACCESSION      CF310516
VERSION      CF310516.1 GI:33682277
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES      source
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Location/Qualifiers
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element binding transcription factor 3 overexpression
line."

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT 2178

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|||||  
1 TTTTTTTTTTTT 13

Db

RESULT 3305  
CF310516/c

LOCUS  
DEFINITION  
ABF--05-D09.b1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.

ACCESSION  
CF310516

VERSION  
CF310516.1 GI:33682277

KEYWORDS  
EST.

SOURCE  
Oryza sativa

ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
1 (bases 1 to 13)

AUTHORS  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE  
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL  
Unpublished (2003)

COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
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QY 2786 AAAAAAAAAAAAAA 2798  
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Db 13 AAAAAAAAAAAAAA 1

RESULT 3306  
CF310517

LOCUS  
DEFINITION  
ABF--05-D09.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.

ACCESSION  
CF310517

VERSION  
CF310517.1 GI:33682278

KEYWORDS  
EST.

SOURCE  
Oryza sativa

ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
1 (bases 1 to 13)

AUTHORS  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE  
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL  
Unpublished (2003)

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of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
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RESULT 3307  
CF310517/c

LOCUS  
DEFINITION  
ABF--05-D09.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.

ACCESSION  
CF310517

VERSION  
CF310517.1 GI:33682278

KEYWORDS  
EST.

SOURCE  
Oryza sativa

ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
1 (bases 1 to 13)

AUTHORS  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE  
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL  
Unpublished (2003)

COMMENT  
Contact: Nahm B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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element binding transcription factor 3 overexpression  
line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
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Db 13 AAAAAAAAAAAAAA 1

RESULT 3308  
CF310517

LOCUS  
DEFINITION  
ABF--05-D09.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.

ACCESSION  
CF310517

VERSION  
CF310517.1 GI:33682278

KEYWORDS  
EST.

SOURCE  
Oryza sativa

ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
1 (bases 1 to 13)

AUTHORS  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE  
Large-scale Sequencing Analysis of Rice ESTs

JOURNAL  
COMMENT

Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
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Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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line."

## Query Match

Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
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## QY

2786 AAAAAAAAAAAAAA 2798

## Db

1 AAAAAAAAAAAAAA 13

## RESULT 3307

## CF310517/c

## LOCUS

DEFINITION  
ABF--05-D09.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--05-D09, mRNA sequence.

## ACCESSION

CF310517

## VERSION

CF310517.1 GI:33682278

## KEYWORDS

EST.

## SOURCE

Oryza sativa

## ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

1 (bases 1 to 13)

## AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

## TITLE

Large-scale Sequencing Analysis of Rice ESTs

## JOURNAL

Unpublished (2003)

## COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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Thu Jun 10 13:10:24 2004

for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
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QY 2166 TTTT TTTT TTTT TTTT 2178  
Db 13 TTTT TTTT TTTT TTTT 1

RESULT 3308  
CF312721 13 bp mRNA linear EST 15-AUG-2003  
LOCUS ABF--08-J13.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--08-J13, mRNA sequence.  
ACCESSION CF312721 GI:33684482  
VERSION  
KEYWORDS  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.  
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Query Match 0.5%; Score 13; DB 1; Length 13;  
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QY 2166 TTTT TTTT TTTT TTTT 2178  
Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3309  
CF312721/c 13 bp mRNA linear EST 15-AUG-2003  
LOCUS ABF--08-J13.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--08-J13, mRNA sequence.  
ACCESSION CF312721  
VERSION CF312721.1 GI:33684482

KEYWORDS Oryza sativa  
SOURCE Oryza sativa  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.  
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Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
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QY 2786 AAAAAAAAAAAAAA 2798  
Db 13 AAAAAAAAAAAAAA 1

RESULT 3310  
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LOCUS HD--01-D10.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (HD) Oryza sativa cDNA clone HD--01-D10, mRNA sequence.  
ACCESSION CF313171 GI:33684932  
VERSION CF313171.1  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.  
Location/Qualifiers  
1. .13  
/organism="Oryza sativa"



```
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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line."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798
|||||
DB 13 AAAAAAAAAAAAAA 1

RESULT 3314
CF314874 13 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
HD--03-J07.g1 OSHDAc1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa clone HD--03-J07, mRNA sequence.
ACCESSION
CF314874.1 GI:33686635
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798
|||||
DB 13 AAAAAAAAAAAAAA 1

RESULT 3314
CF314874 13 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
HD--03-J07.g1 OSHDAc1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa clone HD--03-J07, mRNA sequence.
ACCESSION
CF314874.1 GI:33686635
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.5%; Score 13; DB 1; Length 13;
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QY 2786 AAAAAAAAAAAAAA 2798
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DB 13 AAAAAAAAAAAAAA 1

RESULT 3316
CF315395 13 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
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library (HD) Oryza sativa clone HD--04-E20, mRNA sequence.
ACCESSION
CF315395
VERSION
CF315395.1 GI:33687156
KEYWORDS
EST.
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derived from rice Histone Deacetylase overexpression
line."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178
|||||
DB 1 TTTT TTTT TTTT TTTT 13

RESULT 3315
CF314874/c 13 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
HD--03-J07.g1 OSHDAc1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa clone HD--03-J07, mRNA sequence.
ACCESSION
CF314874.1 GI:33686635
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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cDNA library (HD)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
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reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match 0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798
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DB 13 AAAAAAAAAAAAAA 1

RESULT 3316
CF315395 13 bp mRNA linear EST 15-AUG-2003
LOCUS
DEFINITION
HD--04-E20.b1 OSHDAc1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa clone HD--04-E20, mRNA sequence.
ACCESSION
CF315395
VERSION
CF315395.1 GI:33687156
KEYWORDS
EST.
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SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
AUTHORS  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3317  
CF315395/c  
LOCUS  
DEFINITION  
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library (HD) Oryza sativa cDNA clone HD--04-E20, mRNA sequence.  
ACCESSION  
VERSION  
CF315395  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
AUTHORS  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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derived from rice Histone Deacetylase overexpression  
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Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 13 AAAAAA AAAAAA 1

## RESULT 3318

CF316439  
LOCUS  
DEFINITION  
HD--05-L17.b1 OshDAC1-overexpressing transgenic rice plasmid CDNA  
library (HD) Oryza sativa cDNA clone HD--05-L17, mRNA sequence.  
ACCESSION  
VERSION  
CF316439  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
AUTHORS  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source  
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Query Match 0.5%; Score 13; DB 1; Length 13;  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT 2178  
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Db 1 TTTT TTTT TTTT TTTT 13

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
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Db 1 AAAAAAAAAAAAAA 13

RESULT 3321

CF316440/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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source

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RESULT 3319  
CF316439/c  
LOCUS  
DEFINITION

ACCESSION  
VERSION  
KEYWORDS  
SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

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line."

Query Match 0.5%; Score 13; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798

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Db 13 AAAAAAAAAAAAAA 1

RESULT 3320

CF316440

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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derived from rice Histone Deacetylase overexpression
line."

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178
Db 13 TTTT TTTT TTTT TTTT 1

RESULT 3322
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DEFINITION HD--06-A04.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--06-A04, mRNA sequence.
ACCESSION CF316637
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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line."

Query Match      0.5%; Score 13; DB 1; Length 13;
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178
Db 13 TTTT TTTT TTTT TTTT 13

RESULT 3323
CF316637/c
LOCUS
DEFINITION HD--06-A04.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--06-A04, mRNA sequence.
ACCESSION CF316637
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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line."

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
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QY 2166 TTTT TTTT TTTT TTTT 2178
Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3324
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LOCUS
DEFINITION HD--08-F19.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--08-F19, mRNA sequence.
ACCESSION CF318290
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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line."

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3324
CF318290
LOCUS
DEFINITION HD--08-F19.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
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ACCESSION CF318290
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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line."

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QY 2786 AAAAAA AAAAAA 2798
Db 13 AAAAAA AAAAAA 1
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
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reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178  
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Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3325  
CF318290/c  
LOCUS  
DEFINITION HD--08-F19.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--08-F19, mRNA sequence.

ACCESSION CF318290  
VERSION CF318290.1 GI:33690051  
KEYWORDS  
SOURCE  
ORGANISM Oryza sativa

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
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Fax: 82 31 321 6355  
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FEATURES  
source  
1. 13  
Location/Qualifiers

/organism="Oryza sativa"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
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reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
|||||  
Db 13 AAAAAAAAAAAAAA 1

RESULT 3326

CF319066  
LOCUS  
DEFINITION HD--09-H02.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--09-H02, mRNA sequence.

ACCESSION CF319066  
VERSION CF319066.1 GI:33690827  
KEYWORDS  
SOURCE  
ORGANISM Oryza sativa

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1. 13  
Location/Qualifiers

/organism="Oryza sativa"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178  
|||||  
Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3327

CF319066/c  
LOCUS  
DEFINITION HD--09-H02.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--09-H02, mRNA sequence.

ACCESSION CF319066  
VERSION CF319066.1 GI:33690827  
KEYWORDS  
SOURCE  
ORGANISM Oryza sativa

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

1. .13  
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/lab\_host="E.coli DH10B"  
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cDNA library (HD)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
Db 13 AAAAAAAAAAAAAA 1

## RESULT 3328

CF319531

LOCUS

DEFINITION CF319531 13 bp mRNA linear EST 15-AUG-2003  
HD--10-B03.b1 OSHDAc1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--10-B03, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

JOURNAL

COMMENT

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Contact: Nahm B.H.  
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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

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/organism="Oryza sativa"  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was  
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derived from rice Histone Deacetylase overexpression  
line."

line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178  
Db 1 TTTT TTTT TTTT TTTT 13

## RESULT 3329

CF319531/c

LOCUS

DEFINITION CF319531 13 bp mRNA linear EST 15-AUG-2003  
HD--10-B03.b1 OSHDAc1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--10-B03, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE

JOURNAL

COMMENT

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Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

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cDNA library (HD)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was  
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reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
Db 13 AAAAAAAAAAAAAA 1

## RESULT 3330

CF319532

LOCUS

DEFINITION CF319532 13 bp mRNA linear EST 15-AUG-2003  
HD--10-B03.g1 OSHDAc1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--10-B03, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

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/organism="Oryza sativa"

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/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="HD--10-B03"

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/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798

|||||

1 AAAAAAAAAAAAAA 13

RESULT 3331

CF319532/c

LOCUS  
DEFINITION  
CF319532 13 bp mRNA linear EST 15-AUG-2003  
HD--10-B03.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--10-B03, mRNA sequence.

ACCESSION  
CF319532.1 GI:33691293

VERSION  
EST.

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

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/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

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/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178

|||||

13 TTTT TTTT TTTT TTTT 1

RESULT 3332

CF319919

LOCUS

DEFINITION  
CF319919 13 bp mRNA linear EST 15-AUG-2003  
HD--10-J17.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--10-J17, mRNA sequence.

ACCESSION  
CF319919.1 GI:33691680

VERSION  
EST.

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

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/organism="Oryza sativa"

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/cultivar="Nackdong"

/db\_xref="taxon:4530"

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/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798

|||||

1 AAAAAAAAAAAAAA 13

Db

RESULT 3333  
CF319919/c  
LOCUS  
DEFINITION  
HD--10-J17.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--10-J17, mRNA sequence.  
ACCESSION  
CF319919  
VERSION  
CF319919.1 GI:33691680  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
1 (bases 1 to 13)  
AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE  
Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Nahm B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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derived from rice Histone Deacetylase overexpression  
line."  
Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred.No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT 2178  
Db 13 TTTT TTTT TTTT TTTT 1

RESULT 3334  
CF320017  
LOCUS  
DEFINITION  
HD--10-L20.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--10-L20, mRNA sequence.  
ACCESSION  
CF320017  
VERSION  
CF320017.1 GI:33691778  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
1 (bases 1 to 13)  
AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE  
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COMMENT  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
FEATURES  
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derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred.No. 2.2e+03;  
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QY 2166 TTTT TTTT TTTT TTTT 2178  
Db 1 TTTT TTTT TTTT TTTT 13  
RESULT 3335  
CF320017/c  
LOCUS  
DEFINITION  
HD--10-L20.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--10-L20, mRNA sequence.  
ACCESSION  
CF320017  
VERSION  
CF320017.1 GI:33691778  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
1 (bases 1 to 13)  
AUTHORS  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
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/db\_xref="taxon:4530"  
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/tissue\_type="callus"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
|||||  
Db 13 AAAAAAAAAAAAAA 1

RESULT 3336  
CF320018 13 bp mRNA linear EST 15-AUG-2003  
LOCUS HD--10-L20.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (HD) Oryza sativa cDNA clone HD--10-L20, mRNA sequence.

ACCESSION CF320018 GI:33691779  
VERSION CF320018  
KEYWORDS EST.  
SOURCE Oryza sativa

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
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Fax: 82 31 321 6355  
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FEATURES Location/Qualifiers

1..13  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
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cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
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reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
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Db 1 AAAAAAAAAAAAAA 13

RESULT 3337  
CF320018/c 13 bp mRNA linear EST 15-AUG-2003  
LOCUS HD--10-L20.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (HD) Oryza sativa cDNA clone HD--10-L20, mRNA sequence.

ACCESSION CF320018 GI:33691779  
VERSION CF320018  
KEYWORDS EST.  
SOURCE Oryza sativa

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

1..13  
/organism="Oryza sativa"  
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/clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
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reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTT 2178  
|||||  
Db 13 TTTTTTTTTTTT 1

RESULT 3338

CF320143 13 bp mRNA linear EST 15-AUG-2003  
LOCUS HD--10-O13.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (HD) Oryza sativa cDNA clone HD--10-O13, mRNA sequence.

ACCESSION CF320143 GI:33691904  
VERSION CF320143  
KEYWORDS EST.  
SOURCE Oryza sativa

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

1..13  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
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cDNA library (HD)"  
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

CF320938 13 bp mRNA linear EST 15-AUG-2003  
LOCUS HD--12-A06.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
DEFINITION library (HD) Oryza sativa cDNA clone HD--12-A06, mRNA sequence.

ACCESSION CF320938  
VERSION CF320938.1 GI:33692699  
KEYWORDS EST.  
SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

AUTHORS 1 (bases 1 to 13)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

QY 2166 TTTT TTTT TTTT TTTT 2178  
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Db 1 TTTT TTTT TTTT TTTT 13

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3339  
CF320143/c  
LOCUS CF320143 13 bp mRNA linear EST 15-AUG-2003  
DEFINITION HD--10-O13.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--10-O13, mRNA sequence.

ACCESSION CF320143  
VERSION CF320143.1 GI:33691904  
KEYWORDS EST.  
SOURCE Oryza sativa

ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

AUTHORS 1 (bases 1 to 13)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers  
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/organism="Oryza sativa"  
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
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QY 2786 AAAAAAAAAA 2798  
|||||  
Db 13 AAAAAAAAAA 1

RESULT 3340

CF320938  
LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..13

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

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treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178  
|||||  
Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3341

CF320938/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..13

/organism="Oryza sativa"

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/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
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reverse transcribed and then used for PCR. mRNA was  
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line."

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Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAA 2798  
|||||  
Db 13 AAAAAAAAAA 1

RESULT 3340

CF320938

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

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line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
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QY 2166 TTTT TTTT TTTT TTTT 2178  
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Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3341

CF320938/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

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/organism="Oryza sativa"

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treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
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derived from rice Histone Deacetylase overexpression  
line."

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Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178  
|||||  
Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3341

CF320938

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

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JOURNAL

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source

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treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
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Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
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QY 2166 TTTT TTTT TTTT TTTT 2178  
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Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3341

CF320938

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..13

/organism="Oryza sativa"

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line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
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RESULT 3341

CF320938

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

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treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
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derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178  
|||||  
Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3341

CF320938

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

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/organism="Oryza sativa"

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/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"

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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

## source

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/organism="Oryza sativa"  
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derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798

|||||

Db 13 AAAAAAAAAAAAAA 1

## RESULT 3342

## CF326844

LOCUS  
DEFINITION  
NACL--01-B12.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--01-B12, mRNA sequence.

ACCESSION  
VERSION  
CF326844.1 GI:33801943

KEYWORDS  
EST.

SOURCE  
Oryza sativa

ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

## source

1. .13  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
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/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
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Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
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QY 2166 TTTT TTTT TTTT TTTT 2178

|||||

Db 1 TTTT TTTT TTTT TTTT 13

## RESULT 3343

## CF326844/c

## LOCUS

DEFINITION  
NACL--01-B12.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--01-B12, mRNA sequence.

ACCESSION  
VERSION  
CF326844

KEYWORDS  
EST.

SOURCE  
Oryza sativa

ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

## source

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/organism="Oryza sativa"  
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QY 2786 AAAAAAAAAAAAAA 2798

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Db 13 AAAAAAAAAAAAAA 1

## RESULT 3344

## CF327070

## LOCUS

DEFINITION  
NACL--01-G09.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--01-G09, mRNA sequence.

ACCESSION  
VERSION  
CF327070

KEYWORDS  
EST.

SOURCE  
Oryza sativa

ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 13)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)



Query Match      0.5%;      Score 13;      DB 1;      Length 13;



TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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with oligoribonucleotides and then used as templates for  
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## Query Match

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QY 2166 TTTT TTTT TTTT TTTT 2178

Db 1 TTTT TTTT TTTT TTTT 13

## RESULT 3351

CF327576/c

## LOCUS

DEFINITION NACL--02-B22.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--02-B22, mRNA sequence.

## ACCESSION

VERSION CF327576

KEYWORDS EST.

SOURCE Oryza sativa

## ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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## Query Match

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798

Db 13 AAAAAAAAAAAAAA 1

## RESULT 3352

CF327888

## LOCUS

DEFINITION NACL--02-I22.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--02-I22, mRNA sequence.

## ACCESSION

VERSION CF327888

KEYWORDS EST.

SOURCE Oryza sativa

## ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

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Yongin, Kyeonggi, Korea

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

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Db 1 TTTT TTTT TTTT TTTT 13

## RESULT 3353

CF327888/c

## LOCUS

DEFINITION NACL--02-I22.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--02-I22, mRNA sequence.

## ACCESSION

VERSION CF327888

KEYWORDS EST.

SOURCE Oryza sativa

## ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

TITLE  
JOURNAL  
COMMENT

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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Db 13 AAAAAAAAAAAAAA 1

RESULT 3354  
CF327939

LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CF327939 13 bp mRNA linear EST 18-AUG-2003  
NACL--02-K02.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--02-K02, mRNA sequence.

CF327939  
CF327939.1 GI:33804127  
EST.  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
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Contact: Nahm B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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RT-PCR."

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QY 2166 TTTT TTTT TTTT 2178  
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Db 1 TTTT TTTT TTTT 13

RESULT 3355  
CF327939/c

LOCUS  
DEFINITION

CF327939 13 bp mRNA linear EST 18-AUG-2003  
NACL--02-K02.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--02-K02, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CF327939  
CF327939.1 GI:33804127  
EST.  
Oryza sativa  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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QY 2786 AAAAAAAAAAAAAA 2798  
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Db 13 AAAAAAAAAAAAAA 1

RESULT 3356  
CF328153

LOCUS  
DEFINITION

CF328153 13 bp mRNA linear EST 18-AUG-2003  
NACL--02-O19.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--02-O19, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CF328153  
CF328153.1 GI:33804556  
EST.  
Oryza sativa  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Query Match 0.5%; Score 13; DB 1; Length 13;  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178  
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Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3357  
CF328153/c  
LOCUS CF328153 13 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--02-O19.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--02-O19, mRNA sequence.  
ACCESSION CF328153  
VERSION CF328153.1 GI:33804556  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA 2798  
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Db 13 AAAAAA AAAAAA 1

RESULT 3358  
CF328228  
LOCUS CF328228 13 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--03-A13.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--03-A13, mRNA sequence.  
ACCESSION CF328228  
VERSION CF328228.1 GI:33804702  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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Query Match 0.5%; Score 13; DB 1; Length 13;  
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QY 2166 TTTT TTTT TTTT TTTT 2178  
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## FEATURES

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RT-PCR."

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## FEATURES

source

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RT-PCR."

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REFERENCE
AUTHORS      1 (bases 1 to 13)
              Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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  /organism="Oryza sativa"
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 TTTTAAAAA 2798
Db      13 TTTTAAAAA 1

RESULT 3360
CF328807      13 bp mRNA linear EST 18-AUG-2003
LOCUS      NACL--03-007.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION      sativa cDNA clone NACL--03-007, mRNA sequence.
ACCESSION      CF328807
VERSION      CF328807.1 GI:33805856
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 TTTTAAAAA 2798
Db      13 TTTTAAAAA 1

RESULT 3360
CF328807      13 bp mRNA linear EST 18-AUG-2003
LOCUS      NACL--03-007.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION      sativa cDNA clone NACL--03-007, mRNA sequence.
ACCESSION      CF328807
VERSION      CF328807.1 GI:33805856
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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  /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
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  RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 TTTTAAAAA 2798
Db      13 TTTTAAAAA 1

RESULT 3362
CF329075      13 bp mRNA linear EST 18-AUG-2003
LOCUS      NACL--04-E07.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION      sativa cDNA clone NACL--04-E07, mRNA sequence.
ACCESSION      CF329075
VERSION      CF329075.1 GI:33806393
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 TTTTAAAAA 2798
Db      13 TTTTAAAAA 1

RESULT 3361
CF328807/c
LOCUS      NACL--03-007.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION      sativa cDNA clone NACL--03-007, mRNA sequence.
ACCESSION      CF328807
VERSION      CF328807.1 GI:33805856
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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QY      2786 TTTTAAAAA 2798
Db      13 TTTTAAAAA 1

RESULT 3362
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LOCUS      NACL--04-E07.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION      sativa cDNA clone NACL--04-E07, mRNA sequence.
ACCESSION      CF329075
VERSION      CF329075.1 GI:33806393
KEYWORDS      EST.
SOURCE      Oryza sativa
ORGANISM      Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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REFERENCE  
AUTHORS Ehrhartoideae; Oryzae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES  
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Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3363  
CF329075/c  
LOCUS  
DEFINITION NACL--04-E07.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--04-E07, mRNA sequence.  
ACCESSION  
VERSION CF329075.1 GI:33806393  
KEYWORDS  
SOURCE EST.  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

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Query Match 0.5%; Score 13; DB 1; Length 13;  
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QY 2786 AAAAAA AAAAAA 2798  
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Db 13 AAAAAA AAAAAA 1

RESULT 3364  
CF329076  
LOCUS  
DEFINITION NACL--04-E07.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--04-E07, mRNA sequence.  
ACCESSION  
VERSION CF329076.1 GI:33806395  
KEYWORDS  
SOURCE EST.  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA 2798  
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Db 1 AAAAAA AAAAAA 13

RESULT 3365  
CF329076/c  
LOCUS  
DEFINITION NACL--04-E07.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--04-E07, mRNA sequence.  
ACCESSION  
VERSION CF329076.1 GI:33806395  
KEYWORDS  
SOURCE EST.  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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Query Match 0.5%; Score 13; DB 1; Length 13;  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT 2178

Db 13 TTTT TTTT TTTT 1

## RESULT 3366

CF329417

LOCUS  
DEFINITION  
NACL--04-L19.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--04-L19, mRNA sequence.

ACCESSION CF329417

VERSION CF329417.1 GI:33807072

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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QY 2166 TTTT TTTT TTTT 2178

Db 1 TTTT TTTT TTTT 13

## RESULT 3367

CF329417/c

LOCUS  
DEFINITION  
NACL--04-L19.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--04-L19, mRNA sequence.

ACCESSION CF329417

VERSION CF329417.1 GI:33807072

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 13)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

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RT-PCR."

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QY 2786 AAAAAAAAAAAAAA 2798

Db 13 AAAAAAAAAAAAAA 1

## RESULT 3368

CF329460

LOCUS  
DEFINITION  
NACL--04-M18.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--04-M18, mRNA sequence.

ACCESSION CF329460

VERSION CF329460.1 GI:33807156

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE  
JOURNAL  
COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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## Query Match

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Qy 2166 TTTT TTTT TTTT TTTT 2178

Db 1 TTTT TTTT TTTT TTTT 13

## RESULT 3369

CF329460/c

LOCUS

CF329460 13 bp mRNA linear EST 18-AUG-2003  
NACL--04-M18.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--04-M18, mRNA sequence.

ACCESSION

CF329460

VERSION

CF329460.1 GI:33807156

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2798

Db 13 AAAAAAAAAAAAAA 1

## RESULT 3370

CF329729

LOCUS

CF329729 13 bp mRNA linear EST 18-AUG-2003  
NACL--05-C14.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--05-C14, mRNA sequence.

ACCESSION

CF329729

VERSION

CF329729.1 GI:33807674

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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Best Local Similarity 0.5%; Score 13; DB 1; Length 13;  
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Qy 2786 AAAAAAAAAAAAAA 2798

Db 1 AAAAAAAAAAAAAA 13

## RESULT 3371

CF329729/c

LOCUS

CF329729 13 bp mRNA linear EST 18-AUG-2003  
NACL--05-C14.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--05-C14, mRNA sequence.

ACCESSION

CF329729

VERSION

CF329729.1 GI:33807674

KEYWORDS

SOURCE

Oryza sativa

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ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE     1 (bases 1 to 13)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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             RT-PCR."

Query Match   0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT 2178
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Db       13 TTTT TTTT TTTT TTTT 1

RESULT 3372
CF329800
LOCUS      CF329800
DEFINITION NACL--05-E04.b1 Rice callus plasmid cDNA library (NACL) Oryza
           sativa cDNA clone NACL--05-E04, mRNA sequence.
ACCESSION  CF329800
VERSION     CF329800.1 GI:33807817
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 13)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     Location/Qualifiers
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             /lab_host="E.coli DH10B"
             /clone_lib="Rice callus plasmid cDNA library (NACL)"
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT 2178
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Db       13 TTTT TTTT TTTT TTTT 1

RESULT 3372
CF329800
LOCUS      CF329800
DEFINITION NACL--05-E04.b1 Rice callus plasmid cDNA library (NACL) Oryza
           sativa cDNA clone NACL--05-E04, mRNA sequence.
ACCESSION  CF329800
VERSION     CF329800.1 GI:33807817
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 13)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     Location/Qualifiers
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             /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT 2178
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Db       13 TTTT TTTT TTTT TTTT 1

RESULT 3372
CF329800
LOCUS      CF329800
DEFINITION NACL--05-E04.b1 Rice callus plasmid cDNA library (NACL) Oryza
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ACCESSION  CF329800
VERSION     CF329800.1 GI:33807817
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 13)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     Location/Qualifiers
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QY      2166 TTTT TTTT TTTT TTTT 2178
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Db       13 TTTT TTTT TTTT TTTT 1

RESULT 3372
CF329800
LOCUS      CF329800
DEFINITION NACL--05-E04.g1 Rice callus plasmid cDNA library (NACL) Oryza
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ACCESSION  CF329800
VERSION     CF329800.1 GI:33807819
KEYWORDS   EST.
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RT-PCR."

Query Match   0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT 2178
          |||||
Db       1 TTTT TTTT TTTT TTTT 13

RESULT 3373
CF329800/c
LOCUS      CF329800
DEFINITION NACL--05-E04.b1 Rice callus plasmid cDNA library (NACL) Oryza
           sativa cDNA clone NACL--05-E04, mRNA sequence.
ACCESSION  CF329800
VERSION     CF329800.1 GI:33807817
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 13)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     Location/Qualifiers
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             /tissue_type="callus"
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             /clone_lib="Rice callus plasmid cDNA library (NACL)"
             /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
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             RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAA AAAAAA 2798
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Db       13 AAAAAA AAAAAA 1

RESULT 3374
CF329801
LOCUS      CF329801
DEFINITION NACL--05-E04.g1 Rice callus plasmid cDNA library (NACL) Oryza
           sativa cDNA clone NACL--05-E04, mRNA sequence.
ACCESSION  CF329801
VERSION     CF329801.1 GI:33807819
KEYWORDS   EST.
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SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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QY 2786 AAAAAAAAAAAAAA 2798  
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Db 1 AAAAAAAAAAAAAA 13

RESULT 3375  
CF329801/c  
LOCUS  
DEFINITION NACL--05-E04.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--05-E04, mRNA sequence.  
ACCESSION CF329801  
VERSION CF329801.1 GI:33807819  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
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QY 2166 TTTT TTTT TTTT TTTT 2178  
|||||  
Db 13 TTTT TTTT TTTT TTTT 1

RESULT 3376  
CF329869  
LOCUS  
DEFINITION NACL--05-F18.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--05-F18, mRNA sequence.  
ACCESSION CF329869  
VERSION CF329869.1 GI:33807959  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3377  
CF329869/c  
LOCUS  
DEFINITION NACL--05-F18.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--05-F18, mRNA sequence.  
ACCESSION CF329869  
VERSION CF329869.1 GI:33807959

KEYWORDS  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Tel: 82 31 330 6193  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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QY 2786 AAAAAAAAAAAAAA 2798  
|||||  
Db 13 AAAAAAAAAAAAAA 1

RESULT 3378  
CF329946 13 bp mRNA linear EST 18-AUG-2003  
LOCUS NACL--05-H12.b1 Rice callus plasmid cDNA library (NACL) Oryza  
DEFINITION sativa cDNA clone NACL--05-H12, mRNA sequence.

ACCESSION CF329946.1 GI:33808114  
VERSION  
KEYWORDS  
SOURCE

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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QY 2166 TTTT TTTT TTTT TTTT 2178  
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Db 1 TTTT TTTT TTTT TTTT 13

## RESULT 3379

CF329946/c  
LOCUS NACL--05-H12.b1 Rice callus plasmid cDNA library (NACL) Oryza  
DEFINITION sativa cDNA clone NACL--05-H12, mRNA sequence.

ACCESSION CF329946.1 GI:33808114  
VERSION  
KEYWORDS  
SOURCE

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
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of Bioscience and Bioinformatics, Myongji University  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
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Db 13 AAAAAAAAAAAAAA 1

## RESULT 3380

CF329988 13 bp mRNA linear EST 18-AUG-2003  
LOCUS NACL--05-I10.b1 Rice callus plasmid cDNA library (NACL) Oryza  
DEFINITION sativa cDNA clone NACL--05-I10, mRNA sequence.

ACCESSION CF329988



ACCESSION CF330023  
VERSION CF330023.1 GI:33808268  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
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of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2798  
Db 13 AAAAAAAAAAAAAA 1

RESULT 3384  
CF330725  
LOCUS 13 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--06-J01.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--06-J01, mRNA sequence.  
ACCESSION CF330725  
VERSION CF330725.1 GI:33809672  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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Qy 2786 AAAAAAAAAAAAAA 2798  
Db 13 AAAAAAAAAAAAAA 1

RESULT 3384  
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LOCUS 13 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--06-J01.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--06-J01, mRNA sequence.  
ACCESSION CF330725  
VERSION CF330725.1 GI:33809672  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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RESULT 3385  
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LOCUS 13 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--06-J01.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--06-J01, mRNA sequence.  
ACCESSION CF330725  
VERSION CF330725.1 GI:33809672  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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Db 13 TTTT TTTT TTTT TTTT 1

RESULT 3386  
CF331041  
LOCUS 13 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--07-A04.b1 Rice callus plasmid cDNA library (NACL) Oryza





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DEFINITION NACL--07-F06.b1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION sativa cDNA clone NACL--07-F06, mRNA sequence.
VERSION CF331266.1 GI:33810744
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798
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Db 13 AAAAAAAAAAAAAA 1

RESULT 3390
CF331273
LOCUS NACL--07-F09.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--07-F09, mRNA sequence.
ACCESSION CF331273
VERSION CF331273.1 GI:33810757
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 13 AAAAAAAAAAAAAA 1

RESULT 3390
CF331273
LOCUS NACL--07-F09.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--07-F09, mRNA sequence.
ACCESSION CF331273
VERSION CF331273.1 GI:33810757
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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CF331903
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Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798
|||||
Db 1 AAAAAAAAAAAAAA 13

RESULT 3391
CF331273/c
LOCUS NACL--07-F09.g1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sativa cDNA clone NACL--07-F09, mRNA sequence.
ACCESSION CF331273
VERSION CF331273.1 GI:33810757
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 13 TTTT TTTT TTTT TTTT TTTT 1

RESULT 3392
CF331903
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LOCUS CF331903 13 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--08-D07.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--08-D07, mRNA sequence.  
ACCESSION CF331903  
VERSION CF331903.1 GI:33812027  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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QY 2166 TTTT TTTT TTTT TTTT 2178

Db 1 TTTT TTTT TTTT TTTT 13

## RESULT 3393

CF331903/c

LOCUS CF331903 13 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--08-D07.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--08-D07, mRNA sequence.

ACCESSION CF331903

VERSION CF331903.1 GI:33812027

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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COMMENT

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

Location/Qualifiers

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QY 2786 AAAAAA AAAAAA 2798

Db 13 AAAAAA AAAAAA 1

## RESULT 3394

CF332079

LOCUS

DEFINITION

NACL--08-H04.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--08-H04, mRNA sequence.

ACCESSION

CF332079

VERSION

CF332079.1 GI:33812379

KEYWORDS

EST.

SOURCE

Oryza sativa

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

1 (bases 1 to 13)

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

COMMENT

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Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .13

/organism="Oryza sativa"

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/db\_xref="taxon:4530"

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Best Local Similarity 100.0%; Pred. No. 2.2e+03;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178

Db 1 TTTT TTTT TTTT TTTT 13

## RESULT 3395

CF332079/c  
LOCUS NACL--08-H04 13 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--08-H04.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--08-H04, mRNA sequence.  
ACCESSION CF332079  
VERSION CF332079.1 GI:33812379  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1. .13  
/organism="Oryza sativa"  
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Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
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RESULT 3396  
CF332695 13 bp mRNA linear EST 18-AUG-2003  
LOCUS JMT--01-E21.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--01-E21, mRNA sequence.  
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ACCESSION CF332695.1 GI:33813618  
VERSION CF332695  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
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REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
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Db 13 AAAAAAAAAAAAAA 1

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LOCUS JMT--01-E21.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--01-E21, mRNA sequence.  
DEFINITION CF332695  
ACCESSION CF332695.1 GI:33813618  
VERSION CF332695  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 13)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 13 AAAAAAAAAAAAAA 1

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QY 2166 TTTT TTTT TTTT TTTT 2178  
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Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3397  
CF332695/c  
LOCUS JMT--01-E21.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--01-E21, mRNA sequence.  
DEFINITION CF332695  
ACCESSION CF332695.1 GI:33813618  
VERSION CF332695  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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Location/Qualifiers  
1. .13  
/organism="Oryza sativa"  
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Query Match 0.5%; Score 13; DB 1; Length 13;  
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QY 2786 AAAAAAAAAAAAAA 2798  
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Db 13 AAAAAAAAAAAAAA 1





methyltransferase overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178  
Db 1 TTTT TTTT TTTT TTTT 13

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LOCUS  
DEFINITION  
JMT--02-G11.b1 AtJMT-overexpressing transgenic rice plasmid cDNA  
Library (JMT) Oryza sativa cDNA clone JMT--02-G11, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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FEATURES  
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QY 2786 AAAAAAAAAAAAAA 2798  
Db 13 AAAAAAAAAAAAAA 1

RESULT 3402  
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LOCUS  
DEFINITION  
JMT--03-B12.b1 AtJMT-overexpressing transgenic rice plasmid cDNA  
Library (JMT) Oryza sativa cDNA clone JMT--03-B12, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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QY 2166 TTTT TTTT TTTT TTTT 2178  
Db 1 TTTT TTTT TTTT TTTT 13

RESULT 3403  
CF333972/c  
LOCUS  
DEFINITION  
JMT--03-B12.b1 AtJMT-overexpressing transgenic rice plasmid cDNA  
Library (JMT) Oryza sativa cDNA clone JMT--03-B12, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source

1. .13  
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RESULT 3404  
CF333973

LOCUS  
DEFINITION  
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library (JMT) Oryza sativa cDNA clone JMT--03-B12, mRNA sequence.  
CF333973  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 13)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
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Tel: 82 31 330 6193  
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CF333973/c

LOCUS  
DEFINITION  
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library (JMT) Oryza sativa cDNA clone JMT--03-B12, mRNA sequence.  
CF333973  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 1 AAAAAAAAAAAAAA 13

RESULT 3405  
CF333973/c

LOCUS  
DEFINITION  
JMT--03-B12.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--03-B12, mRNA sequence.  
CF333973  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
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QY 2786 AAAAAAAAAAAAAA 2798  
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Db 13 AAAAAAAAAAAAAA 1

RESULT 3406  
CF333973

LOCUS  
DEFINITION  
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library (JMT) Oryza sativa cDNA clone JMT--03-B12, mRNA sequence.  
CF333973  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
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RESULT 3406  
CF333973

LOCUS  
DEFINITION  
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library (JMT) Oryza sativa cDNA clone JMT--03-B12, mRNA sequence.  
CF333973  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
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Location/Qualifiers  
1. .13  
/organism="Oryza sativa"  
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Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
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QY 2166 TTTT TTTT TTTT TTTT 2178  
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RESULT 3406  
CF333973

LOCUS  
DEFINITION  
JMT--03-B12.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--03-B12, mRNA sequence.  
CF333973  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
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Location/Qualifiers  
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/organism="Oryza sativa"  
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/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="JMT--03-B12"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
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cDNA library (JMT)"  
/note="Vector: pCR4-TOPO; Site\_1: EcoRI; Oligo-capped mRNA  
was reverse transcribed and then used for PCR. mRNA was  
prepared from Arabidopsis Jasmonate Carboxyl  
methyltransferase overexpression line."

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source      1. .13
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/mol_type="mRNA"
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/clone="JMT--03-J19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT 2178
Db      1 TTTT TTTT TTTT TTTT 13

RESULT 3407
CF334347/c
LOCUS
DEFINITION
JMT--03-J19.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--03-J19, mRNA sequence.
CF334347
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--03-J19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT 2178
Db      1 TTTT TTTT TTTT TTTT 13

RESULT 3407
CF334347/c
LOCUS
DEFINITION
JMT--03-J19.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--03-J19, mRNA sequence.
CF334347
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--03-J19"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT 2178
Db      1 TTTT TTTT TTTT TTTT 13

RESULT 3409
CF337022/c
LOCUS
DEFINITION
JMT--07-E22.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--07-E22, mRNA sequence.
CF337022
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
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Db      13 AAAAAAAAAAAAAA 1

RESULT 3408
CF337022
LOCUS
DEFINITION
JMT--07-E22.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--07-E22, mRNA sequence.
CF337022
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .13
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="JMT--07-E22"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="AtJMT-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jasmonate Carboxyl
methyltransferase overexpression line."

Query Match      0.5%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTT TTTT TTTT TTTT 2178
Db      1 TTTT TTTT TTTT TTTT 13

RESULT 3409
CF337022/c
LOCUS
DEFINITION
JMT--07-E22.b1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--07-E22, mRNA sequence.
CF337022
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
1 (bases 1 to 13)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
```



Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1. .13  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
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/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.5%; Score 13; DB 1; Length 13;  
Best Local Similarity 100.0%; Pred. No. 2.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
Db 13 AAAAAAAAAAAAAA 1

RESULT 3410  
CF327203  
LOCUS  
DEFINITION  
NACL--01-J16.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--01-J16, mRNA sequence.  
ACCESSION  
CF327203  
VERSION  
CF327203.1 GI:33802665  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1. .14  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="NACL--01-J16"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
Db 13 AAAAAAAAAAAAAA 1

RESULT 3412  
AW251049  
LOCUS  
DEFINITION  
2821507.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821507 3', mRNA sequence.  
ACCESSION  
AW251049  
VERSION  
AW251049.1 GI:6593995  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2178  
Db 1 TTTT TTTT TTTT TTTT TTTT 13

RESULT 3411  
CF327203/c  
LOCUS  
DEFINITION  
NACL--01-J16.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--01-J16, mRNA sequence.  
ACCESSION  
CF327203  
VERSION  
CF327203.1 GI:33802665  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1. .14  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
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/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.5%; Score 13; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
Db 13 AAAAAAAAAAAAAA 1

RESULT 3412  
AW251049  
LOCUS  
DEFINITION  
2821507.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821507 3', mRNA sequence.  
ACCESSION  
AW251049  
VERSION  
AW251049.1 GI:6593995  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

COMMENT

Other\_ESTs: 2821507.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 10  
contiguous PHRED high quality bases followed 16 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: LCM6 row: P column: 20  
High quality sequence stop: 10.  
Location/Qualifiers

FEATURES

source

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/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 13; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2177 TTTT TTTT TTTT AAC 2189

Db 1 TTTT TTTT TTTT AAC 13

RESULT 3413

AW251033

LOCUS

DEFINITION AW251033 17 bp mRNA linear EST 07-JAN-2000  
2821399.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821399 3',  
mRNA sequence.

ACCESSION AW251033

VERSION AW251033.1 GI:6593979

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2821399.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 17  
contiguous PHRED high quality bases followed 17 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: LCM6 row: L column: 8  
High quality sequence stop: 17.  
Location/Qualifiers

FEATURES

source

1..17  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:2821399"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 13; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1772 TTTT TTTT TTTT GAA 1784

Db 1 TTTT TTTT TTTT GAA 13

RESULT 3414

AW246451

LOCUS

DEFINITION AW246451 18 bp mRNA linear EST 07-JAN-2000  
2821637.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821637 3',  
mRNA sequence.

ACCESSION AW246451

VERSION AW246451.1 GI:6589444

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 18)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2821637.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 9 contiguous

PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 18 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated. Plate: L1CM7 row: F column: 6 High quality sequence stop: 9.

FEATURES

Location/Qualifiers  
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/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="IMAGE:2821637"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 13; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2177 TTTT TTTT TTTT AAC 2189  
Db 1 TTTT TTTT TTTT AAC 13

RESULT 3415

AZ764511  
LOCUS  
DEFINITION 1M0560B08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0560B08 R, genomic survey sequence.

ACCESSION AZ764511  
VERSION AZ764511.1 GI:12879549  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0560 row: B column: 08  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES

Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"

/db\_xref="taxon:10090"  
/clone="UUGC1M0560B08"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA AAAAAA 2798  
Db 1 AAAAAA AAAAAA 13

RESULT 3416

AZ764511/C  
LOCUS  
DEFINITION 1M0560B08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0560B08 R, genomic survey sequence.

ACCESSION AZ764511  
VERSION AZ764511.1 GI:12879549  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

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Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0560 row: B column: 08  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES

Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"



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/clone="UUGC1M0560B08"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
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10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Query Match      0.5%; Score 13; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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          |||||
Db       13 TTTT TTTT TTTT TTTT 1
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RESULT 3417
AZ9951149
LOCUS      2M0280D22R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
DEFINITION clone UUGC2M0280D22 R, genomic survey sequence.
ACCESSION  AZ9951149
VERSION     1
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
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JOURNAL     Unpublished (2000)
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            University of Utah Genome Center
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            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0280 row: D column: 22
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
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/sex="Female"
/lab host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
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with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
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chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

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Query Match      0.5%; Score 13; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db       2 ACCTGCTGCTGCC 14
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RESULT 3418
AZ479732/c
LOCUS      1M0300A09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0300A09 R, genomic survey sequence.
ACCESSION  AZ479732
VERSION     1
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 20)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
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JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
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            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0300 row: A column: 09
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
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                /db_xref="taxon:10090"
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
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was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.5%; Score 13; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAATAAAA 2797  
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Db 13 GAAAAAATAAAA 1

RESULT 3419  
AZ427740/c  
LOCUS  
DEFINITION  
IM0209J23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0209J23 R, genomic survey sequence.

ACCESSION  
AZ427740  
VERSION  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
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plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
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University of Utah Genome Center  
University of Utah  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0209 row: J column: 23  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

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/mol\_type="genomic DNA"  
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/clone="UUGC1M0209J23"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
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ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.5%; Score 13; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2175 TTTTNTTTTATA 2187  
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Db 13 TTTTNTTTTATA 1

RESULT 3420  
AZ506216  
LOCUS  
DEFINITION  
IM0347G11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0347G11 F, genomic survey sequence.

ACCESSION  
AZ506216  
VERSION  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
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COMMENT  
Unpublished (2000)  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0347 row: G column: 11  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
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/mol\_type="genomic DNA"  
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/db\_xref="taxon:10090"  
/clone="UUGC1M0347G11"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
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Db 1 AAAAAAAAAAAAAA 13

RESULT 3421  
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LOCUS  
DEFINITION  
1M0347G11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0347G11 F, genomic survey sequence.

ACCESSION  
AZ506216  
VERSION  
AZ506216.1 GI:10687532

KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

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84112, USA

TEL: 801 585 5606  
FAX: 801 585 7177  
EMAIL: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0347 row: G column: 11  
Seq primer: CGTTGTAACGACGGCCAGT  
Class: plasmid ends

High quality sequence stop: 20.  
Location/Qualifiers  
1. .20

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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/clone="UUGC1M0347G11"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.

FEATURES  
source

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Query Match 0.5%; Score 13; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2178  
|||||  
Db 13 TTTT TTTT TTTT TTTT 1

RESULT 3422  
AZ764514

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Robert B. Weiss

UNIVERSITY OF UTAH

UNIVERSITY OF UTAH

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EMAIL: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0560 row: F column: 09

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. .20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0560F09"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

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(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
|||||||  
Db 1 AAAAAAAAAAAAAA 13

RESULT 3423  
AZ764514/c  
LOCUS AZ764514 20 bp DNA linear GSS 16-FEB-2001  
DEFINITION IM0560F09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0560F09 R, genomic survey sequence.

ACCESSION AZ764514  
VERSION AZ764514.1 GI:12879555  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 20)

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

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Tel: 801 585 5606

Fax: 801 585 7177

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)

Insert Length: 10000 Std Error: 0.00

Plate: 0560 row: F column: 09

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0560F09"  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTT 2178  
|||||||  
Db 13 TTTTTTTTTTTT 1

RESULT 3424  
AZ772040

LOCUS AZ772040

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)

Insert Length: 10000 Std Error: 0.00

Plate: 0574 row: G column: 11

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

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/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA



was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2165 CTTTCTTTTCTTTT 2177  
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Db 1 CTTTCTTTTCTTTT 13

RESULT 3425  
AZ773905  
LOCUS  
DEFINITION  
2M0001C15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0001C15 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0001 row: C column: 15  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

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/db\_xref="taxon:10090"  
/clone="UUGC2M0001C15"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTCTTTTCTTTT 2178  
|||||  
Db 8 TTTTCTTTTCTTTT 20

RESULT 3426  
AZ773905/c  
LOCUS  
DEFINITION  
2M0001C15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0001C15 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0001 row: C column: 15  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
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Location/Qualifiers  
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/mol\_type="genomic DNA"  
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/db\_xref="taxon:10090"  
/clone="UUGC2M0001C15"  
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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA



was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No. 4.3e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
|||||||  
Db 20 AAAAAAAAAAAAAA 8

RESULT 3427  
AZ834769/c  
LOCUS  
DEFINITION  
2M0117F08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0117F08 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0117 row: F column: 08  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0117F08"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred.No. 4.3e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1947 TTGGTTTGTGT 1959  
|||||||  
Db 18 TTGGTTTGTGT 6

RESULT 3428  
AZ589400/c  
LOCUS  
DEFINITION  
AZ589400 21 bp DNA linear GSS 13-DEC-2000  
1M0398C23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0398C23 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

TITLE  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0398 row: C column: 23  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 21.

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/clone="UUGC1M0398C23"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13; DB 1; Length 21;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAA 2798  
|||||  
Db 21 AAAAAAAAAAAAA 9

RESULT 3429  
AZ346714  
LOCUS  
DEFINITION 1M0082N05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0082N05 F, genomic survey sequence.

ACCESSION AZ346714  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Mus musculus (house mouse)

REFERENCE  
AUTHORS  
1 (bases 1 to 21)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0082 row: N column: 05  
Seq primer: CGTTGTAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 21.

JOURNAL  
COMMENT  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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/db\_xref="taxon:10090"  
/clone="UUGC1M0082N05"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

FEATURES  
source  
Location/Qualifiers  
1. .21  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0082N05"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

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Query Match 0.5%; Score 13; DB 1; Length 21;  
Best Local Similarity 76.2%; Pred. No. 4.2e+03;  
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2783 TTGAAAAAAAAAAAAA 2803  
|||||  
Db 1 TTACATAATACAAAAAAA 21

RESULT 3430  
CB305256  
LOCUS  
DEFINITION 3'EST-Nfly-071 Drosophila melanogaster cDNA library Drosophila melanogaster cDNA 3', mRNA sequence.

ACCESSION CB305256  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Drosophila melanogaster (fruit fly)

REFERENCE  
AUTHORS  
1 (bases 1 to 23)  
Lee,S., Zhou,G., Bao,J., Shapiro,J., Xu,J., Sun,M., Lin,W., Zhang,R., Chen,J., Clark,T., Sun,M., Wang,J., Johnson,D., Tseng,C., Yang,H., Wang,J., Du,W., Wu,C.I., Zhang,X. and Wang,S.M.

TITLE  
Novel SAGE tags represent a significant number of novel genes in Drosophila genome  
Unpublished (2003)  
Contact: Wang SM  
Hem/Onc  
University of Chicago Medical Center  
5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA  
Tel: 773-702-6788  
Fax: 773-702-3002  
Email: swangl@midway.uchicago.edu  
This EST was detected from Drosophila melanogaster cDNA Library with GLGI technique (Generation of Longer cDNA fragments from SAGE tags for Gene Identification, Proc. Natl. Acad. Sci. USA 97, 349, 2000; A high-throughput GLGI procedure for converting a large number of SAGE tag sequences into 3' ESTs, Genes, Chromosomes & Cancers 33:252-261, 2002 ), which covers from the 3' end of cDNA till the first CATG.  
Seq primer: M13 Forward.

JOURNAL  
COMMENT  
Location/Qualifiers  
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Query Match 0.5%; Score 13; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1772 TTTTGTGAA 1784  
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Db 1 TTTTGTGAA 13

RESULT 3431  
AZ615086/c

LOCUS AZ615086 23 bp DNA linear GSS 13-DEC-2000  
DEFINITION IM0444C14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0444C14 F, genomic survey sequence.  
ACCESSION AZ615086  
VERSION AZ615086.1 GI:11737276  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0444 row: C column: 14  
Seq primer: CGTTGTAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 23.  
Location/Qualifiers  
1. 23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0444C14"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
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FEATURES source

1. 23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
|||||  
Db 23 AAAAAAAAAAAAAA 11

RESULT 3432  
AZ819376 23 bp DNA linear GSS 20-FEB-2001  
LOCUS AZ819376

DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

2M0089P23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0089P23 R, genomic survey sequence.  
AZ819376  
AZ819376.1 GI:12989284  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0089 row: P column: 23  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 23.  
Location/Qualifiers  
1. 23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0089P23"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES source

1. 23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0089P23"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.5%; Score 13; DB 1; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.9e+03;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798  
|||||  
Db 1 AAAAAAAAAAAAAA 13

RESULT 3433  
AA937877 16 bp mRNA linear EST 30-APR-1998  
LOCUS AA937877  
DEFINITION nw90e06.s1 NCI\_CGAP\_Prl2 Homo sapiens cDNA clone IMAGE:1253890



similar to TR:Q35989 Q35989 CYTOCHROME C OXIDASE SUBUNIT 1 ;, mRNA sequence.  
AA937877  
AA937877.1 GI:3095988  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D., Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: David B. Krizman, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Trace considered overall poor quality  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1253890"  
/sex="male"  
/tissue\_type="metastatic prostate bone lesion"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Pr12"  
/note="Vector: pAMP10; mRNA made from metastatic prostate lesion of the bone, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman, NIH."  
Query Match 0.5%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.8e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT TTTT TTTT 2181  
Db 1 TTGT TTTT TTTT TTTT TTTT 16  
RESULT 3434  
AA937877/c  
LOCUS  
DEFINITION  
similar to TR:Q35989 Q35989 CYTOCHROME C OXIDASE SUBUNIT 1 ;, mRNA sequence.  
AA937877  
AA937877.1 GI:3095988  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D., Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: David B. Krizman, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Trace considered overall poor quality  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1253890"  
/sex="male"  
/tissue\_type="metastatic prostate bone lesion"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Pr12"  
/note="Vector: pAMP10; mRNA made from metastatic prostate lesion of the bone, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Library made by D. Krizman, NIH."  
Query Match 0.5%; Score 12.8; DB 1; Length 16;  
Best Local Similarity 87.5%; Pred. No. 3.8e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2786 AAAAAA AAAAAA AAAAAA 2801  
Db 16 AAAAAA TAAAAA AAAAAA 1  
RESULT 3435  
AW245338/c  
LOCUS  
DEFINITION  
AW245338 16 bp mRNA linear EST 07-JAN-2000  
2822905.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2822905 3', mRNA sequence.  
AW245338  
AW245338.1 GI:6588331  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2822905.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross\_match from University of Washington Genome Center. PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 15 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 16 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.



Plate: LLCM10 row: K column: 2  
High quality sequence stop: 15.  
Location/Qualifiers  
1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2822905"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match  
Best Local Similarity 0.5%; Score 12.8; DB 1; Length 16;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAA 2800  
|||||

Db 16 GAACACAAAAAAA 1

RESULT 3436  
BQ591425  
LOCUS  
DEFINITION BQ591425 16 bp mRNA linear EST 06-DEC-2002  
CDNA clone 024-017-C11-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
BQ591425  
ACCESSION BQ591425  
VERSION BQ591425.1 GI:26121008  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaar@piz-koeln.mpg.de  
Insert Length: 16 Std Error: 0.00  
Plate: 17 row: C column: 11  
Seq primer: T7; GTAATACGACTCACTATAGGC.  
Location/Qualifiers  
1. .16  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:188698"  
/db\_xref="taxon:161934"  
/clone="024-017-C11"  
/tissue\_type="storage root"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-storage root"

/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
SP6-Sali-CCAGCGTCGG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match  
Best Local Similarity 0.5%; Score 12.8; DB 1; Length 16;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1632 CCTTACTATTAAAGA 1647  
|||||

Db 1 CCTTACTATTAAAAA 16

RESULT 3437  
AW247976/c  
LOCUS  
DEFINITION AW247976 17 bp mRNA linear EST 07-JAN-2000  
2820717.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2820717 3', mRNA sequence.  
ACCESSION AW247976  
VERSION AW247976.1 GI:6591064  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 17)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other\_ESTs: 2820717.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 0 contiguous  
PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LLCM4 row: O column: 22.  
Location/Qualifiers  
1. .17  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.5%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 4.1e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2782 ATTGAAAAA 2797  
Db 16 ATTGTA 1

RESULT 3438  
CF312453  
LOCUS  
DEFINITION ABF--08-D15.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--08-D15, mRNA sequence.

ACCESSION CF312453  
VERSION CF312453.1 GI:33684214  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 18)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1..18  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="ABF--08-D15"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid  
cDNA library (ABF)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; Leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.5%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 4.3e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2166 TTTT 2181  
Db 16 TGT 1

RESULT 3440  
A1149192  
LOCUS  
DEFINITION A1149192.1 Soares\_placenta 8to9weeks\_2NbHP8to9W Homo sapiens cDNA  
clone IMAGE:1715537 3, similar to TR:Q39949 Q39949  
HYDROXYPROLINE-RICH PROTEIN. ;contains element TAR1 repetitive  
element ;, mRNA sequence.

ACCESSION A1149192  
VERSION A1149192.1 GI:3677661  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 19)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Insert Length: 675 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
location/Qualifiers  
1..19  
/organism="Homo sapiens"  
/mol\_type="mRNA"

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 18)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
Location/Qualifiers  
1..18  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="ABF--08-D15"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid  
cDNA library (ABF)"  
/note="Vector: PCR4-TOPO; Site\_1: EcoRI; Leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.5%; Score 12.8; DB 1; Length 18;  
Best Local Similarity 87.5%; Pred. No. 4.3e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2166 TTTT 2181  
Db 16 TGT 1

RESULT 3440  
A1149192  
LOCUS  
DEFINITION A1149192.1 Soares\_placenta 8to9weeks\_2NbHP8to9W Homo sapiens cDNA  
clone IMAGE:1715537 3, similar to TR:Q39949 Q39949  
HYDROXYPROLINE-RICH PROTEIN. ;contains element TAR1 repetitive  
element ;, mRNA sequence.

ACCESSION A1149192  
VERSION A1149192.1 GI:3677661  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 19)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall poor quality  
Insert Length: 675 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
location/Qualifiers  
1..19  
/organism="Homo sapiens"  
/mol\_type="mRNA"





QY 2155 TTTTTCCTCCTTTT 2170  
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Db 4 TTTTTCCTCCTTT 19

RESULT 3443  
AZ786308/c  
LOCUS  
DEFINITION  
2M0031B17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0031B17 R, genomic survey sequence.  
ACCESSION  
AZ786308  
VERSION  
AZ786308.1 GI:12923936.  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE  
1 (bases 1 to 19)  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0031 row: B column: 17  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source  
1. 19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0031B17"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.5%; Score 12.8; DB 1; Length 19;  
Best Local Similarity 87.5%; Pred. No. 4.4e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 253 CCCCCACCTCTCCTCC 268

Db 17 CCCCCACCTCCCCGCC 2  
||||||| |||

RESULT 3444  
AZ830469  
LOCUS  
DEFINITION  
2M0109C14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0109C14 R, genomic survey sequence.  
ACCESSION  
AZ830469  
VERSION  
AZ830469.1 GI:13000377  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE  
1 (bases 1 to 19)  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0109 row: C column: 14  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source  
1. 19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0109C14"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.5%; Score 12.8; DB 1; Length 19;  
Best Local Similarity 87.5%; Pred. No. 4.4e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 107 CTTGGGGGCTGGGGG 122  
||||| |||||



Db 2 CTGGGACCTGGGGG 17

RESULT 3445	AZ326642	22 bp	DNA	linear	GSS 29-SEP-2000
LOCUS	1M0049D09R	Mouse 10kb	plasmid	UUGC1M library	Mus musculus genomic
DEFINITION	clone UUGC1M0049D09 R,	genomic survey	sequence.		
ACCESSION	AZ326642				
VERSION	AZ326642.1	GI:10384599			
KEYWORDS	GSS.				
SOURCE	Mus musculus	(house mouse)			
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 22)				
	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss				
	University of Utah Genome Center				
	University of Utah				
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA				
	Tel: 801 585 5606				
	Fax: 801 585 7177				
	Email: ddunn@genetics.utah.edu				
	Insert Length: 10000	Std Error: 0.00			
	Plate: 0049	row: D	column: 09		
	Seq primer: CACACAGGAACAGCTATGACC				
	Class: plasmid ends				
	High quality sequence stop: 22.				

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Query Match      0.5%; Score 12.8; DB 1; Length 22;
Best Local Similarity 87.5%; Pred. No. 4.1e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1494 AGAAAAATGGAGAAACA 1509
      | | | | | | | | | | | | | |
Db 6 AAAAAATGGAGCAACA 21

```

```

RESULT 3446
BG929133/c
LOCUS
DEFINITION
    BG929133
    HNC34-1-E8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
    sequence.
ACCESSION
    BG929133
VERSION
    BG929133.1 GI:14323656
KEYWORDS
    EST.
SOURCE
    Homo sapiens (human)
    ORGANISM
        Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
        1 (bases 1 to 25)
AUTHORS
    Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
    Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
    Lark,M.W.
TITLE
    Identification and initial characterization of 5000 expressed
    sequenced tags (ESTs) each from adult human normal and
    osteoarthritic cartilage cDNA libraries
JOURNAL
    Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE
    21482651
PUBMED
    11597177
COMMENT
    Contact: Sanjay Kumar
    UW2109
    GlaxoSmithKline
    709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
    Tel: 610-270-7245
    Fax: 610-270-5598
    Email: sanjay_kumar-logsk.com
    Seq primer: T7.
FEATURES
    Location/Qualifiers
        1..25
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /tissue_type="cartilage"
            /lab_host="E.coli DH10 B"
            /clone_lib="HNC (Human Normal Cartilage)"
            /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
            Directional"

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Query Match      0.5%; Score 12.8; DB 1; Length 25;
Best Local Similarity 70.8%; Pred. No. 3.6e+03;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAAAAAAAAAAAAAAA 2804
      ||| ||| ||| ||| ||| ||| |||
db 25 AAAAAACACAATAAAGAAAAAAA 2

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RESULT 3447	AI745099	LOCUS	AI745099	25 bp	mrna	linear	EST 21-JUN-1999
		DEFINITION	tr21a09.x1 NCI CGAP Ov23 Homo sapiens cDNA clone IMAGE:2218936 3' similar to TR:Q34096 Q34096 MURF2 PROTEIN. ; contains element L1 L1 repetitive element ;, mRNA sequence.				
		ACCESSION	AI745099				
		VERSION	AI745099.1	GI:5113387			
		KEYWORDS	EST.				
		SOURCE	Homo sapiens (human)				
		ORGANISM	Homo sapiens				
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
		REFERENCE	1 (bases 1 to 25)				
		AUTHORS	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .				
		TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
		JOURNAL	Unpublished (1997)				
		COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: Christopher Moskaluk, M.D., Ph.D. Michael R.				

Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Greg Lemmon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .25  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2218936"  
/tissue\_type="tumor, 5 pooled (see description)"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Ov23"  
/note="Organ: ovary; Vector: pCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.35 kb. Tumor types include: mixed  
Mullerian tumor, papillary serous, clear cell, spindle  
cell. All are primary tumors, metastasis positive. Life  
Technologies catalog #: 11534-013"

Query Match

Best Local Similarity

Matches

17;

Conservative

0;

Mismatches

7;

Indels

0;

Gaps

0;

Qy

2781

AATTGAAAAA

AAAAAAAAAAAAA

AAAAAAAAA

2804

Db

1

AAAGAAACAGATGAGAAAAA

AAAAA

24

RESULT 3448

AZ785005/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AZ785005

2M0028P24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC2M0028P24 F, genomic survey sequence.

AZ785005

GI:12921312

GSS.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 28)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0028 row: P column: 24

Seq primer: CGTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 28.

Location/Qualifiers

1. .28

/organism="Mus musculus"

/mol\_type="genomic DNA"

FEATURES

source

/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0028P24"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match

Best Local Similarity

Matches

17;

Conservative

0;

Mismatches

7;

Indels

0;

Gaps

0;

Qy

2779

AGAAATTGAAAAA

AAAAAAAAAAAAA

AAAAA

2802

Db

24

ACAAACCAAAACGTA

AAAAA

1

RESULT 3449

AI371092/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AI371092

ta07g09.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:2043424 3'

similar to TR:Q26195 Q26195 PVA1 GENE. ;contains Ll.b3 Ll

repetitive element ;, mRNA sequence.

AI371092

GI:4149845

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 19)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BTGP), Tumor Gene Index

Unpublished (1998)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.

cDNA Library Arrayed by: Greg Lemmon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 536 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. .19

/organism="Homo sapiens"

FEATURES

source









Query Match 0.4%; Score 12.6; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1971 TTACCTTGAAAAAAGAAA 1989  
Db 19 TTGGCTTGGAAGAAAAA 1

RESULT 3454

AW246513  
LOCUS  
DEFINITION  
2821739.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821739 3',  
mRNA sequence.

AW246513  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)

NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2821739.5prime

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 17  
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 19 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.

Plate: LLCM7 row: J column: 12  
High quality sequence stop: 17.

FEATURES

source

1..19  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821739"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dr priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 12.6; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2177 TTTTCTTTTAACTTGAA 2195  
Db 1 TTTTCTTTTTCAGGTTCAA 19

RESULT 3455

AW246513/c  
LOCUS  
DEFINITION

2821739.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821739 3',  
mRNA sequence.

AW246513  
VERSION  
KEYWORDS  
SOURCE

ORGANISM  
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)

NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2821739.5prime

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 17  
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 19 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.

Plate: LLCM7 row: J column: 12  
High quality sequence stop: 17.

FEATURES

source

1..19  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821739"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dr priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 12.6; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1970 TTTACCTTGAAAAAAGAA 1988  
Db 19 TTGAACCTGAAAAA 1

RESULT 3456

AW248820

LOCUS

DEFINITION

2821008.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821008 3',  
mRNA sequence.







Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

FEATURES

source

1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0080G12"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0203O11"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.6; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 294 CGCCACCCCTCTCCACAC 312  
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Db 19 CGCCCCCTCCCCCCCC 1

RESULT 3461

AZ424216

LOCUS

DEFINITION 1M0203O11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0203O11 R, genomic survey sequence.

ACCESSION AZ424216

VERSION AZ424216.1 GI:10548229

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

COMMENT Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0203 row: O column: 11

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

FEATURES

source

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/sex="Male"  
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/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.6; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 1 ACAAAACAAACAAACAA 19

RESULT 3462

AZ424216/c

LOCUS

DEFINITION 1M0203O11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0203O11 R, genomic survey sequence.

ACCESSION AZ424216

VERSION AZ424216.1 GI:10548229

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 19)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
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JOURNAL

COMMENT Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0203 row: O column: 11

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends



High quality sequence stop: 19.

## FEATURES

FEATURES source

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 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnares/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Location/Qualifiers

1. .19

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/strain="C57BL/6J"

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/clone="UUGC1M0231A01"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      0.4%; Score 12.6; DB 1; Length 19;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
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Query Match 0.4%; Score 12.6; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 289 CCGCGCGCCACCCCTCTCC 307  
||||| ||||| ||||| |||  
Db 1 CCCCCCGCCCCCCCCCCC 19

RESULT 3465  
AZ595570/c  
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DEFINITION IM0408I15F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0408I15 F, genomic survey sequence.  
ACCESSION AZ595570 GI:11717760  
VERSION AZ595570.1  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0408 row: I column: 15  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers 1. .19  
FEATURES source

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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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Query Match 0.4%; Score 12.6; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2032 AGGCAAGGTTCTATCTGC 2050  
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Db 19 AGGCAAGTTTGGAGCTGC 1

RESULT 3466  
AZ760597  
LOCUS AZ760597 19 bp DNA linear GSS 16-FEB-2001  
DEFINITION IM0554N21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0554N21 F, genomic survey sequence.  
ACCESSION AZ760597  
VERSION AZ760597.1 GI:12868613  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0554 row: N column: 21  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers 1. .19  
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Query Match 0.4%; Score 12.6; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
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RESULT 3467  
AZ761834  
LOCUS  
DEFINITION  
1M0556E19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0556E19 F, genomic survey sequence.  
ACCESSION  
AZ761834  
VERSION  
AZ761834.1 GI:12871174  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE  
1 (bases 1 to 19)  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
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Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0556 row: E column: 19  
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Query Match 0.4%; Score 12.6; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 47 GCGCGCGCGGGGGCGCG 65  
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Db 1 GGGCGCGGTGGGGTGGGG 19

RESULT 3468  
AZ775865/c  
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2M0009P05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0009P05 F, genomic survey sequence.  
ACCESSION  
AZ775865  
VERSION  
AZ775865.1 GI:12902847  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE  
1 (bases 1 to 19)  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
Unpublished (2000)  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
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Query Match 0.4%; Score 12.6; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.5e+03;  
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Db 19 CCCCTCTCTACCACATGCT 1

RESULT 3469  
AZ779094  
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DEFINITION 2M0015E02F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0015E02 F, genomic survey sequence.  
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VERSION AZ779094.1 GI:12909402  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0015 row: E column: 02  
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Class: plasmid ends  
High quality sequence stop: 19.  
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.6; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 2681 TGGTGAAATGGAGATTG 2699  
|||||  
Db 1 TTGGTAAATGGTGTGTTG 19

RESULT 3470  
AZ782026  
LOCUS  
DEFINITION 2M0021I23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0021I23 R, genomic survey sequence.  
ACCESSION AZ782026  
VERSION AZ782026.1 GI:12915307  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0021 row: I column: 23  
Seq primer: CACACAGGAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0021I23"



/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.6; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 792 GTCAGAGGAGCTGGTGGG 810  
| | | | | | | | | | | | | | |  
Db 1 GGCAGAGGTGCGGTGGG 19

RESULT 3471  
AZ789674 19 bp DNA linear GSS 16-FEB-2001  
LOCUS  
DEFINITION 2M0037L08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0037L08 R, genomic survey sequence.

ACCESSION AZ789674  
VERSION AZ789674.1 GI:12930742  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0037 row: L column: 08  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0037L08"  
/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.6; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT TTTT 2184  
| | | | | | | | | | | | | | |  
Db 1 TTTGGTTGTTTATTTT 19

RESULT 3472  
AZ789674/c 19 bp DNA linear GSS 16-FEB-2001  
LOCUS  
DEFINITION 2M0037L08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0037L08 R, genomic survey sequence.

ACCESSION AZ789674  
VERSION AZ789674.1 GI:12930742  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0037 row: L column: 08  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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/db\_xref="taxon:10090"  
/clone="UUGC2M0037L08"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.6; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
||||| ||||| ||||| |||||  
Db 19 AAAAAATAAACAAACCAA 1

RESULT 3473  
AZ807440  
LOCUS AZ807440 19 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0070K18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0070K18 F, genomic survey sequence.

ACCESSION AZ807440  
VERSION AZ807440.1 GI:12971791  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0070 row: K column: 18  
Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0070K18"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.6; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2599 GAAACTCTCTGTTACAGAA 2617  
||||| ||||| ||||| |||||  
Db 1 GAATCGCTGTGTTAAGAA 19

RESULT 3474  
AZ962769  
LOCUS AZ962769 19 bp DNA linear GSS 27-APR-2001  
DEFINITION 2M0231P08R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
clone UUGC2M0231P08 R, genomic survey sequence.

ACCESSION AZ962769  
VERSION AZ962769.1 GI:13833996  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0231 row: P column: 08  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0231P08"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.6; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 289 CCCC GCCGCCACCCCTCTCC 307  
||||| ||| ||||| |||  
Db 1 CCCCCCCCCCCCCCTTCC 19

RESULT 3475  
AL587630/c  
LOCUS  
DEFINITION AL587630 BP Chicken Brain Library Gallus gallus cdna clone  
ROS060A07, mRNA sequence.  
ACCESSION AL587630  
VERSION AL587630.1 GI:13192664  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
1 (bases 1 to 20)  
Murray,F.  
AUTHORS BP Chicken Brain Library  
TITLE Unpublished (2001)  
JOURNAL  
COMMENT Contact: Frazer Murray  
Dept. Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UK  
Tel: +44 (0)131 527 4200  
Fax: +44 (0)131 440 0434  
Email: frazer.murray@bbsrc.ac.uk  
CGCGCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clonetech (\*6854-

Seq primer: M13F.  
Location/Qualifiers  
1..20  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9031"  
/clone="ROS060A07"  
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/dev\_stage="Unknown"  
/lab\_host="DH10B"  
/clone\_lib="BP Chicken Brain Library"  
/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. 5' adaptor sequence: 5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5' CGCGCGCTTTT TTTT TTTT TTTT TTTT 3' Poly A RNA purchased from Clonetech (\*6854-1)"

Query Match 0.4%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 4.4e+03;

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
||||| ||| ||||| |||  
Db 20 AAAAAAAAAAAACTGGAAA 2

RESULT 3476  
AU264645  
LOCUS  
DEFINITION AU264645 VS Dictyostelium discoideum cDNA clone VSD846 5', mRNA  
sequence.  
ACCESSION AU264645  
VERSION AU264645.1 GI:20523443  
KEYWORDS EST.  
SOURCE Dictyostelium discoideum  
ORGANISM Dictyostelium discoideum  
REFERENCE Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
1 (bases 1 to 20)  
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriiki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.  
TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum  
JOURNAL Unpublished (2002)  
COMMENT Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664  
Fax: 81-298-53-6614  
Email: hideko@biol.tsukuba.ac.jp.  
Location/Qualifiers  
1..20  
/organism="Dictyostelium discoideum"  
/mol\_type="mRNA"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="VSD846"  
/sex="mat A"  
/dev\_stage="vegetative"  
/clone\_lib="VS"

Query Match 0.4%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 4.4e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAAAAAAAAAA 2797  
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Db 2 AAAAAATTTTAAAAAAAAAAAA 20

RESULT 3477  
AU267884  
LOCUS  
DEFINITION AU267884 VS Dictyostelium discoideum cDNA clone VSH730 3', mRNA  
sequence.  
ACCESSION AU267884  
VERSION AU267884.1 GI:20526682  
KEYWORDS EST.  
SOURCE Dictyostelium discoideum  
ORGANISM Dictyostelium discoideum  
REFERENCE Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.  
1 (bases 1 to 20)  
AUTHORS Urushihara,H., Morio,T., Saito,T., Koriiki,E., Ochiai,H., Maeda,M., Takeuchi,I., Kohara,Y. and Tanaka,Y.  
TITLE Population analysis of cDNAs from unicellular and multicellular stages of Dictyostelium discoideum  
JOURNAL Unpublished (2002)  
COMMENT Contact: Hideko Urushihara  
Institute of Biological Sciences  
University of Tsukuba  
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan  
Tel: 81-298-53-4664

Fax: 81-298-53-6614  
Email: hideko@biol.tsukuba.ac.jp.  
Location/Qualifiers  
1. .20  
/organism="Dictyostelium discoideum"  
/mol\_type="mRNA"  
/strain="AX4"  
/db\_xref="taxon:44689"  
/clone="VSH730"  
/sex="mat A"  
/dev\_stage="vegetative"  
/clone\_lib="VS"

Query Match 0.4%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 4.4e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2157 TTTTCTCCTTTTTTTT 2175  
||||| ||||||| |||  
Db 2 TTTTTCGCTTTTCTCT 20

RESULT 3478  
CF301021  
LOCUS  
DEFINITION 7LEAF--05-L10.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--05-L10, mRNA sequence.  
ACCESSION CF301021  
VERSION CF301021.1 GI:33672782  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers  
1. .14  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--05-L10"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 3.3e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTCTTTTCTTTT 2179  
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Db 14 TTTTCTATTTT 1

RESULT 3480  
CF543203  
LOCUS  
DEFINITION S014679-024-030-D05-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone 024-030-D05 5-PRIME, mRNA sequence.  
ACCESSION CF543203  
VERSION CF543203.1 GI:34891643  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany

Query Match 0.4%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 3.3e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2799  
||||| ||||||  
Db 1 AAAAAATAAAAAA 14

RESULT 3479  
CF301021/c

LOCUS  
DEFINITION 7LEAF--05-L10.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--05-L10, mRNA sequence.  
ACCESSION CF301021  
VERSION CF301021.1 GI:33672782  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 14)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers  
1. .14  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--05-L10"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 12.4; DB 1; Length 14;  
Best Local Similarity 92.9%; Pred. No. 3.3e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTCTTTTCTTTT 2179  
||||| ||||||  
Db 14 TTTTCTATTTT 1

RESULT 3480  
CF543203  
LOCUS  
DEFINITION S014679-024-030-D05-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone 024-030-D05 5-PRIME, mRNA sequence.  
ACCESSION CF543203  
VERSION CF543203.1 GI:34891643  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany



Fax: 004922215062851  
Email: weisshaa@piz-koeln.mpg.de  
Insert Length: 15 Std Error: 0.00  
Plate: 30 row: D column: 05  
Seq primer: SP6.

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FEATURES
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Location/Qualifiers
1..15
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:936579"
/db_xref="taxon:161934"
/clone="024-030-D05"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MPIZ-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzucht AG Einbeck, Germany, conta
b.schulz@kws.de; cloning sites SalI-NotI, primer site
orientation:
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; N
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinat
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"
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Query Match	0.4%;	Score 12.4;	DB 1;	Length 15;
Best Local Similarity	92.9%;	Pred. No. 3.8e+03;		
Matches 13;	Conservative	0;	Mismatches 1;	Indels 0;
QY	2784	TGAAAAAAAAAAAA	2797	
db	2	TCAAAAAAAAAAAA	15	

RESULT 3481	AW245585	LOCUS	AW245585	15 bp	linear	EST 07-JAN-2000
DEFINITION	2822740.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822740 3', mRNA sequence.					
ACCESSION	AW245585					
VERSION	AW245585.1 GI:6588578					
KEYWORDS	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	1 (bases 1 to 15)					
TITLE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .					
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)					
COMMENT	Unpublished (1999)					
	Other_ESTs: 2822740.5prime					
	Contact: Robert Strausberg, Ph.D.					
	Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a>					
	Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling					
	Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.					
	Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing					
	project Clone distribution: MGC clone distribution information can					
	be found through the I.M.A.G.E. Consortium/LLNL at:					
	<a href="http://www-bio.llnl.gov/bbrp/image/image.html">www-bio.llnl.gov/bbrp/image/image.html</a> Base Calling / Quality					
	Scores: PHRED from University of Washington Genome Center. Vector					
	Trimming: cross match from University of Washington Genome Center					
	PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley					
	Drosophila Genome Project. University of Washington Genome Center:					
	<a href="http://www.genome.washington.edu">http://www.genome.washington.edu</a> Low Quality Sequence: 6 contiguous					
	PHRED high quality bases following vector sequence. Very Low					
	Quality Sequence: Trace file contained 15 contiguous distinct peaks					
	following vector sequence. Polyadenylation: Based upon the presence					
	of a XhoI site followed by a run of 14 or more T residues at the					
	beginning of the sequence, this cDNA insert was polyadenylated.					
	Plate: LLCW10 row: D column: 5					

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High quality sequence stop: 6.
FEATURES
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      /db_xref="taxon:9606"
      /clone="IMAGE:2822740"
      /tissue type="small cell carcinoma"
      /cell_line="MGC3"
      /lab_host="DH10B (phage-resistant)"
      /clone_lib="NIH_MGC_7"
      /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
      EcoRI; cDNA made by oligo-dT priming. Directionally
      cloned into EcoRI/XhoI sites using the following 5'
      adaptor: GGCACGAG(G). Size-selected >500bp for average
      insert size 1.8kb. Library constructed by Ling Hong in
      the laboratory of Gerald M. Rubin (University of
      California, Berkeley) using ZAP-cDNA synthesis kit
      (Stratagene) and Superscript II RT (Life Technologies)."
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Query Match	0.4%;	Score 12.4;	DB 1;	Length 15;
Best Local Similarity	92.9%;	Pred. NO. 3.8e+03;		
Matches 13;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps	0;			
QY	2177	TTTTTTTTTAACT	2190	
Db	1	TTTTTTTTTAAAT	14	

RESULT 3482	
AW2455585/c	
LOCUS	AW2455585 15 bp mRNA linear EST 07-JAN-2000
DEFINITION	2822740.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822740 3', mRNA sequence.
ACCESSION	AW2455585
VERSION	AW245585.1 GI:6588578
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 15)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Other_ESTs: 2822740.5prime Contact: Robert Strausberg, Ph.D.

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FEATURES
  source
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      1..15
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        /clone="IMAGE:2822740"
        /tissue type="small cell carcinoma"

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/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

Query Match 0.4%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3.8e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2781 AATTGAAAAAAA 2794  
|||||  
Db 14 AATTAAAAAAA 1

RESULT 3483  
AW246494  
LOCUS  
DEFINITION  
2821595.3prime NIH\_MGC\_7 15 bp mRNA linear EST 07-JAN-2000  
mRNA sequence.  
ACCESSION  
AW246494  
VERSION  
AW246494.1 GI:6589487  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 15)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2821595.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-re@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 14  
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 15 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: LLCW7 row: D column: 12  
High quality sequence stop: 14.  
Location/Qualifiers  
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/organism="Homo sapiens"  
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/clone="IMAGE:2821595"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average

```

insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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Query Match 0.4%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3.8e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1772 TTTT TTTT TTTT GAAC 1785  
|||||  
Db 1 TTTT TTTT TTTT GATC 14

RESULT 3484  
AW246551  
LOCUS  
DEFINITION  
2822090.3prime NIH\_MGC\_7 15 bp mRNA linear EST 07-JAN-2000  
mRNA sequence.  
ACCESSION  
AW246551  
VERSION  
AW246551.1 GI:6589544  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 15)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2822090.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-re@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 14  
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 15 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: LLCM8 row: I column: 3  
High quality sequence stop: 14.  
Location/Qualifiers  
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/organism="Homo sapiens"  
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/clone="IMAGE:2822090"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 12.4; DB 1; Length 15;  
Best Local Similarity 92.9%; Pred. No. 3.8e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1772 TTTT TTTT TTTT GAAC 1785  
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Db 1 TTTT TTTT TTTT AAAC 14

RESULT 3485  
CF299603/c

LOCUS 7LEAF--03-L01.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--03-L01, mRNA sequence.

ACCESSION CF299603.1 GI:33671364

VERSION EST.

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 15)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Title Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

1. .15

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="7LEAF--03-L01"

/tissue\_type="leaf"

/dev\_stage="7 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match 0.4%; Score 12.4; DB 1; Length 15;

Best Local Similarity 92.9%; Pred. No. 3.8e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2179 TTTT TTTT TTTT AACTTT 2192  
|||||  
Db 15 TTTT TTTT TTTT AATT 2

RESULT 3486  
CF319827

LOCUS HD--10-H16.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA

DEFINITION library (HD) Oryza sativa cDNA clone HD--10-H16, mRNA sequence.

ACCESSION CF319827.1 GI:33691588

VERSION EST.

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 16)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Title Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

JOURNAL  
COMMENT

Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

1. .16

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="HD--10-H16"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_host="E.coli DH10B"

/clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid

cDNA library (HD)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was

treated with ABA(20um) for 1hr. Oligo-capped mRNA was

reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression

line."

Query Match 0.4%; Score 12.4; DB 1; Length 16;

Best Local Similarity 92.9%; Pred. No. 4.2e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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|||||  
Db 2 AATTAAAAA 15

RESULT 3487  
AI564678/c

LOCUS tq78g03.x1 NCI CGAP Ut1 Homo sapiens cDNA clone IMAGE:2214964 3'

DEFINITION similar to TR:Q15214 Q15214 SALIVARY PROLINE-RICH PROTEIN 1

ACCESSION AI564678.1 GI:4523135

VERSION EST.

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 16)

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 1719 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1

POLYA=No.

FEATURES

source

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/mol\_type="mRNA"



/db\_xref="taxon:9606"  
/clone="IMAGE:2214964"  
/tissue\_type="well-differentiated endometrial  
adenocarcinoma, 7 pooled tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP\_Utl1"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: Sali;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.75 kb. Life Technologies catalog #:  
11538-014"

Query Match 0.4%; Score 12.4; DB 1; Length 16;  
Best Local Similarity 92.9%; Pred. No. 4.2e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 51 GCGGCGGGGCGGC 64  
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Db 14 GCGGAGGGGCGGC 1

RESULT 3488  
AW246490/c  
LOCUS  
DEFINITION AW246490.1 16 bp mRNA linear EST 07-JAN-2000  
2821591.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821591 3',  
mRNA sequence.  
ACCESSION AW246490  
VERSION AW246490.1 GI:6589483  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2821591.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 12  
contiguous PHRED high quality bases followed by vector sequence. Very  
Low Quality Sequence: trace file contained 16 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: LLCM7 row: D column: 8  
High quality sequence stop: 12.  
Location/Qualifiers  
1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821591"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 12.4; DB 1; Length 16;  
Best Local Similarity 92.9%; Pred. No. 4.2e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2783 TTGAAAAA 2796  
|||||  
Db 14 TTGAAAAA 1

RESULT 3489  
BQ588093/c  
LOCUS  
DEFINITION BQ588093.1 16 bp mRNA linear EST 06-DEC-2002  
E012336-024-009-A19-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
024-009-A19 5-PRIME, mRNA sequence.  
ACCESSION BQ588093  
VERSION BQ588093.1 GI:26117675  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 16)  
Herwig,R.; Schulz,B.; Weisshaar,B.; Hennig,S.; Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698  
Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 16 Std Error: 0.00  
Plate: 9 row: A column: 19  
Seq primer: SP6; CATACGATTAGGTGACACTATAG.  
Location/Qualifiers  
1. .16  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:184766"  
/db\_xref="taxon:161934"  
/clone="024-009-A19"  
/tissue\_type="leaf"  
/lab\_host="EMDH10B"  
/clone\_lib="MPIZ-ADIS-024-leaf"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match 0.4%; Score 12.4; DB 1; Length 16;  
Best Local Similarity 92.9%; Pred. No. 4.2e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2159 TTTCTCCTTTT 2172  
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Db      14 TTTCTCCCTTTTTT 1

RESULT 3490
AW245664/c
LOCUS   AW245664          17 bp   mRNA   linear   EST 07-JAN-2000
DEFINITION  2822994.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822994 3',
            mRNA sequence.
ACCESSION  AW245664
VERSION    AW245664.1   GI:6588657
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 17)
            NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS    National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE      Unpublished (1999)
JOURNAL
COMMENT     Other_ESTs: 2822994.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
            Hong/Rubin laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 17 contiguous distinct peaks
            following vector sequence.
            Plate: LLCM10 row: N column: 19.
FEATURES             Location/Qualifiers
     source           1..17
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2822994"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
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Query Match      0.4%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 4.5e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2799
        |||||
Db      17 AAAAAAAAAAAAAACA 4

RESULT 3491
BM398017/c
LOCUS   BM398017          18 bp   mRNA   linear   EST 17-JAN-2002
DEFINITION  5009-0-4-D05.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM398017
VERSION    BM398017.1   GI:18198070
KEYWORDS   EST.
```

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SOURCE
ORGANISM Tetrahymena thermophila
            Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE  1 (bases 1 to 18)
AUTHORS    Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL    Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source           1..18
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: Bluescript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
Query Match      0.4%; Score 12.4; DB 1; Length 18;
Best Local Similarity 92.9%; Pred. No. 4.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      219 GCCACGCGGGAGC 232
        |||||
Db      17 GCCACGCGGGAGC 4

RESULT 3492
AZ774536
LOCUS   AZ774536          19 bp   DNA   linear   GSS 16-FEB-2001
DEFINITION  2M0004P01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0004P01 F, genomic survey sequence.
ACCESSION  AZ774536
VERSION    AZ774536.1   GI:12900089
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0004 row: P column: 01
            Seq primer: CGTTGTAACGACGCGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source           1..19
                     /organism="Mus musculus"
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0004P01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

Query Match 0.4%; Score 12.4; DB 1; Length 19;  
Best Local Similarity 92.9%; Pred. No. 4.5e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2783 TTGAAAAA 2796  
Db 4 TTA 17

RESULT 3493  
AI648553/c

LOCUS AI648553 19 bp mRNA linear EST 16-DEC-1999  
DEFINITION tz55e07.x1 NCI CGAP Ov35 Homo sapiens cDNA clone IMAGE:2292516 3', similar to TR:004216 O04216 EXTENSIN ;, mRNA sequence.

ACCESSION AI648553  
VERSION AI648553.1 GI:4729387  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-re@mail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Insert Length: 249 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"

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/clone="IMAGE:2292516"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/clone_lib="NCI CGAP_Ov35"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site: 1: Sali; Site 2: NotI; This library represents the normalized version of NCI CGAP Ov23. Cloned unidirectionally. Primer: Oligo dT. Average insert size 0.86 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Constructed by Life Technologies."
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Query Match 0.4%; Score 12.4; DB 1; Length 19;  
Best Local Similarity 92.9%; Pred. No. 4.5e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 542 CCCACCTCTCCGG 555  
Db 14 CCCCCCTCTCCGG 1

RESULT 3494  
AZ369369

LOCUS AZ369369 19 bp DNA linear GSS 02-OCT-2000  
DEFINITION 1M0119K19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0119K19 R, genomic survey sequence.

ACCESSION AZ369369  
VERSION AZ369369.1 GI:10483069  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0119 row: K column: 19  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0119K19"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.4; DB 1; Length 19;  
Best Local Similarity 92.9%; Pred. No. 4.5e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2673 AGTGTGTGTGGTG 2686  
|||||||  
Db 1 AGTGTGTGTGGGG 14

RESULT 3495  
AZ510143  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

AZ510143 19 bp DNA linear GSS 05-OCT-2000  
1M0354P21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0354P21 F, genomic survey sequence.

ACCESSION AZ510143  
VERSION AZ510143.1 GI:10691459  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0354 row: P column: 21  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0354P21"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.4; DB 1; Length 19;  
Best Local Similarity 92.9%; Pred. No. 4.5e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 346 TCCCCCTCCCTACC 359  
|||||||  
Db 5 TCCCCCTCCCCACC 18

RESULT 3496  
AZ514586/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

AZ514586 19 bp DNA linear GSS 05-OCT-2000  
1M0361B17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0361B17 F, genomic survey sequence.

ACCESSION AZ514586  
VERSION AZ514586.1 GI:10695818  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0361 row: B column: 17  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0361B17"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel



electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.4; DB 1; Length 19;  
Best Local Similarity 92.9%; Pred. No. 4.5e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1772 TTTT TTTT TTTT GAAC 1785  
Db 17 TTTT TTTT TTTT GCAC 4

RESULT 3497  
AZ827164  
LOCUS  
DEFINITION 19 bp DNA linear GSS 20-FEB-2001  
clone UUGC2M0103M22 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE  
AUTHORS  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0103 row: M column: 22  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
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/mol\_type="genomic DNA"  
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/db\_xref="taxon:10090"  
/clone="UUGC2M0103M22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.4; DB 1; Length 19;  
Best Local Similarity 92.9%; Pred. No. 4.5e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 831 AGGTCTTCTGCTCA 844  
Db 6 AGGTCTTCTGCTCA 19

RESULT 3498  
CF302637/c  
LOCUS  
DEFINITION 20 bp mRNA linear EST 15-AUG-2003  
7LEAF--08-F12.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--08-F12, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
AUTHORS  
1 (bases 1 to 20)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE  
JOURNAL  
COMMENT  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1. 20  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--08-F12"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.4%; Score 12.4; DB 1; Length 20;  
Best Local Similarity 92.9%; Pred. No. 4.4e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2783 TTGAAAAA AAAAA 2796  
Db 18 TTTTAAAAA AAAAA 5

RESULT 3499  
AZ772040/c  
LOCUS  
DEFINITION 20 bp DNA linear GSS 16-FEB-2001  
1M0574G11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0574G11 R, genomic survey sequence.  
ACCESSION  
VERSION  
AZ772040.1 GI:12894936



KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0574 row: G column: 11  
Seq primer: CACACAGGAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
FEATURES Location/Qualifiers  
source 1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0574G11"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."  
Query Match 0.4%; Score 12.4; DB 1; Length 20;  
Best Local Similarity 92.9%; Pred. No. 4.4e+03;  
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 2784 TGAATAAAAAAAAAA 2797  
Db 15 TCAAAAAAAAAAAAAA 2  
RESULT 3500  
AZ355624  
LOCUS AZ355624 22 bp DNA linear GSS 02-OCT-2000  
DEFINITION 1M0095E22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0095E22 F, genomic survey sequence.  
ACCESSION AZ355624  
VERSION AZ355624.1 GI:10468133  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 22)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0095 row: E column: 22  
Seq primer: CGTTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.  
FEATURES Location/Qualifiers  
source 1..22  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0095E22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."  
Query Match 0.4%; Score 12.4; DB 1; Length 22;  
Best Local Similarity 72.7%; Pred. No. 4.1e+03;  
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
Qy 2772 TCCTGTTAGAAATGAAAAAAA 2793  
Db 1 TCCTCTTCTAAATTAAAAAAA 22  
RESULT 3501  
BH856226/c  
LOCUS BH856226 25 bp DNA linear GSS 08-JUL-2002  
DEFINITION SALK 083159.52.35.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK\_083159.52.35.x, genomic survey sequence.  
ACCESSION BH856226  
VERSION BH856226.1 GI:21705816  
KEYWORDS GSS.



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FEATURES
  source
Plate: LLCMS row: L column: 8.
  Location/Qualifiers
1. .17
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:2821015"
  /tissue_type="small cell carcinoma"
  /cell_line="MGC3"
  /lab_host="DH10B (phage-resistant)"
  /clone_lib="NIH_MGC_7"
  /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

  Query Match      0.4%; Score 12.2; DB 1; Length 17;
  Best Local Similarity 82.4%; Pred. No. 4.6e+03;
  Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1773 TTTTGTGACCCCA 1789
      |||||
Db 1 TTTTTCAGCCTA 17

RESULT 3504
AW246528
LOCUS
DEFINITION
  AW246528
  17 bp mRNA linear EST 07-JAN-2000
  2821879.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821879 3',
  mRNA sequence.
ACCESSION
  AW246528
VERSION
  AW246528.1 GI:6589521
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 17)
REFERENCE
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Other ESTs: 2821879.5prime
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
  Hong/Rubin Laboratory: DCTD/DTP cDNA Library Arrayed by: The I.M.A.G.E.
  Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
  project Clone distribution: MGC clone distribution information can
  be found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
  Scores: PHRED from University of Washington Genome Center. Vector
  Trimming: cross match from University of Washington Genome Center
  PHRAP suite. Poly-T identification: patMatch.pl from Berkeley
  Drosophila Genome Project. University of Washington Genome Center:
  http://www.genome.washington.edu Low Quality Sequence: 13
  contiguous PHRED high quality bases following vector sequence. Very
  Low Quality Sequence: Trace file contained 17 contiguous distinct
  peaks following vector sequence. Polyadenylation: Based upon the
  presence of a XhoI site followed by a run of 14 or more T residues
  at the beginning of the sequence, this cDNA insert was
  polyadenylated.
Plate: LLCM7 row: P column: 8
High quality sequence stop: 13.
  Location/Qualifiers
1. .17
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:2821879"
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  Query Match      0.4%; Score 12.2; DB 1; Length 17;
  Best Local Similarity 82.4%; Pred. No. 4.6e+03;
  Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1773 TTTTGTGACCCCA 1789
      |||||
Db 1 TTTTTCAGCCTA 17

RESULT 3504
AW246528
LOCUS
DEFINITION
  AW246528
  17 bp mRNA linear EST 07-JAN-2000
  2821879.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821879 3',
  mRNA sequence.
ACCESSION
  AW246528
VERSION
  AW246528.1 GI:6589521
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 17)
REFERENCE
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Other ESTs: 2821879.5prime
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
  Hong/Rubin Laboratory: DCTD/DTP cDNA Library Arrayed by: The I.M.A.G.E.
  Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
  project Clone distribution: MGC clone distribution information can
  be found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
  Scores: PHRED from University of Washington Genome Center. Vector
  Trimming: cross match from University of Washington Genome Center
  PHRAP suite. Poly-T identification: patMatch.pl from Berkeley
  Drosophila Genome Project. University of Washington Genome Center:
  http://www.genome.washington.edu Low Quality Sequence: 13
  contiguous PHRED high quality bases following vector sequence. Very
  Low Quality Sequence: Trace file contained 17 contiguous distinct
  peaks following vector sequence. Polyadenylation: Based upon the
  presence of a XhoI site followed by a run of 14 or more T residues
  at the beginning of the sequence, this cDNA insert was
  polyadenylated.
Plate: LLCM7 row: P column: 8
High quality sequence stop: 13.
  Location/Qualifiers
1. .17
  /organism="Homo sapiens"
  /mol_type="mRNA"
  /db_xref="taxon:9606"
  /clone="IMAGE:2821879"
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  Query Match      0.4%; Score 12.2; DB 1; Length 17;
  Best Local Similarity 82.4%; Pred. No. 4.6e+03;
  Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1771 TTTTGTGACCC 1787
      |||||
Db 1 TTTTTCAGCCTA 17

RESULT 3505
AZ924200
LOCUS
DEFINITION
  AZ924200
  18 bp DNA linear GSS 01-APR-2001
  4906.ic27n17.s1 Saccharomyces mikatae IFO 1815 Saccharomyces
  mikatae genomic clone 4906.ic27n17.s1, genomic survey sequence.
ACCESSION
  AZ924200
VERSION
  AZ924200.1 GI:13495098
KEYWORDS
  GSS.
SOURCE
  Saccharomyces mikatae
  ORGANISM
  Saccharomyces mikatae
  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
  Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
  1 (bases 1 to 18)
REFERENCE
  Clifton,P.F., Hillier,L.W., Fulton,L., Graves,T., Miner,T.,
  Gish,W.R., Waterston,R.H. and Johnston,M.
  Surveying Saccharomyces genomes to identify functional elements by
  comparative DNA sequence analysis
  Unpublished (2001)
  Contact: Johnston M
  Department of Genetics
  Washington University Medical School
  Box 8232, 4566 Scott Ave., St. Louis, MO 63110, USA
  Tel: 314 362 2735
  Fax: 314 362 7855
  Email: mj@genetics.wustl.edu
  Class: random plasmid subclone.
  Location/Qualifiers
1. .18
  /organism="Saccharomyces mikatae"
  /mol_type="genomic DNA"
  /strain="IFO 1815"
  /db_xref="taxon:114525"
  /clone="4906.ic27n17.s1"
  /clone_lib="Saccharomyces mikatae IFO 1815"
  /note="Random genomic sequence"
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  Query Match      0.4%; Score 12.2; DB 1; Length 18;
  Best Local Similarity 82.4%; Pred. No. 4.7e+03;
  Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2783 TTGAAAAA 2799
      |||||
Db 1 TTAAAGACAAAAA 17

RESULT 3506
AW246520/c
LOCUS
DEFINITION
  AW246520
  18 bp mRNA linear EST 07-JAN-2000
  2821787.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821787 3',
  mRNA sequence.
ACCESSION
  AW246520
```



VERSION AW246520.1 GI:6589513  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 18)  
NIH-MGC <http://mgc.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2821787.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: DCTD/DTP CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross\_match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu/LowQuality> Sequence: 16 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 18 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LCM7 row: L column: 12  
High quality sequence stop: 16.  
Location/Qualifiers  
1..18  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="IMAGE:2821787"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
Query Match 0.4%; Score 12.2; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 4.7e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2783 TTGAAAAA 2799  
Db 17 TTGAGGCA 1  
RESULT 3507  
AI476315  
LOCUS  
DEFINITION tal5c09.x1 NCI CGAP\_Lym5 Homo sapiens CDNA clone IMAGE:2044144 3' similar to TR:Q61431 Q61431 PROCOLLAGEN TYPE V ALPHA 2. ;contains OFR.b3 MSRI repetitive element ;, mRNA sequence.  
ACCESSION AI476315  
VERSION AI476315.1 GI:4329360  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 19)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Mark Raffeld, M.D.  
cDNA Library Preparation: Stratagene, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Trace considered overall poor quality  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1..19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2044144"  
/tissue\_type="follicular lymphoma"  
/lab\_host="SOLR (Stratagene, kanamycin resistant)"  
/clone\_lib="NCI CGAP Lym5"  
/note="Organ: lymph node; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.2 kb. Non-amplified library. ~5' adaptor sequence: 5' GAATTCGGCAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'"  
Query Match 0.4%; Score 12.2; DB 1; Length 19;  
Best Local Similarity 82.4%; Pred. No. 4.6e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1599 CCCTCTGGCCTGGGG 1615  
Db 1 CCCCCCTGGCCTGGGG 17  
RESULT 3508  
AI357421  
LOCUS  
DEFINITION AI357421 19 bp mRNA linear EST 06-JAN-1999  
qu01c02.x1 NCI CGAP\_Col4 Homo sapiens CDNA clone IMAGE:1963490 3' similar to TR:O20200 O20200 ORF54D. ;, mRNA sequence.  
ACCESSION AI357421  
VERSION AI357421.1 GI:4109042  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Trace considered overall poor quality  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.



FEATURES  
source  
Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="mrna"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1963490"  
/tissue\_type="moderately-differentiated adenocarcinoma"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Col4"  
/note="Organ: colon; Vector: pcMV-SPORT6; Site 1: Sali;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.7 kb. Life Technologies catalog #:  
11531-019"

Query Match 0.4%; Score 12.2; DB 1; Length 19;  
Best Local Similarity 82.4%; Pred. No. 4.6e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1972 TACCTTGAAAAAAGAA 1988  
||| |||||  
Db 3 TAAATTAAAAAAGAA 19

RESULT 3509  
AZ608537/c  
LOCUS  
DEFINITION  
AZ608537 19 bp DNA linear GSS 13-DEC-2000  
1M0432N14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0432N14 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
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University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0432 row: N column: 14  
Seq primer: CACACAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4

FEATURES  
source  
Location/Qualifiers  
1. .19  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.4%; Score 12.2; DB 1; Length 19;  
Best Local Similarity 82.4%; Pred. No. 4.6e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAAAA 2795  
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Db 17 AGAGGGGAAAAAAA 1

RESULT 3510  
AZ404619  
LOCUS  
DEFINITION  
AZ404619 25 bp DNA linear GSS 03-OCT-2000  
1M0173L20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0173L20 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS  
1 (bases 1 to 25)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
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Seq primer: CGTTGTAAACGACGCCAGT  
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/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were

FEATURES  
source  
Location/Qualifiers  
1. .25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
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/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
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polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12.2; DB 1; Length 25;  
Best Local Similarity 68.0%; Pred. No. 3.6e+03;  
Matches 17; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 2180 TTTTAACTTTGAAAGTTAACTC 2204  
||||| | ||||| | |||||  
Db 1 TTATTGATATTGTAATGGCTACTC 25

RESULT 3511  
BG668943  
LOCUS  
DEFINITION BG668943 12 bp mRNA linear EST 30-APR-2001  
DRN03E05 Rat DRG Library Rattus norvegicus cDNA clone DRN03E05.5',  
mRNA sequence.

ACCESSION BG668943  
VERSION BG668943.1 GI:13890865  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 12)  
AUTHORS Xiao,H.S., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,  
Yang,L., Huang,Z., Han,Z.G. and Zhang,X.

TITLE Identification of gene expression profile of dorsal root ganglion  
in the rat peripheral axotomy model of neuropathic pain  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)  
MEDLINE 22056133  
PUBMED 12060780

COMMENT Contact: Zhang Xu  
Laboratory of Sensory System  
Institute of Neuroscience  
320 Yue Yang Road, Shanghai 200031, P.R.China  
Tel: 86-21-64748700-121  
Fax: 86-21-64713446  
Email: xu.zhang@ion.ac.cn

This clone is also available at Chinese National Human Genome  
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,  
Pudong New Area, P.R.China. Please contact with Zhang Xu  
(xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)

PCR Primers  
FORWARD: T3  
BACKWARD: T7  
Seq primer: T3  
POLYA=No.

FEATURES Location/Qualifiers  
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/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clone="DRN03E05"  
/sex="male"  
/tissue\_type="dorsal root ganglion"  
/dev\_stage="adult"  
/clone\_lib="Rat DRG Library"

Query Match 0.4%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAA 2797  
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Db 1 AAAAAAAAAAAAA 12

RESULT 3512  
BG668943/c  
LOCUS  
DEFINITION BG668943 12 bp mRNA linear EST 30-APR-2001  
DRN03E05 Rat DRG Library Rattus norvegicus cDNA clone DRN03E05.5',  
mRNA sequence.

ACCESSION BG668943  
VERSION BG668943.1 GI:13890865  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 12)  
AUTHORS Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C.,  
Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D.,  
Zhang,X., Chen,Z., Han,Z.G. and Zhang,X.

TITLE Identification of gene expression profile of dorsal root ganglion  
in the rat peripheral axotomy model of neuropathic pain  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)  
MEDLINE 22056133  
PUBMED 12060780

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Institute of Neuroscience  
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Tel: 86-21-64748700-121  
Fax: 86-21-64713446  
Email: xu.zhang@ion.ac.cn

This clone is also available at Chinese National Human Genome  
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,  
Pudong New Area, P.R.China. Please contact with Zhang Xu  
(xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)

PCR Primers  
FORWARD: T3  
BACKWARD: T7  
Seq primer: T3  
POLYA=No.

FEATURES Location/Qualifiers  
source 1..12  
/organism="Rattus norvegicus"  
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/clone="DRN03E05"  
/sex="male"  
/tissue\_type="dorsal root ganglion"  
/dev\_stage="adult"  
/clone\_lib="Rat DRG Library"

Query Match 0.4%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTNTTTTTTTT 2177  
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Db 12 TTTTNTTTTTTTT 1

RESULT 3513  
BQ582536  
LOCUS  
DEFINITION BQ582536 12 bp mRNA linear EST 06-DEC-2002  
S013300-024-007-P01-T7 MP1Z-ADIS-024-inflorescence Beta vulgaris  
cDNA clone 024-007-P01 3-PRIME, mRNA sequence.  
ACCESSION BQ582536  
VERSION BQ582536.1 GI:26112113

KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaam@piz-koeln.mpg.de  
Insert Length: 12 Std Error: 0.00  
Plate: 7 row: P column: 01  
Seq primer: T7; GTAATACGACTCACTATAGGGC.  
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1..12  
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/mol\_type="mRNA"  
/cultiyar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:184167"  
/db\_xref="taxon:161934"  
/clone="024-007-P01"  
/tissue\_type="inflorescence"  
/lab\_host="EMDH10B"  
/clone\_lib="MPIZ-ADIS-024-inflorescence"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"  
Query Match 0.4%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT 2177  
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Db 1 TTTT TTTT TTTT 12  
RESULT 3514  
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LOCUS  
DEFINITION S013300-024-007-P01-T7 MPIZ-ADIS-024-inflorescence Beta vulgaris  
CDNA clone 024-007-P01 3-PRIME, mRNA sequence.  
ACCESSION BQ582536  
VERSION BQ582536.1 GI:26112113  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaam@piz-koeln.mpg.de  
Insert Length: 12 Std Error: 0.00  
Plate: 7 row: P column: 01  
Seq primer: T7; GTAATACGACTCACTATAGGGC.  
FEATURES source  
1..12  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultiyar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:184167"  
/db\_xref="taxon:161934"  
/clone="024-007-P01"  
/tissue\_type="inflorescence"  
/lab\_host="EMDH10B"  
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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"  
Query Match 0.4%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAAAAAAAAAA 2797  
|||||  
Db 12 AAAAAAAAAAAAAA 1  
RESULT 3515  
BQ588719  
LOCUS  
DEFINITION BQ588719 12 bp mRNA linear EST 06-DEC-2002  
S013713-024-014-P24-T7 MPIZ-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-014-P24 3-PRIME, mRNA sequence.  
ACCESSION BQ588719  
VERSION BQ588719.1 GI:26118302  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851

Email: weissshaampiz-koeln.mpg.de  
Insert Length: 12 Std Error: 0.00  
Plate: 14 row: P column: 24  
Seq primer: T7; GTAATACGACTCACTATAGGCG.  
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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.4%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2177  
Db 1 TTTT TTTT TTTT 12

RESULT 3516  
BQ588719/c  
LOCUS  
DEFINITION S013713-024-014-P24-T7 MPIZ-ADIS-024-storage root Beta vulgaris  
CDNA clone 024-014-P24 3-PRIME, mRNA sequence.  
ACCESSION BQ588719.1 GI:261118302  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
REFERENCE  
AUTHORS  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
TITLE  
Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT  
Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaampiz-koeln.mpg.de  
Insert Length: 12 Std Error: 0.00  
Plate: 14 row: P column: 24  
Seq primer: T7; GTAATACGACTCACTATAGGCG.  
Location/Qualifiers  
1..12  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"

/db\_xref="GABI:187286"  
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/clone="024-014-P24"  
/tissue\_type="storage root"  
/lab\_host="EMDH10B"  
/clone\_lib="MPIZ-ADIS-024-storage root"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.4%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAA 2797  
Db 12 AAAAAAAAAA 1

RESULT 3517  
BQ594698  
LOCUS  
DEFINITION E012404-024-024-E05-T7 MPIZ-ADIS-024-developing root Beta vulgaris  
CDNA clone 024-024-E05 3-PRIME, mRNA sequence.  
ACCESSION BQ594698  
VERSION BQ594698.1 GI:26124281  
KEYWORDS  
SOURCE  
ORGANISM  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
REFERENCE  
AUTHORS  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M., Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radelof,U.  
TITLE  
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Plant J. 32 (5), 845-857 (2002)  
JOURNAL  
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ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weissshaampiz-koeln.mpg.de  
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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and



orientation:  
SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

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Db 1 TTTT TTTT TTTT TTTT 12

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E012404-024-024-E05-T7 MP1Z-ADIS-024-developing root Beta vulgaris  
CDNA clone 024-024-E05 3-PRIME, mRNA sequence.  
ACCESSION BQ594698.1 GI:26124281  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 12 Std Error: 0.00  
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Seq primer: T7; GTAATACGACTCACTATAGGCG.  
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cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.4%; Score 12; DB 1; Length 12;  
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QY 2786 AAAAAAAAAAAAAA 2797  
Db 12 AAAAAAAAAAAAAA 1

RESULT 3519  
CF279278  
LOCUS  
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14ETL--05-I10.b1 Rice etiolated leaf plasmid cDNA library (14ETL)  
Oryza sativa cDNA clone 14ETL--05-I10, mRNA sequence.  
ACCESSION CF279278  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.  
FEATURES  
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with oligoribonucleotides and then used as templates for  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2177  
Db 1 TTTT TTTT TTTT TTTT 12

RESULT 3520  
CF279278/c  
LOCUS  
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Oryza sativa cDNA clone 14ETL--05-I10, mRNA sequence.  
ACCESSION CF279278  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL  
COMMENT

Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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Query Match      0.4%; Score 12; DB 1; Length 12;
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Db      12 AAAAAAAAAAAAAA 1

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RESULT 3521

CF291428

LOCUS

DEFINITION

CF291428 12 bp mRNA linear EST 14-AUG-2003  
14ROOT--01-N14.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-N14, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 12)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Query Match      0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2797
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Db      1 AAAAAAAAAAAAAA 12

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RESULT 3522  
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DEFINITION 14ROOT--01-N14.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--01-N14, mRNA sequence.  
ACCESSION CF291428  
VERSION CF291428.1 GI:33660461  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 12)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

Query Match	0.4%	Score 12;	DB 1;	Length 12;
Best Local Similarity	100.0%;	Pred. No. 2.6e+03;		
Matches 12;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	12	TTTTTTTTTTTT	1	

RESULT 3523	
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LOCUS	CF291800 12 bp mRNA linear EST 14-AUG-2003
DEFINITION	14ROOT--02-G04.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--02-G04, mRNA sequence.
ACCESSION	CF291800
VERSION	CF291800.1 GI:33660833
KEYWORDS	EST.
SOURCE	Oryza sativa
ORGANISM	Oryza sativa
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE	1 (bases 1 to 12)
AUTHORS	Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.

TITLE  
JOURNAL  
COMMENT

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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QY 2166 TTTT TTTT TTTT 2177  
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Db 1 TTTT TTTT TTTT 12

## RESULT 3524

CF291800/c  
LOCUS  
DEFINITION  
CF291800  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

CF291800 12 bp mRNA linear EST 14-AUG-2003  
14ROOT--02-G04.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--02-G04, mRNA sequence.

CF291800  
EST.  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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QY 2786 AAAAAAAAAAAAAA 2797  
|||||  
Db 12 AAAAAAAAAAAAAA 1

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LOCUS  
DEFINITION  
CF291801  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

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14ROOT--02-G04.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--02-G04, mRNA sequence.

CF291801  
EST.  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 12)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 1 AAAAAAAAAAAAAA 12

## RESULT 3526

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LOCUS  
DEFINITION  
CF291801  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

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14ROOT--02-G04.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--02-G04, mRNA sequence.

CF291801  
EST.  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
1 (bases 1 to 12)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTT 2177  
Db 12 TTTTTTTTTT 1

RESULT 3527  
CF291885 12 bp mRNA linear EST 14-AUG-2003  
LOCUS 14ROOT--02-I01.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
DEFINITION sativa cDNA clone 14ROOT--02-I01, mRNA sequence.  
ACCESSION CF291885  
VERSION CF291885.1 GI:336660918  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RT-PCR."  
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QY 2166 TTTTTTTTTT 2177  
Db 1 TTTTTTTTTT 12

RESULT 3528  
CF291885/C 12 bp mRNA linear EST 14-AUG-2003  
LOCUS 14ROOT--02-I01.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
DEFINITION sativa cDNA clone 14ROOT--02-I01, mRNA sequence.  
ACCESSION CF291885  
VERSION CF291885.1 GI:336660918  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source  
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Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAA 2797  
Db 12 AAAAAAAAAA 1

RESULT 3529  
CF291886 12 bp mRNA linear EST 14-AUG-2003  
LOCUS 14ROOT--02-I01.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
DEFINITION sativa cDNA clone 14ROOT--02-I01, mRNA sequence.  
ACCESSION CF291886  
VERSION CF291886.1 GI:336660919  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.



REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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1. .12  
/organism="Oryza sativa"  
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Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAA 2797

Db 1 AAAAAAAAAA 12

## RESULT 3530

CF291886/c

LOCUS CF291886 12 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--02-I01.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--02-I01, mRNA sequence.

ACCESSION CF291886  
VERSION CF291886.1 GI:33660919  
KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 12)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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JOURNAL Unpublished (2003)

COMMENT

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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

## FEATURES

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1. .12  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT 2177

Db 12 TTTT TTTT TTTT 1

## RESULT 3531

CF292107

LOCUS CF292107 12 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--02-M21.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--02-M21, mRNA sequence.

ACCESSION CF292107

VERSION CF292107.1 GI:33661140

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 12)

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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/organism="Oryza sativa"  
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with oligoribonucleotides and then used as templates for  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT 2177

Db 1 TTTT TTTT TTTT 12

## RESULT 3532

CF292107/c

LOCUS CF292107 12 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--02-M21.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--02-M21, mRNA sequence.

ACCESSION CF292107

VERSION CF292107.1 GI:33661140

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE  
AUTHORS Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 12)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
Location/Qualifiers

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/organism="Oryza sativa"  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAA 2797  
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Db 12 AAAAAAAAAAAA 1

RESULT 3533  
CF295593  
LOCUS 12 bp mRNA linear EST 14-AUG-2003  
DEFINITION 30DGS--05-J18.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa cDNA clone 30DGS--05-J18, mRNA sequence.

ACCESSION CF295593  
VERSION CF295593.1 GI:33664626  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
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FEATURES  
Location/Qualifiers

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/organism="Oryza sativa"  
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RT-PCR."

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTT 2177  
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Db 1 TTTTTTTTTTTT 12

RESULT 3534  
CF295593/c

LOCUS 12 bp mRNA linear EST 14-AUG-2003  
DEFINITION 30DGS--05-J18.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
sativa cDNA clone 30DGS--05-J18, mRNA sequence.

ACCESSION CF295593  
VERSION CF295593.1 GI:33664626  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 12)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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COMMENT Contact: Nahm B.H.

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FEATURES  
Location/Qualifiers

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/organism="Oryza sativa"  
/mol\_type="mRNA"  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAA 2797  
|||||  
Db 12 AAAAAAAAAAAA 1

RESULT 3535  
CF298686

LOCUS 12 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--02-D15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--02-D15, mRNA sequence.

ACCESSION CF298686  
VERSION CF298686.1 GI:33670447  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 12)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

1. .12  
/organism="Oryza sativa"  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2177

Db 1 TTTT TTTT TTTT TTTT 12

## RESULT 3536

CF298686/c

LOCUS CF298686 12 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--02-D15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--02-D15, mRNA sequence.

ACCESSION CF298686

VERSION CF298686.1 GI:33670447

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

TITLE

JOURNAL

COMMENT

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

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RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 12;  
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QY 2786 AAAAAA AAAAAA 2797

Db 12 AAAAAA AAAAAA 1

## RESULT 3537

CF298872

LOCUS

DEFINITION 7LEAF--02-I17.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--02-I17, mRNA sequence.

ACCESSION CF298872

VERSION CF298872.1 GI:33670633

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

AUTHORS

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Unpublished (2003)

TITLE

JOURNAL

COMMENT

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Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

1. .12  
/organism="Oryza sativa"  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2177

Db 1 TTTT TTTT TTTT TTTT 12

## RESULT 3538

CF298872/c

LOCUS

DEFINITION 7LEAF--02-I17.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--02-I17, mRNA sequence.

ACCESSION CF298872

VERSION CF298872.1 GI:33670633

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.



Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
1 (bases 1 to 12)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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#### FEATURES

source

Location/Qualifiers

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/organism="Oryza sativa"

/mol\_type="mRNA"

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/note="Vector: pCR4-TOPO; Site\_1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2797

Db 12 AAAAAAAAAAAAAA 1

#### RESULT 3539

CF299343

LOCUS

DEFINITION 7LEAF--03-F06.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--03-F06, mRNA sequence.

ACCESSION CF299343

VERSION CF299343.1 GI:33671104

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

#### FEATURES

source

Location/Qualifiers

1..12

/organism="Oryza sativa"

/mol\_type="mRNA"

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/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site\_1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match

Best Local Similarity 0.4%; Score 12; DB 1; Length 12;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2797

Db 1 AAAAAAAAAAAAAA 12

#### RESULT 3540

CF299343/C

LOCUS

DEFINITION 7LEAF--03-F06.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--03-F06, mRNA sequence.

ACCESSION CF299343

VERSION CF299343.1 GI:33671104

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,

Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

#### FEATURES

source

Location/Qualifiers

1..12

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="7LEAF--03-F06"

/tissue\_type="leaf"

/dev\_stage="7 days after germination"

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/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="Vector: pCR4-TOPO; Site\_1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for

RT-PCR."

Query Match

Best Local Similarity 0.4%; Score 12; DB 1; Length 12;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTT 2177

Db 12 TTTTTTTTTTTT 1

#### RESULT 3541

CF299514

LOCUS

DEFINITION 7LEAF--03-J03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--03-J03, mRNA sequence.

ACCESSION CF299514

VERSION CF299514.1 GI:33671275

KEYWORDS EST.

SOURCE Oryza sativa

CF299514

7LEAF--03-J03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza

sativa cDNA clone 7LEAF--03-J03, mRNA sequence.

CF299514

CF299514.1 GI:33671275

EST.

Oryza sativa

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

1. .12  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
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/db\_xref="taxon:4530"  
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/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
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Db 1 TTTT TTTT TTTT TTTT 12

RESULT 3542  
CF299514/c  
LOCUS 12 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--03-J03.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--03-J03, mRNA sequence.

ACCESSION CF299514  
VERSION CF299514.1 GI:33671275  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

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Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES Location/Qualifiers

1. .12  
/organism="Oryza sativa"  
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QY 2786 AAAAAAAAAA 2797  
|||||  
Db 12 AAAAAAAAAA 1

RESULT 3543  
CF300272

LOCUS 12 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--04-J19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--04-J19, mRNA sequence.

ACCESSION CF300272  
VERSION CF300272.1 GI:33672033  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)

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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

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Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

1. .12  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
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Db 1 TTTT TTTT TTTT TTTT 12

RESULT 3544  
CF300272/c

LOCUS 12 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--04-J19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--04-J19, mRNA sequence.

ACCESSION CF300272  
VERSION CF300272.1 GI:33672033  
KEYWORDS EST.

SOURCE  
ORGANISM Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
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FEATURES  
source  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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|||||  
Db 12 AAAAAAAAAAAAAA 1

RESULT 3545  
CF300420  
LOCUS CF300420 12 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--04-M23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--04-M23, mRNA sequence.  
ACCESSION CF300420  
VERSION CF300420.1 GI:33672181  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
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FEATURES  
source  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTT TTTT TTTT 12

RESULT 3546  
CF300420/c  
LOCUS CF300420 12 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--04-M23.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--04-M23, mRNA sequence.  
ACCESSION CF300420  
VERSION CF300420.1 GI:33672181  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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1. .12  
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Db 12 AAAAAAAAAAAAAA 1

RESULT 3547  
CF300558  
LOCUS CF300558 12 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--05-B09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--05-B09, mRNA sequence.  
ACCESSION CF300558  
VERSION CF300558.1 GI:33672319



KEYWORDS  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
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Db 1 TTTT TTTT TTTT TTTT 12

RESULT 3548  
CF300558/c  
LOCUS 12 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--05-B09.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--05-B09, mRNA sequence.

ACCESSION CF300558  
VERSION CF300558.1 GI:33672319  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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Db 12 AAAAAA AAAAAA 1

RESULT 3549  
CF300881  
LOCUS 12 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--05-I10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--05-I10, mRNA sequence.

ACCESSION CF300881  
VERSION CF300881.1 GI:33672642  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

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AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
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JOURNAL Unpublished (2003)  
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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Db 1 TTTT TTTT TTTT TTTT 12

RESULT 3550  
CF300881/c  
LOCUS 12 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--05-I10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--05-I10, mRNA sequence.

ACCESSION CF300881

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VERSION CF300881.1 GI:33672642
KEYWORDS
SOURCE EST.
ORGANISM Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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/organism="Oryza sativa"
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QY 2786 AAAAAAAAAAAA 2797
Db 12 AAAAAAAAAAAA 1

RESULT 3551
CF301006
LOCUS 12 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-L02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-L02, mRNA sequence.
ACCESSION CF301006
VERSION CF301006.1 GI:33672767
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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FEATURES             source
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Best Local Similarity 100.0%; Pred. No. 2.6e+03;
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QY 2786 AAAAAAAAAAAA 2797
Db 12 AAAAAAAAAAAA 1

RESULT 3551
CF301006
LOCUS 12 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-L02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-L02, mRNA sequence.
ACCESSION CF301006
VERSION CF301006.1 GI:33672767
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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FEATURES             source
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/organism="Oryza sativa"
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RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAA 2797
Db 12 AAAAAAAAAAAA 1

RESULT 3553
CF301075
LOCUS 12 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-M15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-M15, mRNA sequence.
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2177
Db 1 TTTT TTTT TTTT TTTT 12
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LOCUS 12 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-L02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-L02, mRNA sequence.
ACCESSION CF301006
VERSION CF301006.1 GI:33672767
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 12)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAA 2797
Db 12 AAAAAAAAAAAA 1

RESULT 3553
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LOCUS 12 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-M15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAA 2797
Db 12 AAAAAAAAAAAA 1

RESULT 3553
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LOCUS 12 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--05-M15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--05-M15, mRNA sequence.
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ACCESSION      CF301075
VERSION        CF301075.1  GI:33672836
KEYWORDS
SOURCE         Oryza sativa
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 12)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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Qy 2166 TTTT TTTT TTTT TTTT 2177
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Db 1 TTTT TTTT TTTT TTTT 12

RESULT 3554
CF301075/c
LOCUS          CF301075
DEFINITION    7LEAF--05-M15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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ACCESSION     CF301075
VERSION       CF301075.1  GI:33672836
KEYWORDS
SOURCE        Oryza sativa
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 12)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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Db 1 TTTT TTTT TTTT TTTT 12

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CF301075/c
LOCUS          CF301075
DEFINITION    7LEAF--05-M15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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ACCESSION     CF301075
VERSION       CF301075.1  GI:33672836
KEYWORDS
SOURCE        Oryza sativa
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 12)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
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               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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Qy 2166 TTTT TTTT TTTT TTTT 2177
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Qy 2786 AAAAAA AAAAAA 2797
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Db 12 AAAAAA AAAAAA 1

RESULT 3555
CF301489
LOCUS          CF301489
DEFINITION    7LEAF--06-G01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
               sativa cDNA clone 7LEAF--06-G01, mRNA sequence.
ACCESSION     CF301489
VERSION       CF301489.1  GI:33673250
KEYWORDS
SOURCE        Oryza sativa
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 12)
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, Myongji University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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Qy 2166 TTTT TTTT TTTT TTTT 2177
      ||| ||| ||| |||
Db 1 TTTT TTTT TTTT TTTT 12

RESULT 3556
CF301489/c
LOCUS          CF301489
DEFINITION    7LEAF--06-G01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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sativa cDNA clone 7LEAF--06-G01, mRNA sequence.
CF301489
VERSION CF301489.1 GI:33673250
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2786 AAAAAAAAAAAAAA 2797
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Db 12 AAAAAAAAAAAAAA 1

RESULT 3557
CF301940
LOCUS 12 bp mRNA linear EST 15-AUG-2001
DEFINITION 7LEAF--07-A01.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-A01, mRNA sequence.
ACCESSION CF301940
VERSION CF301940.1 GI:33673701
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .12
/organism="Oryza sativa"

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DEFINITION 7LEAF--07-C18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--07-C18, mRNA sequence.  
ACCESSION CF302029  
VERSION CF302029.1 GI:33673790  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 TTTT TTTT TTTT 12

RESULT 3560  
CF302029/c  
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DEFINITION 7LEAF--07-C18.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--07-C18, mRNA sequence.  
ACCESSION CF302029  
VERSION CF302029.1 GI:33673790  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
FEATURES  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2786 AAAAAA AAAAAA 2797  
Db 12 AAAAAA AAAAAA 1

RESULT 3561  
CF302122  
LOCUS CF302122 12 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--07-F15.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--07-F15, mRNA sequence.  
ACCESSION CF302122  
VERSION CF302122.1 GI:33673883  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2166 TTTT TTTT TTTT 2177  
Db 1 TTTT TTTT TTTT 12

RESULT 3562  
CF302122/c



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CF302486
LOCUS       CF302486               12 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--08-B02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
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ACCESSION   CF302486
VERSION     CF302486.1  GI:33674247
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTTtttttttt 2177
Db      1 TTTTtttttttt 12

RESULT 3566
CF302486/c
LOCUS       CF302486               12 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   7LEAF--08-B02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
              sativa cDNA clone 7LEAF--08-B02, mRNA sequence.
ACCESSION   CF302486
VERSION     CF302486.1  GI:33674247
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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FEATURES             Location/Qualifiers
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                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2797
Db      12 AAAAAAAAAAAAAA 1

RESULT 3567
CF308112
LOCUS       CF308112               12 bp    mRNA    linear    EST 15-AUG-2003
DEFINITION   ABF--01-M19.b1 ABF3-overexpressing transgenic rice plasmid cDNA
              library (ABF) Oryza sativa cDNA clone ABF--01-M19, mRNA sequence.
ACCESSION   CF308112
VERSION     CF308112.1  GI:33679873
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 12)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongji University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /cultivar="Nackdong"
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                     /lab_host="E.coli DH10B"
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                     cDNA library (ABF)"
                     /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
                     for 2hrs. Oligo-capped mRNA was reverse transcribed and
                     then used for PCR. mRNA was prepared from ABA-responsive
                     element binding transcription factor 3 overexpression
                     line."

Query Match      0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTTtttttttt 2177
Db      1 TTTTtttttttt 12
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Db      1 TTTTTTTTTTTT 12

RESULT 3568
CF308112/c
LOCUS
DEFINITION ABF--01-M19.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--01-M19, mRNA sequence.
ACCESSION CF308112
VERSION   CF308112.1 GI:33679873
KEYWORDS
SOURCE
ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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                    /mol_type="mRNA"
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                    /lab_host="E.coli DH10B"
                    /clone_lib="ABF3-overexpressing transgenic rice plasmid
                    cDNA library (ABF)"
                    /note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
                    for 2hrs. Oligo-capped mRNA was reverse transcribed and
                    then used for PCR. mRNA was prepared from ABA-responsive
                    element binding transcription factor 3 overexpression
                    line."

            Query Match      0.4%; Score 12; DB 1; Length 12;
            Best Local Similarity 100.0%; Pred. No. 2.6e+03;
            Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2797
Db      12 AAAAAAAAAAAAAA 1

RESULT 3569
CF311835
LOCUS
DEFINITION ABF--07-E11.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--07-E11, mRNA sequence.
ACCESSION CF311835
VERSION   CF311835.1 GI:33683596
KEYWORDS
SOURCE
ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)

            Query Match      0.4%; Score 12; DB 1; Length 12;
            Best Local Similarity 100.0%; Pred. No. 2.6e+03;
            Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2797
Db      12 AAAAAAAAAAAAAA 1

RESULT 3569
CF311835
LOCUS
DEFINITION ABF--07-E11.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--07-E11, mRNA sequence.
ACCESSION CF311835
VERSION   CF311835.1 GI:33683596
KEYWORDS
SOURCE
ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
```

```
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
            Location/Qualifiers
                1..12
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                    /mol_type="mRNA"
                    /cultivar="Nackdong"
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                    /tissue_type="leaf"
                    /dev_stage="14 days after germination"
                    /lab_host="E.coli DH10B"
                    /clone_lib="ABF3-overexpressing transgenic rice plasmid
                    cDNA library (ABF)"
                    /note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
                    for 2hrs. Oligo-capped mRNA was reverse transcribed and
                    then used for PCR. mRNA was prepared from ABA-responsive
                    element binding transcription factor 3 overexpression
                    line."

            Query Match      0.4%; Score 12; DB 1; Length 12;
            Best Local Similarity 100.0%; Pred. No. 2.6e+03;
            Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2166 TTTTTTTTTTTT 2177
Db      1 TTTTTTTTTTTT 12

RESULT 3570
CF311835/c
LOCUS
DEFINITION ABF--07-E11.b1 ABF3-overexpressing transgenic rice plasmid cDNA
            library (ABF) Oryza sativa cDNA clone ABF--07-E11, mRNA sequence.
ACCESSION CF311835
VERSION   CF311835.1 GI:33683596
KEYWORDS
SOURCE
ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             source
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                    /lab_host="E.coli DH10B"
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                    cDNA library (ABF)"
                    /note="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
                    for 2hrs. Oligo-capped mRNA was reverse transcribed and
                    then used for PCR. mRNA was prepared from ABA-responsive
                    element binding transcription factor 3 overexpression
                    line."
                    for 2hrs. Oligo-capped mRNA was reverse transcribed and
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then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.4%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAA 2797  
|||||  
Db 12 AAAAAAAAAA 1

RESULT 3571  
CF311836 12 bp mRNA linear EST 15-AUG-2003  
LOCUS  
DEFINITION ABF--07-E11.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa CDNA clone ABF--07-E11, mRNA sequence.

ACCESSION CF311836  
VERSION CF311836.1 GI:33683597  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source Location/Qualifiers  
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/organism="Oryza sativa"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.4%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAA 2797  
|||||  
Db 1 AAAAAAAAAA 12

RESULT 3572  
CF311836/c 12 bp mRNA linear EST 15-AUG-2003  
LOCUS  
DEFINITION ABF--07-E11.g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa CDNA clone ABF--07-E11, mRNA sequence.

ACCESSION CF311836  
VERSION CF311836.1 GI:33683597  
KEYWORDS EST.

SOURCE  
ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source Location/Qualifiers  
1..12

/organism="Oryza sativa"  
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/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.4%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2177  
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Db 12 TTTT TTTT TTTT TTTT 1

RESULT 3573  
CF313356 12 bp mRNA linear EST 15-AUG-2003  
LOCUS  
DEFINITION HD--01-H09.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa CDNA clone HD--01-H09, mRNA sequence.

ACCESSION CF313356  
VERSION CF313356.1 GI:33685117  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source Location/Qualifiers  
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/mol\_type="mRNA"

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cDNA library (HD)"  
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
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derived from rice Histone Deacetylase overexpression  
line."
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Query Match 0.4%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2166 TTTT TTTT TTTT 2177  
Db 1 TTTT TTTT TTTT 12
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RESULT 3574  
CF313356/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 12)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhna@mgbio.com, bhna@mgbio.myongji.ac.kr.
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/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
/note="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."
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Query Match 0.4%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2786 AAAAAAAAAA 2797  
Db 12 AAAAAAAAAA 1
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RESULT 3575  
CF315565  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 12)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhna@mgbio.com, bhna@mgbio.myongji.ac.kr.
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treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."
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Query Match 0.4%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2166 TTTT TTTT TTTT 2177  
Db 1 TTTT TTTT TTTT 12
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RESULT 3576  
CF315565/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 12)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.
```

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source

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/lab\_host="E.coli DH10B"  
/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
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Best Local Similarity 100.0%; Pred.No. 2.6e+03;  
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QY 2786 AAAAAAAAAAAAAA 2797

Db 12 AAAAAAAAAAAAAA 1

## RESULT 3577

CF317551

LOCUS

DEFINITION HD--07-E16.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--07-E16, mRNA sequence.

ACCESSION

VERSION CF317551.1 GI:33689312

KEYWORDS

SOURCE

ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

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Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 12)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
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CF317798.1 GI:33689559  
VERSION  
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 12)  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
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ACCESSION  
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VERSION  
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KEYWORDS  
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ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
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CF320426  
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library (HD) Oryza sativa cDNA clone HD--11-F02, mRNA sequence.  
ACCESSION  
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VERSION  
EST.  
KEYWORDS  
Oryza sativa  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 12)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
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Db 1 TTTT TTTT TTTT TTTT 12



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CF320426/c
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DEFINITION
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library (HD) Oryza sativa cDNA clone HD--11-F02, mRNA sequence.
ACCESSION
CF320426
VERSION
CF320426.1 GI:33692187
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 12)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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COMMENT
Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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DEFINITION
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cDNA library (JMT1) Oryza sativa cDNA clone JMT1--01-H22, mRNA
sequence.
ACCESSION
CF324793
VERSION
CF324793.1 GI:33797867
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 12)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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Contact: Nahm B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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cDNA library (JMT1) Oryza sativa cDNA clone JMT1--01-H22, mRNA
sequence.
ACCESSION
CF324793
VERSION
CF324793.1 GI:33797867
KEYWORDS
EST.
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ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 12)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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```
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            methyltransferase overexpression line."

Query Match      0.4%; Score 12; DB 1; Length 12;
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RESULT 3584
CF324793/c
LOCUS
DEFINITION
JMT1--01-H22.g1 AtJMT-overexpressing transgenic rice lambda phage
cDNA library (JMT1) Oryza sativa cDNA clone JMT1--01-H22, mRNA
sequence.
ACCESSION
CF324793
VERSION
CF324793.1 GI:33797867
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 12)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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LOCUS
DEFINITION
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sequence.
ACCESSION
CF324793
VERSION
CF324793.1 GI:33797867
KEYWORDS
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Oryza sativa
ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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REFERENCE
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Query Match 0.4%; Score 12; DB 1; Length 12;  
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VERSION CF326913.1 GI:33802082  
KEYWORDS EST.  
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ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
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Query Match 0.4%; Score 12; DB 1; Length 12;  
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Db 1 TTTTTTTTTTTT 12

RESULT 3586  
CF326913/c  
LOCUS CF326913 12 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--01-D01.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--01-D01, mRNA sequence.  
ACCESSION CF326913  
VERSION CF326913.1 GI:33802082  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAA 2797  
Db 12 AAAAAAAAAAAAA 1

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ACCESSION CF326913  
VERSION CF326913.1 GI:33802082  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

Query Match 0.4%; Score 12; DB 1; Length 12;  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2166 TTTTTTTTTTTT 2177  
Db 1 TTTTTTTTTTTT 12

RESULT 3586  
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LOCUS CF326913 12 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--01-D01.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--01-D01, mRNA sequence.  
ACCESSION CF326913  
VERSION CF326913.1 GI:33802082  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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Qy 2786 AAAAAAAAAAAAA 2797  
Db 12 AAAAAAAAAAAAA 1

RESULT 3587  
CF327376  
LOCUS CF327376 12 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--01-N10.b1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--01-N10, mRNA sequence.  
ACCESSION CF327376  
VERSION CF327376.1 GI:33803011  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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with oligoribonucleotides and then used as templates for  
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Db 1 TTTT TTTT TTTT TTTT 12

RESULT 3588  
CF327376/c

LOCUS CF327376 12 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--01-N10.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--01-N10, mRNA sequence.

ACCESSION CF327376  
VERSION CF327376.1 GI:33803011  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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Db 12 AAAAAAAAAA 1

RESULT 3589  
CF327962

LOCUS CF327962 12 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--02-K14.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--02-K14, mRNA sequence.

ACCESSION CF327962  
VERSION CF327962.1 GI:33804174  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

REFERENCE  
AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

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Db 1 TTTT TTTT TTTT TTTT 12

RESULT 3590  
CF327962/c

LOCUS CF327962 12 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--02-K14.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--02-K14, mRNA sequence.

ACCESSION CF327962  
VERSION CF327962.1 GI:33804174  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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QY      2786 AAAAAAAAAAAAAA 2797
Db      12 AAAAAAAAAAAAAA 1

RESULT 3591
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DEFINITION NACL--03-A13.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-A13, mRNA sequence.
ACCESSION  CF328229
VERSION     CF328229.1 GI:33804704
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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with oligoribonucleotides and then used as templates for
RT-PCR."

REFERENCE  1 (bases 1 to 12)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RT-PCR."

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 AAAAAAAAAAAAAA 12

RESULT 3592
CF328229/c
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DEFINITION NACL--03-A13.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-A13, mRNA sequence.
ACCESSION  CF328229
VERSION     CF328229.1 GI:33804704
KEYWORDS   EST.
SOURCE     Oryza sativa
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
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of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db      12 TTTT TTTT TTTT 1

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DEFINITION NACL--04-F18.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--04-F18, mRNA sequence.
ACCESSION  CF329141
VERSION     CF329141.1 GI:33806519
KEYWORDS   EST.
SOURCE     Oryza sativa
ORGANISM   Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 12)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 1 TTTT TTTT TTTT 12

RESULT 3594  
CF329141/c  
LOCUS  
DEFINITION NACL--04-F18.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--04-F18, mRNA sequence.

ACCESSION  
VERSION CF329141.1 GI:33806519  
KEYWORDS  
SOURCE

ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Location/Qualifiers

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAA 2797  
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Db 12 AAAAAAAAAA 1

RESULT 3595  
CF329142  
LOCUS  
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sativa cDNA clone NACL--04-F18, mRNA sequence.

ACCESSION  
VERSION CF329142.1 GI:33806520  
KEYWORDS  
EST.

SOURCE  
ORGANISM

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Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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Location/Qualifiers

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Db 1 AAAAAAAAAA 12

RESULT 3596  
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LOCUS  
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sativa cDNA clone NACL--04-F18, mRNA sequence.

ACCESSION  
VERSION CF329142.1 GI:33806520  
KEYWORDS  
SOURCE

ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Location/Qualifiers

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/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
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Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT 2177
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Db 1 TTTT TTTT TTTT 12

RESULT 3600
CF329872/c
LOCUS      CF329872      12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-F19.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--05-F19, mRNA sequence.
ACCESSION  CF329872
VERSION     CF329872.1 GI:33807965
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 12)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
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of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 12 AAAAAA AAAAAA 1

RESULT 3601
CF329929
LOCUS      CF329929      12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-H03.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--05-H03, mRNA sequence.
ACCESSION  CF329929
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VERSION  CF329929.1 GI:33808079
KEYWORDS EST.
SOURCE    Oryza sativa
ORGANISM  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 12)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 1 TTTT TTTT TTTT 12

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LOCUS      CF329929      12 bp mRNA linear EST 18-AUG-2003
DEFINITION NACL--05-H03.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--05-H03, mRNA sequence.
ACCESSION  CF329929
VERSION     CF329929.1 GI:33808079
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 12)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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    /lab_host="E.coli DH10B"
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTT TTTT TTTT 12
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RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAA 2797  
Db 12 AAAAAAAAAAAAA 1

RESULT 3603  
CF331241  
LOCUS CF331241 12 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--07-E15.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--07-E15, mRNA sequence.  
ACCESSION CF331241  
VERSION CF331241.1 GI:33810705  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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with oligoribonucleotides and then used as templates for  
RT-PCR."

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTT 2177  
Db 1 TTTTTTTTTTTT 12

RESULT 3604  
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LOCUS CF331241 12 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--07-E15.b1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--07-E15, mRNA sequence.

ACCESSION CF331241  
VERSION CF331241.1 GI:33810705  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 12 AAAAAAAAAAAAA 1

RESULT 3605  
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LOCUS CF331858 12 bp mRNA linear EST 18-AUG-2003  
DEFINITION NACL--08-C08.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--08-C08, mRNA sequence.  
ACCESSION CF331858  
VERSION CF331858.1 GI:33811939  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 12)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      2786 AAAAAAAAAA 2797  
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Db      1 AAAAAAAAAA 12
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RESULT 3606  
CF331858/c
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DEFINITION NACL--08-C08.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--08-C08, mRNA sequence.
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ACCESSION  CF331858  
VERSION     CF331858.1 GI:33811939  
KEYWORDS    EST.
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SOURCE     Oryza sativa  
ORGANISM    Oryza sativa
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REFERENCE   1 (bases 1 to 12)  
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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TITLE       Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL     Unpublished (2003)  
COMMENT     Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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Qy      2166 TTTT TTTT TTTT 2177  
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Db      12 TTTT TTTT TTTT 1
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RESULT 3607
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CF331904
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DEFINITION NACL--08-D07.g1 Rice callus plasmid cDNA library (NACL) Oryza
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ACCESSION  CF331904  
VERSION     CF331904.1 GI:33812029  
KEYWORDS    EST.
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SOURCE     Oryza sativa  
ORGANISM    Oryza sativa
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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Ehrhartoideae; Oryzeae; Oryza.
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1 (bases 1 to 12)
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AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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TITLE       Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL     Unpublished (2003)
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COMMENT     Contact: Nahm B.H.
```

```
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, MyongJi University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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FEATURES
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source
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Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      2786 AAAAAAAAAA 2797  
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Db      1 AAAAAAAAAA 12
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RESULT 3608  
CF331904/c
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LOCUS      CF331904      12 bp      mRNA      linear      EST 18-AUG-2003  
DEFINITION NACL--08-D07.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--08-D07, mRNA sequence.
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ACCESSION  CF331904  
VERSION     CF331904.1 GI:33812029  
KEYWORDS    EST.
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SOURCE     Oryza sativa  
ORGANISM    Oryza sativa
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.
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1 (bases 1 to 12)
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AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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TITLE       Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL     Unpublished (2003)
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COMMENT     Contact: Nahm B.H.
```

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Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
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FEATURES
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RT-PCR."

Query Match      0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2177
      |||||
Db 12 TTTT TTTT TTTT TTTT 1

RESULT 3609
CF331950
LOCUS
DEFINITION NACL--08-E07.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--08-E07, mRNA sequence.
ACCESSION CF331950
VERSION CF331950.1 GI:33812121
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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with oligoribonucleotides and then used as templates for
RT-PCR."

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Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2177
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Db 1 TTTT TTTT TTTT TTTT 12

RESULT 3610
CF331950/c
LOCUS
DEFINITION NACL--08-E07.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--08-E07, mRNA sequence.
ACCESSION CF331950
VERSION CF331950.1 GI:33812121
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2177
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Db 1 TTTT TTTT TTTT TTTT 12

RESULT 3611
CF332993
LOCUS
DEFINITION JMT--01-L10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--01-L10, mRNA sequence.
ACCESSION CF332993
VERSION CF332993.1 GI:33814228
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Db 12 AAAAAA AAAAAA 1
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ACCESSION CF331950
VERSION CF331950.1 GI:33812121
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.4%; Score 12; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      |||||
Db 12 AAAAAA AAAAAA 1

RESULT 3611
CF332993
LOCUS
DEFINITION JMT--01-L10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--01-L10, mRNA sequence.
ACCESSION CF332993
VERSION CF332993.1 GI:33814228
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 12)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
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Db 12 AAAAAA AAAAAA 1
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prepared from Arabidopsis Jasmonate Carboxyl  
methyltransferase overexpression line."

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Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT 2177  
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Db 1 TTTT TTTT TTTT 12

RESULT 3612  
CF332993/c  
LOCUS  
DEFINITION  
JMT--01-L10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--01-L10, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
1 (bases 1 to 12)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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prepared from Arabidopsis Jasmonate Carboxyl  
methyltransferase overexpression line."

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Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||  
Db 12 AAAAAAAAAA 1

RESULT 3613  
CF333992  
LOCUS

DEFINITION  
JMT--03-B22.b1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--03-B22, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
1 (bases 1 to 12)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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Query Match 0.4%; Score 12; DB 1; Length 12;  
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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTT TTTT TTTT 12

RESULT 3614  
CF333992/c  
LOCUS

DEFINITION  
JMT--03-B22.b1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--03-B22, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Oryza sativa

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
1 (bases 1 to 12)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

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/note="Vector: PCR4-TOPO; Site\_1: EcoRI; Oligo-capped mRNA  
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methyltransferase overexpression line."

Query Match 0.4%; Score 12; DB 1; Length 12;  
Best Local Similarity 100.0%; Pred.No. 2.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 12 AAAAAAAAAA 1

RESULT 3615

BQ591949

LOCUS

DEFINITION BQ591949 14 bp mRNA linear EST 06-DEC-2002  
cDNA clone 024-016-Cl15-SP6 MP1Z-ADIS-024-storage root Beta vulgaris

ACCESSION BQ591949

VERSION BQ591949.1

KEYWORDS EST. GI:26121532

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 14)

AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE

Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189

PUBMED 12472698

COMMENT

Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
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Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.4%; Score 12; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred.No. 3.8e+03;  
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Db 2 TTTTTTTTTTTT 13

RESULT 3616

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LOCUS

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cDNA clone 024-016-Cl15-SP6 MP1Z-ADIS-024-storage root Beta vulgaris

ACCESSION BQ591949

VERSION BQ591949.1

KEYWORDS EST. GI:26121532

SOURCE Beta vulgaris

ORGANISM Beta vulgaris

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 14)

AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

TITLE

Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)

MEDLINE 22362189

PUBMED 12472698

COMMENT

Contact: Weisshaar B  
ADIS DNA core facility at MPIZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851

Email: weisshaar@mpiz-koeln.mpg.de

Insert Length: 14 Std Error: 0.00

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Seq primer: SP6; CATACGATTAGGTGACACTATAG.

FEATURES

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1. .14  
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/clone="024-016-Cl15"  
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/note="Vector: pCMVSPORT6; Site\_1: SalI; Site\_2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by



RZPD/GABI-Primary database: <http://gabi.rzpd.de>

Query Match 0.4%; Score 12; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 13 AAAAAAAAAAAA 2

RESULT 3617  
CF291593  
LOCUS  
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sativa cDNA clone 14ROOT--02-B10, mRNA sequence.

ACCESSION CF291593  
VERSION CF291593.1 GI:33660626  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source Location/Qualifiers

1. .14  
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RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTT TTTT TTTT TTTG 12

RESULT 3618  
CF330198  
LOCUS  
DEFINITION NACL--05-N04.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--05-N04, mRNA sequence.

ACCESSION CF330198  
VERSION CF330198.1 GI:33808624  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
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Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source Location/Qualifiers

1. .14  
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with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTT TTTT TTTT TTTT 2177  
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Db 3 TTTT TTTT TTTT TTTT 14

RESULT 3619  
CF330198/c

LOCUS  
DEFINITION NACL--05-N04.g1 Rice callus plasmid cDNA library (NACL) Oryza  
sativa cDNA clone NACL--05-N04, mRNA sequence.

ACCESSION CF330198  
VERSION CF330198.1 GI:33808624  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 14)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source Location/Qualifiers

1. .14  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="NACL--05-N04"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: pCR4-TOPO; Site\_1: EcoRI; mRNA was capped

with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 12; DB 1; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.8e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2797  
Db 14 AAAAAAAAAAAAAA 3

RESULT 3620  
AW249689/c  
LOCUS  
DEFINITION 2819706.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819706 3',  
mRNA sequence.  
ACCESSION AW249689  
VERSION AW249689.1 GI:6592682  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 15)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2819706.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 13  
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 15 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: LCM2 row: E column: 19  
High quality sequence stop: 13.  
Location/Qualifiers  
1. .15  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2819706"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2784 TGAATAAAAAAAAA 2795  
Db 12 TGAATAAAAAAAAA 1

RESULT 3621  
AW250976/c  
LOCUS  
DEFINITION 2822229.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2822229 3',  
mRNA sequence.  
ACCESSION AW250976  
VERSION AW250976.1 GI:6594065  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 15)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2822229.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 11  
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 15 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: LCM8 row: N column: 22  
High quality sequence stop: 11.  
Location/Qualifiers  
1. .15  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2822229"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.3e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2784 TGAATAAAAAAAAA 2795  
Db 12 TGAATAAAAAAAAA 1

RESULT 3622  
AW248540

LOCUS AW248540 16 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2820844.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2820844 3',  
mRNA sequence.  
ACCESSION AW248540  
VERSION AW248540.1 GI:6591533  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 16)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2820844.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 15  
contiguous PHRED high quality bases followed by vector sequence. Very  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: LLCM5 row: E column: 5  
High quality sequence stop: 15.  
Location/Qualifiers  
1. 16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2820844"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
Query Match 0.4%; Score 12; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2177 TTTT TTTT TTTT TTTT AA 2188  
|||||  
Db 1 TTTT TTTT TTTT AA 12  
RESULT 3623  
AW246518/c  
LOCUS AW246518 17 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2821785.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821785 3',  
mRNA sequence.  
ACCESSION AW246518  
VERSION AW246518.1 GI:6589511  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2821785.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 15  
contiguous PHRED high quality bases followed by vector sequence. Very  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: LLCM7 row: L column: 10  
High quality sequence stop: 15.  
Location/Qualifiers  
1. 17  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:2821785"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC 7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
Query Match 0.4%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2784 TGAAAAA AAAAAA 2795  
|||||  
Db 12 TGAAAAA AAAAAA 1  
RESULT 3624  
AW249853/c  
LOCUS AW249853 18 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2821520.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821520 3',  
mRNA sequence.  
ACCESSION AW249853  
VERSION AW249853.1 GI:6592846  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 18)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)









0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12; DB 1; Length 20;  
Best Local Similarity 75.0%; Pred. No. 4.5e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1854 ACAGACCCACACACTTAGCC 1873  
|||||  
Db 20 ACACACACACACACTGCC 1

RESULT 3629  
CF322590/c  
LOCUS  
DEFINITION HDN--01-I03.g1 OSHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--01-I03, mRNA sequence.  
ACCESSION CF322590 20 bp mRNA linear EST 18-AUG-2003  
VERSION CF322590.1 GI:33793421  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1..20  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="HDN--01-I03"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli SOLR"  
/clone\_lib="OSHDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN)"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end with XhoI site. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 12; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAA 2796

Db 12 GAAAAA 1  
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RESULT 3630  
AZ427740  
LOCUS  
DEFINITION AZ427740 Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0209J23 R, genomic survey sequence.  
ACCESSION AZ427740  
VERSION AZ427740.1 GI:10551753  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 20)  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0209 row: J column: 23  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0209J23"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 12; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 4.5e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAA 2797  
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Db      2 AAAAAAAAAA 13

RESULT 3631
AZ967472
LOCUS
DEFINITION 2M0238L20F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0238L20 F, genomic survey sequence.
ACCESSION AZ967472
VERSION AZ967472.1 GI:13838699
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0238 row: L column: 20
Seq primer: CGTTGTAAACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
FEATURES
Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0238L20"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.4%; Score 12; DB 1; Length 21;
Best Local Similarity 75.0%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 555 GGCTGGAGGCGGCGCGGTG 574
||| ||| ||| ||| ||| ||| |||
Db 1 GGGGGGGGGGGGGCGCGGGG 20

Db      2 AAAAAAAAAA 13

RESULT 3631
AZ967472
LOCUS
DEFINITION 2M0238L20F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0238L20 F, genomic survey sequence.
ACCESSION AZ967472
VERSION AZ967472.1 GI:13838699
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0238 row: L column: 20
Seq primer: CGTTGTAAACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
FEATURES
Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0238L20"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.4%; Score 12; DB 1; Length 21;
Best Local Similarity 75.0%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 555 GGCTGGAGGCGGCGCGGTG 574
||| ||| ||| ||| ||| ||| |||
Db 1 GGGGGGGGGGGGGCGCGGGG 20

Db      2 AAAAAAAAAA 13

RESULT 3632
AW248826/c
LOCUS
DEFINITION 2821056.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821056 3',
mRNA sequence.
ACCESSION AW248826
VERSION AW248826.1 GI:6591819
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 21)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other_ESTs: 2821056.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center
Trimming: cross match from University of Washington Genome Center
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 21
contiguous PHRED high quality bases followed 21 contiguous distinct
Low Quality Sequence: Trace file contained 21 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a xhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LLCM5 row: N column: 1
High quality sequence stop: 21.
FEATURES
Location/Qualifiers
1..21
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821056"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```
QY 2777 TTAGAATTGAAAAA 2796
||||| ||| ||| ||| ||| ||| |||
Db 20 TTAGGGTCCCAAAAAA 1

RESULT 3633
AZ665864/c
LOCUS
DEFINITION AZ665864
IM0547I04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0547I04 R, genomic survey sequence.

Query Match 0.4%; Score 12; DB 1; Length 21;
Best Local Similarity 75.0%; Pred. No. 4.3e+03;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 24 bp DNA linear GSS 14-DEC-2000
IM0547I04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0547I04 R, genomic survey sequence.
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ACCESSION AZ665864  
VERSION AZ665864.1 GI:11803010  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0547 row: 1 column: 04  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 24.  
FEATURES  
source  
1. .24  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0547I04"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."  
Query Match 0.4%; Score 12; DB 1; Length 24;  
Best Local Similarity 75.0%; Pred. No. 3.8e+03;  
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 433 CTTGACACCGCGCGGCCCA 452  
Db 24 CTTACACCCCGCGGCCCA 5  
RESULT 3634  
CF330669  
LOCUS  
DEFINITION NACL--06-H16.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa cDNA clone NACL--06-H16, mRNA sequence.  
ACCESSION CF330669

VERSION CF330669.1 GI:33809573  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhnm@ggbio.com, bnhnm@bio.myongji.ac.kr.  
FEATURES  
source  
1. .15  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="NACL--06-H16"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."  
Query Match 0.4%; Score 11.8; DB 1; Length 15;  
Best Local Similarity 86.7%; Pred. No. 4.5e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 2779 AGAATTGAAAAAAA 2793  
Db 1 AAAATTAAAAAAA 15  
RESULT 3635  
AW246494/c  
LOCUS  
DEFINITION AW246494.1 GI:6589487  
mRNA sequence.  
ACCESSION AW246494  
VERSION AW246494.1 GI:6589487  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other ESTs: 2821595.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html  
Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 14



contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 15 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LiCM7 row: D column: 12

High quality sequence stop: 14.

Location/Qualifiers

source

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1. .15
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2821595"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

Query Match 0.4%; Score 11.8; DB 1; Length 15;

Best Local Similarity 86.7%; Pred. No. 4.5e+03;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2784 TGAATAAAAAAAAAA 2798

Db 15 TGATCAAAAAAAAAA 1

RESULT 3636

CF299603

LOCUS

DEFINITION 7LEAF--03-L01.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--03-L01, mRNA sequence.

ACCESSION CF299603

VERSION CF299603.1 GI:33671364

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 15)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source

```
1. .15
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--03-L01"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped"
```

with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.4%; Score 11.8; DB 1; Length 15;

Best Local Similarity 86.7%; Pred. No. 4.5e+03;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2779 AGAATTGAAAAAAA 2793

Db 1 AAAATTAAAAAAA 15

RESULT 3637

BM658732

LOCUS

DEFINITION BM658732 15 bp mRNA linear EST 27-FEB-2002 LZW602768445.R1 CSEQFXL37 pig adrenal Sus scrofa cDNA, mRNA sequence.

ACCESSION BM658732

VERSION BM658732.1 GI:18959003

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 15)

AUTHORS Adelson,D.L. and Gill,C.A.

TITLE Porcine ESTs

JOURNAL Unpublished (2002)

COMMENT Contact: David L. Adelson

Animal Breeding and Genetics

Texas A&M University

Animal Science Dept., TAMU-2471, College Station, TX 77843-2471, USA

Tel: 9798452616

Fax: 9798456970

Email: david.adelson@tamu.edu.

FEATURES

source

Location/Qualifiers

1. .15

/organism="Sus scrofa"

/mol\_type="mRNA"

/db\_xref="taxon:9823"

/clone\_lib="CSEQFXL37 pig adrenal"

/note="Organ: adrenal gland; Vector: pBluescript SK+;

Site\_1: NotI; Site\_2: EcoRI; sequence 5' of the insert

(5'-NNN...NNNinsert)

GCGAATTGGAGCTCCACCGCGGTGGCGCGCGGTCGAG. Sequence 3' of

the inserts (AAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG.

non-normalized library, sequenced 3' with M13R primer."

Query Match

Best Local Similarity 0.4%; Score 11.8; DB 1; Length 15;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2158 TTTTCTCTTTT 2172

Db 1 TTTTTCGTTTTT 15

RESULT 3638

BM658732/c

LOCUS

DEFINITION BM658732 15 bp mRNA linear EST 27-FEB-2002 LZW602768445.R1 CSEQFXL37 pig adrenal Sus scrofa cDNA, mRNA sequence.

ACCESSION BM658732

VERSION BM658732.1 GI:18959003

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 15)

AUTHORS Adelson,D.L. and Gill,C.A.

TITLE Porcine ESTs

```
JOURNAL Unpublished (2002)
COMMENT Contact: David L. Adelson
        Animal Breeding and Genetics
        Texas A&M University
        Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
        USA
        Tel: 9798452616
        Fax: 9798456970
        Email: david.adelson@tamu.edu.

FEATURES source
LOCUS      CF332179
DEFINITION NACL--08-J10.g1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION  CF332179
VERSION     CF332179.1 GI:33812582
KEYWORDS   EST.
SOURCE     Oryza sativa
           Oryza sativa
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
LOCUS      CF332179
DEFINITION NACL--08-J10.g1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION  CF332179
VERSION     CF332179.1 GI:33812582
KEYWORDS   EST.
SOURCE     Oryza sativa
           Oryza sativa
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Query Match      0.4%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 4.5e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2800
Db      15 AAAAAACGAAAAAA 1

RESULT 3639
CF332179
LOCUS      CF332179
DEFINITION NACL--08-J10.g1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION  CF332179
VERSION     CF332179.1 GI:33812582
KEYWORDS   EST.
SOURCE     Oryza sativa
           Oryza sativa
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
LOCUS      CF332179
DEFINITION NACL--08-J10.g1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION  CF332179
VERSION     CF332179.1 GI:33812582
KEYWORDS   EST.
SOURCE     Oryza sativa
           Oryza sativa
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Query Match      0.4%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 4.5e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2782 ATTGAAAAAAAAAAAA 2796
Db      1 ATTTATAAAAAAAAAA 15

RESULT 3640
CF332179/c
LOCUS      CF332179
DEFINITION NACL--08-J10.g1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION  CF332179
VERSION     CF332179.1 GI:33812582
KEYWORDS   EST.
SOURCE     Oryza sativa
           Oryza sativa
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
LOCUS      CF332179
DEFINITION NACL--08-J10.g1 Rice callus plasmid cDNA library (NACL) Oryza
ACCESSION  CF332179
VERSION     CF332179.1 GI:33812582
KEYWORDS   EST.
SOURCE     Oryza sativa
           Oryza sativa
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
           Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 15)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Query Match      0.4%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 4.5e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2176 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db      15 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 3641
AW245338
LOCUS      AW245338
DEFINITION 2822905.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822905 3',
           mRNA sequence.
ACCESSION  AW245338
VERSION     AW245338.1 GI:6588331
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
           Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 16)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
           National Institutes of Health, Mammalian Gene Collection (MGC)
           Unpublished (1999)
           Other_ESTs: 2822905.5prime

Query Match      0.4%; Score 11.8; DB 1; Length 15;
Best Local Similarity 86.7%; Pred. No. 4.5e+03;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2176 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db      15 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 3641
AW245338
LOCUS      AW245338
DEFINITION 2822905.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822905 3',
           mRNA sequence.
ACCESSION  AW245338
VERSION     AW245338.1 GI:6588331
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
           Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 16)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
           National Institutes of Health, Mammalian Gene Collection (MGC)
           Unpublished (1999)
           Other_ESTs: 2822905.5prime
```

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTP/DTP CDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image.html Base Calling / Quality Scores: PHRED from University of Washington Genome Center Trimming: cross match from University of Washington Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: http://www.genome.washington.edu Low Quality Sequence: 15 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 16 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LLCM10 row: K column: 2  
High quality sequence stop: 15.  
Location/Qualifiers

FEATURES

source

1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2822905"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC 7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11.8; DB 1; Length 16;  
Best Local Similarity 86.7%; Pred. No. 4.7e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1922 TTTTTCAGTGT 1936

Db 1 TTTTTCAGTGT 15

RESULT 3642

AI798250

LOCUS

DEFINITION

AI798250 16 bp mRNA linear EST 06-JUL-1999  
tr32b08.x1 NCI CGAP Ov23 Homo sapiens cDNA clone IMAGE:2219991 3'  
similar to TR:O79354 O79354 CYTOCHROME OXIDASE SUBUNIT III. ; mRNA

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 16)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cdNA Library Preparation: Life Technologies, Inc.

cdNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

FEATURES

source

1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:2219991"  
/tissue\_type="tumor, 5 pooled (see description)"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Ov23"  
/note="Organ: ovary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"

Query Match 0.4%; Score 11.8; DB 1; Length 16;  
Best Local Similarity 86.7%; Pred. No. 4.7e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800

Db 2 AAAAAAAAAAAAAA 16

RESULT 3643

AI798250/c

LOCUS

DEFINITION

AI798250 16 bp mRNA linear EST 06-JUL-1999  
tr32b08.x1 NCI CGAP Ov23 Homo sapiens cDNA clone IMAGE:2219991 3'  
similar to TR:O79354 O79354 CYTOCHROME OXIDASE SUBUNIT III. ; mRNA

sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 16)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cdNA Library Preparation: Life Technologies, Inc.

cdNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

FEATURES

source

1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2219991"  
/tissue\_type="tumor, 5 pooled (see description)"  
/lab\_host="DH10B"



/clone\_lib="NCI\_CGAP\_Ov23"  
/note="Organ: ovary; Vector: PCMV-SPORT6; Site 1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.35 kb. Tumor types include: mixed  
Mullerian tumor, papillary serous, clear cell, spindle  
cell. All are primary tumors, metastasis positive. Life  
Technologies catalog #: 11534-013"

Query Match 0.4%; Score 11.8; DB 1; Length 16;  
Best Local Similarity 86.7%; Pred. No. 4.7e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2166 TTTTCTTTTCTTTTGT 2180  
Db 16 TTTCTTTTCTTTTGT 2

RESULT 3644  
AW250449/c  
LOCUS  
DEFINITION AW250449 18 bp mRNA linear EST 07-JAN-2000  
2822458.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2822458 3',  
mRNA sequence.  
ACCESSION AW250449  
VERSION AW250449.1 GI:6593442  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 18)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2822458.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project  
Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
<http://www.genome.washington.edu/LowQuality> Sequence: 18  
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 18 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: LCM9 row: H column: 11  
High quality sequence stop: 18.  
Location/Qualifiers  
1. 18  
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/db\_xref="taxon:9606"  
/clone="IMAGE:2822458"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC 7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

/clone\_lib="NCI\_CGAP\_Ov23"  
/note="Organ: ovary; Vector: PCMV-SPORT6; Site 1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.35 kb. Tumor types include: mixed  
Mullerian tumor, papillary serous, clear cell, spindle  
cell. All are primary tumors, metastasis positive. Life  
Technologies catalog #: 11534-013"

Query Match 0.4%; Score 11.8; DB 1; Length 18;  
Best Local Similarity 86.7%; Pred. No. 4.8e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2781 AATTGAAAAA 2795  
Db 15 AAGGAAAAA 1

RESULT 3645  
AZ323986/c  
LOCUS  
DEFINITION AZ323986 19 bp DNA linear GSS 29-SEP-2000  
1M0045P09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0045P09 R, genomic survey sequence.  
ACCESSION AZ323986  
VERSION AZ323986.1 GI:10379252  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0045 row: P column: 09  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
1. 19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0045P09"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."



Query Match 0.4%; Score 11.8; DB 1; Length 19;  
Best Local Similarity 86.7%; Pred. No. 4.7e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800  
| | | | | | | | | | | | | | | | |  
Db 19 AAACAACAAACAAA 5

RESULT 3646  
AZ810717/c  
LOCUS  
DEFINITION  
2M0076N24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0076N24 F, genomic survey sequence.  
AZ810717  
AZ810717.1 GI:12978242  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0076 row: N column: 24  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
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1. .19  
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/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0076N24"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.4%; Score 11.8; DB 1; Length 19;

Best Local Similarity 86.7%; Pred. No. 4.7e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2174 TTTTTTTTTTTTAA 2188  
| | | | | | | | | | | | | | | | |  
Db 19 TTTTTTTTTTCCAA 5

RESULT 3647  
AZ786781/c  
LOCUS  
DEFINITION  
2M0032C05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0032C05 R, genomic survey sequence.  
AZ786781  
AZ786781.1 GI:12924886  
GSS.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0032 row: C column: 05  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0032C05"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.4%; Score 11.8; DB 1; Length 20;  
Best Local Similarity 86.7%; Pred. No. 4.5e+03;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800  
Db 20 AAAAAAAAAATATA 6

RESULT 3648  
AZ810709 23 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M0076M20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
DEFINITION clone UUGC2M0076M20 F, genomic survey sequence.  
ACCESSION AZ810709  
VERSION AZ810709.1 GI:12978228  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 23)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0076 row: M column: 20  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 23.

FEATURES source  
1. .23  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0076M20"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 11.8; DB 1; Length 23;  
Best Local Similarity 86.7%; Pred. No. 3.9e+03;  
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2758 TATAATAAAAGTATT 2772  
Db 1 TATAATAAAATTTT 15

RESULT 3649  
AI364573/C 19 bp mRNA linear EST 15-FEB-1999  
LOCUS AI364573  
DEFINITION qw37g03.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:1993300 3', similar to TR:Q39835 Q39835 EXTENSIN. ;, mRNA sequence.  
ACCESSION AI364573  
VERSION AI364573.1 GI:4124262  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Insert Length: 1632 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.  
Location/Qualifiers  
1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1993300"  
/tissue\_type="serous papillary carcinoma, high grade, 2 pooled tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Ut4"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: SalI; Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"

Query Match 0.4%; Score 11.6; DB 1; Length 19;  
Best Local Similarity 77.8%; Pred. No. 4.7e+03;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 49 GCGCGCGGGGGCGGCGG 66  
Db 19 GTGGGGGGGGGTGGCGG 2

RESULT 3650  
AW248167  
LOCUS AW248167  
DEFINITION 2819811.5prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819811 5', mRNA sequence.  
ACCESSION AW248167  
VERSION AW248167.1 GI:6591160  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 19)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other ESTs: 2819811.3prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
<http://www.genome.washington.edu> Low Quality Sequence: 14  
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 19 contiguous distinct  
peaks following vector sequence. Possible inverted insert: Based  
upon the presence of a XhoI site followed by a run of 14 or more T  
residues at the beginning of the sequence, this clone probably  
contains an inverted cDNA insert. EST# does not reflect transcript  
orientation. Possible Chimera: Based upon the presence of a XhoI  
site followed by a run of 14 or more T residues at the beginning of  
this sequence and at the beginning of the sequence from the 3' read  
of this clone, this cDNA insert appears to be chimeric.  
Plate: LLCM2 row: J column: 4  
High quality sequence stop: 14.  
Location/Qualifiers

FEATURES source

1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2819811"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11.6; DB 1; Length 19;  
Best Local Similarity 77.8%; Pred. No. 4.7e+03;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1773 TTTT TTTT TTTGAACCCCAT 1790  
|||||  
Db 1 TTTT TTTT TTTCTTCCCAT 18

RESULT 3651  
AW249918  
LOCUS AW249918 19 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2821753.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821753 3',  
mRNA sequence.  
ACCESSION AW249918  
VERSION AW249918.1 GI:6592911  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE JOURNAL COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2821753.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
<http://www.genome.washington.edu> Low Quality Sequence: 11  
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 19 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: LLCM7 row: K column: 2  
High quality sequence stop: 11.  
Location/Qualifiers

FEATURES source

1. .19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821753"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11.6; DB 1; Length 19;  
Best Local Similarity 77.8%; Pred. No. 4.7e+03;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2171 TTTT TTTT TTTTTTAA 2188  
|||||  
Db 1 TTTT TTTT TTTGTCATCA 18

RESULT 3652  
AZ447864/c  
LOCUS AZ447864 19 bp DNA linear GSS 04-OCT-2000  
DEFINITION 1M0245A14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0245A14 F, genomic survey sequence.  
ACCESSION AZ447864  
VERSION AZ447864.1 GI:106000087  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss



University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0245 row: A column: 14  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source

1. 19  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0245A14"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

University of Utah  
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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0245 row: A column: 14  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

FEATURES  
source

1. 19  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0080P01"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0080 row: P column: 01  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.

Query Match 0.4%; Score 11.6; DB 1; Length 19;  
Best Local Similarity 77.8%; Pred. No. 4.7e+03;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2778 TAGAATTGAAAAA 2795  
||| ||||| |||||  
Db 18 TAAAAATGAATATAAAA 1

RESULT 3653  
AZ345537

LOCUS  
DEFINITION  
1M0080P01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0080P01 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center

REFERENCE  
AUTHORS

TITLE  
JOURNAL  
COMMENT

Query Match 0.4%; Score 11.6; DB 1; Length 19;  
Best Local Similarity 77.8%; Pred. No. 4.7e+03;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2786 AAAAAA 2803  
||||| ||||| |||||  
Db 2 AAAAAATAAATTTAAAAA 19

RESULT 3654  
AZ493581/C

LOCUS  
DEFINITION  
1M0328A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0328A24 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center

TITLE  
JOURNAL  
COMMENT



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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
 Insert Length: 1000 Std Error: 0.00  
 Plate: 0328 row: A column: 24  
 Seq primer: CGTTGTAACGACGGCCACT  
 Class: plasmid ends  
 High quality sequence stop: 19

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FEATURES
source
1. 19
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0328A24"
/sex="Male"
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Query Match	0.4%;	Score 11.6;	DB 1;	Length 19;
Best Local Similarity	77.8%;	Pred. NO. 4.7e+03;		
Matches 14; Conservative		0; Mismatches 4;	Indels 0;	Gaps 0;
QY	49	GC GCG CGG GGG GCG GCG G	66	
Dh	19			
		GGGGGGGGGGGGGGGGGG	2	

RESULT	3655
AZ369369/c	
LOCUS	AZ369369
DEFINITION	1M0119K19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0119K19 R, genomic survey sequence.
ACCESSION	AZ369369
VERSION	AZ369369.1 GI:10483069
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 19)
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT

84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0119 row: K column: 19  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends

FEATURES	source
Location/Qualifiers	1..19
	/organism="Mus musculus"
	/mol_type="genomic DNA"
	/strain="C57BL/6J"
	/db_xref="taxon:10090"
	/clone="UUGClM0119K19"
	/sex="Male"

Query Match	0.4%;	Score 11.6;	DB 1;	Length 19;
Best Local Similarity	77.8%;	Pred. No. 4.7e+03;		
Matches 14;	Conservative	0;	Mismatches 4;	Indels 0;
			Gaps	0;
QY	296	CCACCCCTCTCCACACT	313	
dh	18	CCCCCCCCCACACT	1	

RESULT 3656	
AA888191	
LOCUS	AA888191 22 bp mRNA linear EST 31-MAR-1998
DEFINITION	of82a05.s1 NCI CGAP_Li5 Homo sapiens cDNA clone IMAGE:1436816 3', similar to TR:Q33563 Q33563 EATRO 164 KINETOPLAST ;, mRNA sequence.
ACCESSION	AA888191
VERSION	AA888191.1 GI:3003866
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 22)
TITLE	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lemmon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.

FEATURES

source  
1. .22  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1436816"  
/tissue\_type="hepatic adenoma"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Li5"  
/note="Organ: liver; Vector: pCMV-SPORT4; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 0.8 Kb."

Query Match 0.4%; Score 11.6; DB 1; Length 22;  
Best Local Similarity 77.8%; Pred. No. 4.1e+03;  
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2803  
Db 2 AACAAATAAAGAAGAA 19

RESULT 3657  
CF291593/c

LOCUS  
DEFINITION  
14ROOT--02-B10.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--02-B10, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 14)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source  
1. .14  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="14ROOT--02-B10"  
/tissue\_type="root"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.4%; Score 11.4; DB 1; Length 14;  
Best Local Similarity 92.3%; Pred. No. 4.5e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAA 2797

Db 13 GCAAAAAAAAAA 1

RESULT 3658

AW246551/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 15)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other ESTs: 2822090.5prime

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling

Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.

Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing

project Clone distribution: MGC clone distribution information can

be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality

Scores: PHRED from University of Washington Genome Center. Vector

Trimming: cross match from University of Washington Genome Center

PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley

Drosophila Genome Project. University of Washington Genome Center:

http://www.genome.washington.edu Low Quality Sequence: 14

contiguous PHRED high quality bases following vector sequence. Very

Low Quality Sequence: Trace file contained 15 contiguous distinct

peaks following vector sequence. Polyadenylation: Based upon the

presence of a XhoI site followed by a run of 14 or more T residues

at the beginning of the sequence, this cDNA insert was

polyadenylated.

Plate: LLCM8 row: I column: 3

High quality sequence stop: 14.

Location/Qualifiers

1. .15

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2822090"

/tissue\_type="small cell carcinoma"

/cell\_line="MGC3"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH MGC 7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally

cloned into EcoRI/XhoI sites using the following 5'

adaptor: GGACGAG(G). Size-selected >500bp for average

insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

Query Match

Best Local Similarity 92.3%; Pred. No. 4.9e+03;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2783 TTGAAAAAAAAA 2795

Db 13 TTTAAAAAAAAA 1

RESULT 3659

AW249689

LOCUS

AW249689 15 bp mRNA linear EST 07-JAN-2000

DEFINITION 2819706.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819706 3', mRNA sequence.

ACCESSION AW249689

VERSION AW249689.1 GI:6592682

KEYWORDS EST

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 15)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other\_ESTs: 2819706.5prime

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-re@mail.nih.gov](mailto:cgapbs-re@mail.nih.gov)

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www.llnl.gov/bbrp/image/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 13 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 15 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LLCM2 row: E column: 19

High quality sequence stop: 13.

Location/Qualifiers

1. .15

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2819706"

/tissue\_type="small cell carcinoma"

/cell\_line="MGC3"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11.4; DB 1; Length 15;

Best Local Similarity 92.3%; Pred. No. 4.9e+03;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2177 TTTTTCCTTAAAC 2189

Db 1 TTTTTCCTTTCAC 13

RESULT 3660

AW246490

LOCUS AW246490

DEFINITION 2821591.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821591 3', mRNA sequence.

ACCESSION AW246490

VERSION AW246490.1 GI:6589483

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 16)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other\_ESTs: 2820844.5prime

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-re@mail.nih.gov](mailto:cgapbs-re@mail.nih.gov)

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 12 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 16 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LLCM7 row: D column: 8

High quality sequence stop: 12.

Location/Qualifiers

1. .16

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2821591"

/tissue\_type="small cell carcinoma"

/cell\_line="MGC3"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11.4; DB 1; Length 16;

Best Local Similarity 92.3%; Pred. No. 5e+03;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1772 TTTTTCCTTGAA 1784

Db 1 TTTTTCCTTGCA 13

RESULT 3661

AW248540/C

LOCUS AW248540

DEFINITION 2820844.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2820844 3', mRNA sequence.

ACCESSION AW248540

VERSION AW248540.1 GI:6591533

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 16)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other\_ESTs: 2820844.5prime

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 16)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other\_ESTs: 2821591.5prime

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-re@mail.nih.gov](mailto:cgapbs-re@mail.nih.gov)

Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 12 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 16 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LLCM7 row: D column: 8

High quality sequence stop: 12.

Location/Qualifiers

1. .16

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2821591"

/tissue\_type="small cell carcinoma"

/cell\_line="MGC3"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_7"

/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11.4; DB 1; Length 16;

Best Local Similarity 92.3%; Pred. No. 5e+03;

Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1772 TTTTTCCTTGAA 1784

Db 1 TTTTTCCTTGCA 13

RESULT 3661

AW248540/C

LOCUS AW248540

DEFINITION 2820844.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2820844 3', mRNA sequence.

ACCESSION AW248540

VERSION AW248540.1 GI:6591533

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 16)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other\_ESTs: 2820844.5prime



Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 15  
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 16 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: LLCM5 row: E column: 5  
High quality sequence stop: 15.  
Location/Qualifiers  
1. 16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2820844"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: POTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

FEATURES  
source

1. 17  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821399"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: POTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11.4; DB 1; Length 16;  
Best Local Similarity 92.3%; Pred. No. 5e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2783 TTGAATAAAAAA 2795  
||| ||||| |||||  
Db 13 TTTAAAAA 1

RESULT 3662  
AW251033/c

LOCUS AW251033 17 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2821399.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821399 3',  
mRNA sequence.  
ACCESSION AW251033  
VERSION AW251033.1 GI:6593979  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2821399.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 17  
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 17 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.  
Plate: LLCM6 row: L column: 8  
High quality sequence stop: 17.  
Location/Qualifiers  
1. 17  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821399"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: POTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

FEATURES  
source

1. 17  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821399"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: POTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 5e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2783 TTGAATAAAAAA 2795  
||| ||||| |||||  
Db 13 TTTAAAAA 1

RESULT 3663  
AW246528/c

LOCUS AW246528 17 bp mRNA linear EST 07-JAN-2000  
DEFINITION 2821879.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821879 3',  
mRNA sequence.  
ACCESSION AW246528  
VERSION AW246528.1 GI:6589521  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)  
NIH-MGC http://mgc.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2821879.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 13  
contiguous PHRED high quality bases following vector sequence. Very

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT



Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LLCM7 row: P column: 8

High quality sequence stop: 13.

FEATURES source

Location/Qualifiers  
1. .17  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821879"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 5e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2783 TTGAAAAA 2795  
|||  
Db 13 TTTAAAAA 1

RESULT 3664  
AW246518

LOCUS  
DEFINITION  
AW246518  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AW246518 17 bp mRNA linear EST 07-JAN-2000  
2821785.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821785 3',  
mRNA sequence.  
AW246518 GI:6589511  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 17)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2821785.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-re@mail.nih.gov](mailto:cgapbs-re@mail.nih.gov)  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 15 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 17 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LLCM7 row: L column: 10  
High quality sequence stop: 15.

FEATURES source

Location/Qualifiers  
1. .17  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821785"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11.4; DB 1; Length 17;  
Best Local Similarity 92.3%; Pred. No. 5e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2177 TTTTAAAA 2189  
|||||  
Db 1 TTTTAAAA 13

RESULT 3665  
AW249853

LOCUS  
DEFINITION  
AW249853  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AW249853 18 bp mRNA linear EST 07-JAN-2000  
2821520.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821520 3',  
mRNA sequence.  
AW249853 GI:6592846  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 18)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other\_ESTs: 2821520.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-re@mail.nih.gov](mailto:cgapbs-re@mail.nih.gov)  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing project Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html) Base Calling / Quality Scores: PHRED from University of Washington Genome Center. Vector Trimming: cross match from University of Washington Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washington Genome Center: <http://www.genome.washington.edu> Low Quality Sequence: 0 contiguous PHRED high quality bases following vector sequence. Very Low Quality Sequence: Trace file contained 18 contiguous distinct peaks following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.

Plate: LLCM7 row: A column: 9.

FEATURES source

Location/Qualifiers  
1. .18  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821520"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"

/clone lib="NIH\_MGC 7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11.4; DB 1; Length 18;  
Best Local Similarity 92.3%; Pred. No. 4.9e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2177 TTTT TTTT TTTT AAC 2189  
          |||||  
Db 1 TTTT TTTT TTTT CAC 13

RESULT 3666  
LOCUS AW251048/c  
DEFINITION AW251048 18 bp mRNA linear EST 07-JAN-2000  
          2821495.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821495 3',  
          mRNA sequence.  
ACCESSION AW251048  
VERSION AW251048.1 GI:65933994  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other\_ESTs: 2821495.5prime  
          Contact: Robert Strausberg, Ph.D.  
          Email: cgapbs-r@mail.nih.gov  
          Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
          Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
          Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
          project Clone distribution: MGC clone distribution information can  
          be found through the I.M.A.G.E. Consortium/LLNL at:  
          www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
          Scores: PHRED from University of Washington Genome Center. Vector  
          Trimming: cross match from University of Washington Genome Center  
          PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
          Drosophila Genome Project. University of Washington Genome Center:  
          http://www.genome.washington.edu Low Quality Sequence: 10  
          contiguous PHRED high quality bases following vector sequence. Very  
          Low Quality Sequence: Trace file contained 18 contiguous distinct  
          peaks following vector sequence. Polyadenylation: Based upon the  
          presence of a XhoI site followed by a run of 14 or more T residues  
          at the beginning of the sequence, this cDNA insert was  
          polyadenylated.  
          Plate: LLCM6 row: P column: 8  
          High quality sequence stop: 10.

Location/Qualifiers  
1. .18  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821495"  
/tissue type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone lib="NIH\_MGC 7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of

FEATURES  
source  
1. .18  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821495"  
/tissue type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone lib="NIH\_MGC 7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of

California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."  
Query Match 0.4%; Score 11.4; DB 1; Length 18;  
Best Local Similarity 92.3%; Pred. No. 4.9e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2783 TTGA AAAAAA AAA 2795  
          |||  
Db 13 TTTA AAAAAA AAA 1

RESULT 3667  
LOCUS AZ995149/c  
DEFINITION AZ995149 19 bp DNA linear GSS 27-APR-2001  
          2M0280D22R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
          clone UUGC2M0280D22 R, genomic survey sequence.

ACCESSION AZ995149  
VERSION AZ995149.1 GI:13866376  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
          plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
          University of Utah Genome Center  
          University of Utah  
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
          84112, USA  
          Tel: 801 585 5606  
          Fax: 801 585 7177  
          Email: ddunn@genetics.utah.edu  
          Insert Length: 10000 Std Error: 0.00  
          Plate: 0280 row: D column: 22  
          Seq primer: CACACAGGAAACAGCTATGACC  
          Class: plasmid ends  
          High quality sequence stop: 19.

FEATURES  
source  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0280D22"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, Tl-resistant, F-"  
/clone lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
          (http://www.jax.org/resources/documents/dnares/). The DNA  
          was hydrodynamically sheared by repeated passage through a  
          0.005 inch orifice at constant velocity. The sheared DNA  
          was blunt end-repaired with T4 DNA polymerase and T4  
          polynucleotide kinase. Adaptor oligonucleotides were  
          ligated to the blunt ends in high molar excess. The  
          adaptored DNA was purified and size-selected for a 9.5 to  
          10.5 kb range using preparative agarose gel  
          electrophoresis. Vector DNA was prepared from a derivative  
          of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
          inducible derivative of plasmid R1. The vector was ligated  
          with adaptors complementary to the insert adaptors and  
          purified. The sheared, adaptored mouse DNA was annealed to  
          adaptored vector DNA, and transformed into  
          chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.4%; Score 11.4; DB 1; Length 19;  
Best Local Similarity 92.3%; Pred. No. 4.7e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 458 AGCCAGCAGCAGG 470  
||| |||||  
Db 15 AGGCAGCAGCAGG 3

RESULT 3668  
AZ514586 19 bp DNA linear GSS 05-OCT-2000  
LOCUS  
DEFINITION 1M0361B17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0361B17 F, genomic survey sequence.

ACCESSION AZ514586  
VERSION AZ514586.1 GI:10695818  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)

REFERENCE  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0361 row: B column: 17  
Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends  
High quality sequence stop: 19.

Location/Qualifiers

FEATURES  
source

1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0361B17"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.4%; Score 11.4; DB 1; Length 19;  
Best Local Similarity 92.3%; Pred. No. 4.7e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2784 TGAAAAA 2796  
||| |||||  
Db 5 TGCAAAAA 17

RESULT 3669  
AZ308410

LOCUS  
DEFINITION 20 bp DNA linear GSS 29-SEP-2000  
1M0011A24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0011A24 F, genomic survey sequence.

ACCESSION AZ308410  
VERSION AZ308410.1 GI:10348378  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)

REFERENCE  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0011 row: A column: 24  
Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends  
High quality sequence stop: 20.

Location/Qualifiers

FEATURES  
source

1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0011A24"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."



Query Match 0.4%; Score 11.4; DB 1; Length 20;  
Best Local Similarity 92.3%; Pred. No. 4.5e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 110 GGGGGCTGGGGG 122  
|||||  
DB 2 GGGGGCGGGGG 14

RESULT 3670  
AZ469472/c  
LOCUS  
DEFINITION  
1M0283A06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0283A06.F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)

AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0283 row: A column: 06  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends

High quality sequence stop: 20.

FEATURES  
source

1. .20  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0283A06"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.4%; Score 11.4; DB 1; Length 20;

Best Local Similarity 92.3%; Pred. No. 4.5e+03;  
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1979 AAAAAAGAAAAG 1991  
|||||  
DB 20 AAAAAACAAAAG 8

RESULT 3671  
AZ303903

LOCUS

DEFINITION  
IM0003B18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0003B18 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)

AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Unpublished (2000)

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0003 row: B column: 18  
Seq primer: CACACAGGAACACGCTATGACC  
Class: plasmid ends

High quality sequence stop: 20.

FEATURES

source

1. .20  
Location/Qualifiers  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0003B18"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.4%; Score 11.4; DB 1; Length 20;  
Best Local Similarity 92.3%; Pred. No. 4.5e+03;



Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2568 CTGTTCTTGGCTT 2580  
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Db 1 CTGTTCTTGGCTT 13

RESULT 3672  
BQ583458  
LOCUS  
DEFINITION B011979-024-005-J11-SP6 MP1Z-ADIS-024-inflorescence Beta vulgaris  
CDNA clone 024-005-J11 5-PRIME, mRNA sequence.  
ACCESSION BQ583458  
VERSION BQ583458.1 GI:26113035  
KEYWORDS EST.  
SOURCE Beta vulgaris  
ORGANISM Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lebrach,H.  
and Radelof,U.  
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
JOURNAL Plant J. 32 (5), 845-857 (2002)  
MEDLINE 22362189  
PUBMED 12472698  
COMMENT Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 16 Std Error: 0.00  
Plate: 5 Row: J Column: 11  
Seq primer: SP6; CATACGATTAGTGACACTATAG.  
FEATURES  
source  
1..16  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:183240"  
/db\_xref="taxon:161934"  
/clone="024-005-J11"  
/tissue\_type="inflorescence"  
/lab\_host="EMDH10B"  
/clone\_lib="MP1Z-ADIS-024-inflorescence"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.4%; Score 11.2; DB 1; Length 16;  
Best Local Similarity 81.2%; Pred. No. 5.2e+03;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1980 AAAAAAGAAAGTGTG 1995  
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Db 1 AAAAAAGAAAGGGG 16

RESULT 3673  
AZ440413/c  
LOCUS  
DEFINITION 2M0225101F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

DEFINITION 1M0231A01R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0231A01 R, genomic survey sequence.

ACCESSION AZ440413  
VERSION AZ440413.1 GI:10564426  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 19)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0231 row: A column: 01  
Seq primer: CACACAGGAACACGCTATGACC  
CLASS: plasmid ends  
High quality sequence stop: 19.  
FEATURES  
source  
1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0231A01"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Ti-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.4%; Score 11.2; DB 1; Length 19;  
Best Local Similarity 81.2%; Pred. No. 4.7e+03;  
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2785 GAAAAAAGAAAAA 2800  
||||| |||||

Db 18 GAAAGAAAGAGAAAAA 3

RESULT 3674  
AZ957966/c  
LOCUS  
DEFINITION 2M0225101F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

```
clone UUGC2M0225I01 F, genomic survey sequence.

ACCESSION      AZ957966
VERSION        AZ957966.1  GI:13829193
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 20)
AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
               University of Utah Genome Center
               University of Utah
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
               Plate: 0225 row: 1 column: 01
               Seq primer: CGTTGTAACGACGCCAGT
               Class: plasmid ends
               High quality sequence stop: 20.

FEATURES             Location/Qualifiers
     source           1..20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0225I01"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match          0.4%; Score 11.2; DB 1; Length 20;
Best Local Similarity 81.2%; Pred. No. 4.5e+03;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1980 AAAAAAGAAAAGTGTG 1995
Db      20 AAAAAAAGGCGG 5

RESULT 3675
D20705
LOCUS      HUMGS01681 Human promyelocyte Homo sapiens CDNA clone pm2012 3',
DEFINITION mRNA sequence.

Query Match          0.4%; Score 11.2; DB 1; Length 22;
Best Local Similarity 76.5%; Pred. No. 4.1e+03;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2777 TTAGAATTGAAAAAAA 2793
Db      6 TTAAAGTNAATAAA 22

RESULT 3676
CF291636/c
LOCUS      CF291636
DEFINITION 14ROOT--02-C09.g1 Rice root plasmid CDNA library (14ROOT) Oryza
sativa CDNA clone 14ROOT--02-C09, mRNA sequence.
ACCESSION  CF291636
VERSION     CF291636.1  GI:33660669
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 24)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
               Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
               of Bioscience and Bioinformatics, MyongJi University
               Yongin, Kyeonggi, Korea
               Tel: 82 31 330 6193
               Fax: 82 31 321 6355
               Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..24
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="14ROOT--02-C09"
                     /tissue_type="root"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli DH10B"
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/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.4%; Score 11.2; DB 1; Length 24;  
Best Local Similarity 66.7%; Pred. No. 3.8e+03;  
Matches 16; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 50 CGCGGCGGGCGCGCGGACGCG 73  
|||||  
Db 24 CGCGGCGCGCGCGCGCGCGCG 1

RESULT 3677  
AW250976 15 bp mRNA linear EST 07-JAN-2000  
LOCUS 28222229.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:28222229 3',  
DEFINITION mRNA sequence.  
ACCESSION AW250976  
VERSION AW250976.1 GI:6594065  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other\_ESTs: 2822229.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross\_match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 11  
contiguous PHRED high quality bases followed by vector sequence. Very  
Low Quality Sequence: Trace file contained 15 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.

FEATURES  
source  
1..15  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2822229"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.2e+03;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1922 TTTTTCAG 1932  
|||||  
Db 3 TTTTTCAG 13

RESULT 3678  
AW246520  
LOCUS 2821787.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821787 3',  
DEFINITION mRNA sequence.  
ACCESSION AW246520  
VERSION AW246520.1 GI:6589513  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 18)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Other\_ESTs: 2821787.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross\_match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 16  
contiguous PHRED high quality bases followed by vector sequence. Very  
Low Quality Sequence: Trace file contained 18 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.

FEATURES  
source  
1..18  
Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821787"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site\_2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5e+03;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1772 TTTTTCAG 1782  
|||||  
Db 1 TTTTTCAG 11



RESULT 3679  
AZ328922/c  
LOCUS  
DEFINITION  
AZ328922  
1M0052L2R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0052L22 R, genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0052 row: L column: 22  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
FEATURES  
source  
1. .19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0052L22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.4%; Score 11; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 4.8e+03;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 19 AAGAAGAAAGTAGAAAAA 1

RESULT 3680

AW248934/c  
LOCUS  
DEFINITION  
AW248934  
2819262.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2819262 3',  
mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 19)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Other ESTs: 2819262.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
Project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center. Vector  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 8 contiguous  
PHRED high quality bases following vector sequence. Very Low  
Quality Sequence: Trace file contained 19 contiguous distinct peaks  
following vector sequence. Polyadenylation: Based upon the presence  
of a XhoI site followed by a run of 14 or more T residues at the  
beginning of the sequence, this cDNA insert was polyadenylated.  
Plate: LLCM1 row: C column: 7  
High quality sequence stop: 8.  
FEATURES  
source  
1. .19  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2819262"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5',  
adaptor: GGCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.4%; Score 11; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 4.8e+03;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAAAAAAAAAA 2803  
|||||  
Db 19 GAAAGTCCCAAAAAAAAAA 1

RESULT 3681

CF317946/c  
LOCUS  
DEFINITION  
CF317946  
HD--07-N06.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA  
library (HD) Oryza sativa cDNA clone HD--07-N06, mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
Oryza sativa

Query Match 0.4%; Score 11; DB 1; Length 19;  
Best Local Similarity 73.7%; Pred. No. 4.8e+03;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 19 AAGAAGAAAGTAGAAAAA 1

RESULT 3680



ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 20)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1..20  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="HD-07-N06"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli DH10B"  
/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match 0.4%; Score 11; DB 1; Length 20;  
Best Local Similarity 73.7%; Pred. No. 4.5e+03;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 432 CCTGTGACACGCGCGGCC 450  
||| | | | | | | | | | | | | | |  
Db 20 CGCTGCGCGCGCGCGGCC 2

RESULT 3682  
AZ512414/c  
LOCUS AZ512414 20 bp DNA linear GSS 05-OCT-2000  
DEFINITION IM0357J21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0357J21 R, genomic survey sequence.  
ACCESSION AZ512414  
VERSION AZ512414.1 GI:10693730  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0357 row: J column: 21

Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0357J21"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 11; DB 1; Length 20;  
Best Local Similarity 73.7%; Pred. No. 4.5e+03;  
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 471 CCTGGCCCGCGCGCCAG 489  
||| | | | | | | | | | | | | | |  
Db 19 CCGCGCCCGCGCGCCAG 1

RESULT 3683  
AZ331046/c  
LOCUS AZ331046 21 bp DNA linear GSS 29-SEP-2000  
DEFINITION IM0056K08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0056K08 R, genomic survey sequence.  
ACCESSION AZ331046  
VERSION AZ331046.1 GI:10393185  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 21)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0056 row: K column: 08  
Seq primer: CACACAGGAAACAGCTATGACC



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(Stratagene) and Superscript II RT (Life Technologies)."

Query Match      0.4%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 5.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2784 TGAAGAAAAA 2797
Db      14 TGTAAAAA 1

RESULT 3686
LOCUS      BQ588093
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            16 bp mRNA linear EST 06-DEC-2002
ACCESSION  E012336-024-009-A19-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
VERSION     024-009-A19 5-PRIME, mRNA sequence.
KEYWORDS    BQ588093
SOURCE      BQ588093.1 GI:26117675
            EST.
ORGANISM    Beta vulgaris
            Beta vulgaris
REFERENCE   1 (bases 1 to 16)
AUTHORS     Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
TITLE       Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL     Plant J. 32 (5), 845-857 (2002)
MEDLINE     22362189
PUBMED      12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaar@piz-koeln.mpg.de
            Insert length: 16 Std Error: 0.00
            Plate: 9 row: A column: 19
            Seq primer: SP6; CATACGATTAGGTGACACTATAG.
FEATURES    Location/Qualifiers
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                line)"
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                /db_xref="taxon:161934"
                /clone="024-009-A19"
                /tissue_type="leaf"
                /lab_host="EMDH10B"
                /clone_lib="MP1Z-ADIS-024-leaf"
                /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
            b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
            orientation:
            SP6-SalI-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Beet
            project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
            RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match      0.4%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 5.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1494 AGAAATGGAGAAA 1507
Db      1 AAAAAAGGAGAAA 14

(Stratagene) and Superscript II RT (Life Technologies)."

Query Match      0.4%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 5.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2784 TGAAGAAAAA 2797
Db      14 TGTAAAAA 1

RESULT 3686
LOCUS      BQ588093
DEFINITION E012336-024-009-A19-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
            16 bp mRNA linear EST 06-DEC-2002
ACCESSION  E012336-024-009-A19-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
VERSION     024-009-A19 5-PRIME, mRNA sequence.
KEYWORDS    BQ588093
SOURCE      BQ588093.1 GI:26117675
            EST.
ORGANISM    Beta vulgaris
            Beta vulgaris
REFERENCE   1 (bases 1 to 16)
AUTHORS     Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
TITLE       Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL     Plant J. 32 (5), 845-857 (2002)
MEDLINE     22362189
PUBMED      12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MP1Z
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaar@piz-koeln.mpg.de
            Insert length: 16 Std Error: 0.00
            Plate: 9 row: A column: 19
            Seq primer: SP6; CATACGATTAGGTGACACTATAG.
FEATURES    Location/Qualifiers
             1..16
                /organism="Beta vulgaris"
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                line)"
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                /db_xref="taxon:161934"
                /clone="024-009-A19"
                /tissue_type="leaf"
                /lab_host="EMDH10B"
                /clone_lib="MP1Z-ADIS-024-leaf"
                /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
            b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
            orientation:
            SP6-SalI-CCACGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Beet
            project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
            RZPD/GABI-Primary database:http://gabi.rzpd.de"

Query Match      0.4%; Score 10.8; DB 1; Length 16;
Best Local Similarity 85.7%; Pred. No. 5.4e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1494 AGAAATGGAGAAA 1507
Db      1 AAAAAAGGAGAAA 14
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RESULT 3687
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LOCUS      AW246451
DEFINITION 2821637.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821637 3',
            mRNA sequence.
ACCESSION  AW246451
VERSION     AW246451.1 GI:6589444
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Homo sapiens
REFERENCE   1 (bases 1 to 18)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Other ESTs: 2821637.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/FTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patWatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 9 contiguous
            PHRED high quality bases following vector sequence. Very Low
            Quality Sequence: Trace file contained 18 contiguous distinct peaks
            following vector sequence. Polyadenylation: Based upon the presence
            of a XhoI site followed by a run of 14 or more T residues at the
            beginning of the sequence, this cDNA insert was polyadenylated.
            Plate: L1CM7 row: F column: 6
            High quality sequence stop: 9.
FEATURES    Location/Qualifiers
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                /mol_type="mRNA"
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                /clone="IMAGE:2821637"
                /tissue_type="small cell carcinoma"
                /cell_line="MGC3"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH MGC 7"
                /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
            EcoRI; cDNA made by oligo-dT priming. Directionally
            cloned into EcoRI/XhoI sites using the following 5',
            adaptor: GGCACGAG(G). Size-selected >500bp for average
            insert size 1.8kb. Library constructed by Ling Hong in
            the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies)."
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Query Match      0.4%; Score 10.8; DB 1; Length 18;
Best Local Similarity 85.7%; Pred. No. 5e+03;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2784 TGAAGAAAAA 2797
Db      14 TGTAAAAA 1
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RESULT 3688
AZ803756/c
LOCUS      AZ803756
DEFINITION 2M0064M15F Mouse 10kb plasmid UUC1M library Mus musculus genomic
            clone UUGC2M0064M15 F, genomic survey sequence.
ACCESSION  AZ803756
VERSION     AZ803756.1 GI:12956079
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KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source  
QY  
Db  
RESULT 3689  
AZ786308  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0064 row: M column: 15  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.4%; Score 10.8; DB 1; Length 19;  
Best Local Similarity 85.7%; Pred. No. 4.8e+03;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2026 GGTAGGAGGCAAG 2039  
||| |||||  
Db 15 GGAACGAGGCAAG 2

RESULT 3689  
AZ786308  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS

AZ786308  
2M0031B17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0031B17 R, genomic survey sequence.  
AZ786308  
AZ786308.1 GI:12923936  
GSS.

SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source  
QY  
Db  
RESULT 3690  
AZ595570  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0031 row: B column: 17  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
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/clone="UUGC2M0031B17"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.4%; Score 10.8; DB 1; Length 19;  
Best Local Similarity 85.7%; Pred. No. 4.8e+03;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 110 GGGGGCTGGGGGA 123  
||| |||||  
Db 6 GGGAGGTGGGGGA 19

RESULT 3690  
AZ595570  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE

AZ595570  
1M0408115F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0408115 F, genomic survey sequence.  
AZ595570  
AZ595570.1 GI:11717760  
GSS.  
Mus musculus (house mouse)



```

ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE     1 (bases 1 to 19)
AUTHORS       Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE         Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL       Unpublished (2000)
COMMENT       Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0408 row: I column: 15
              Seq primer: CGTGTAAACGACGGCCAGT
              Class: plasmid ends
              High quality sequence stop: 19.
FEATURES             Location/Qualifiers
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     /mol_type="genomic DNA"
     /strain="C57BL/6J"
     /db_xref="taxon:10090"
     /clone="UUGC1M0408I15"
     /sex="Male"
     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
     /clone_lib="Mouse 10kb plasmid UUGC1M library"
     /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
     Query Match      0.4%; Score 10.8; DB 1; Length 19;
     Best Local Similarity 85.7%; Pred. No. 4.8e+03;
     Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1710 ATCTCCTAACTTTG 1723
      |||||
Db       3 AGTCCAAACTTTG 16

RESULT 3691
AU257221/c
LOCUS
DEFINITION AU257221 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0010046 3', mRNA sequence.
ACCESSION AU257221
VERSION AU257221.1 GI:20321628
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

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/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 10.8; DB 1; Length 20;  
Best Local Similarity 85.7%; Pred. No. 4.5e+03;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2782 ATTGAAAAAATA 2795  
||| |||||  
Db 5 ATTAATAATA 18

RESULT 3693  
AZ629111/c  
LOCUS  
DEFINITION  
1M0481D22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0481D22 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 21)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0481 row: D column: 22  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.

Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0481 row: D column: 22  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 21.

Location/Qualifiers  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0481D22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 10.8; DB 1; Length 21;  
Best Local Similarity 85.7%; Pred. No. 4.3e+03;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1854 ACAGACCCACAC 1867  
||| |||||  
Db 15 ACACACACACAC 2

RESULT 3694  
BH791022  
LOCUS  
DEFINITION  
SALK 058381.35.95.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK\_058381.35.95.x, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 25)  
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.  
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
Unpublished (2001)  
Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGnAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At4g36950.  
Class: TDNA tagged.

Location/Qualifiers  
1. .25  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_058381.35.95.x"  
/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at

Location/Qualifiers  
1. .25  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"  
/clone="SALK\_058381.35.95.x"  
/note="PCR was performed on Arabidopsis thaliana TDNA insertion lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)

Query Match 0.4%; Score 10.8; DB 1; Length 25;  
Best Local Similarity 85.7%; Pred. No. 3.6e+03;  
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1825 AGAATCTTTTAAAT 1838  
|||||  
Db 10 AGAATATTTTAAAT 23

RESULT 3695  
AA878744  
LOCUS  
DEFINITION  
of85a08.s1 NCI CGAP\_Li5 Homo sapiens cDNA clone IMAGE:1437110 3'  
similar to TR:Q67633 Q67633 ECO Q PROTEIN. [1]; contains TAR1.t2  
TAR1 repetitive element ; mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
unknown library type  
Trace considered overall poor quality  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

FEATURES  
source  
1..19  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1437110"  
/tissue\_type="hepatic adenoma"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP\_Li5"  
/note="Organ: liver; Vector: pCMV-SPORT4; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 0.8 kb."

Query Match 0.4%; Score 10.6; DB 1; Length 19;  
Best Local Similarity 76.5%; Pred. No. 4.8e+03;  
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1660 TCTGCATCACCCGCCCC 1676  
|||||  
Db 2 TCTGCCCCCGCCCGCC 18

RESULT 3696  
AZ782026/c  
LOCUS  
DEFINITION  
2M0021I23R Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
clone UUGC2M002I123 R, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)

REFERENCE  
AUTHORS  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

TITLE  
JOURNAL  
COMMENT

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausen,A. and Wright,D., Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0021 row: I column: 23  
Seq primer: CACACAGGAACACGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 19.  
Location/Qualifiers

FEATURES  
source  
1..19  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M002I123"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCLM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.4%; Score 10.6; DB 1; Length 19;  
Best Local Similarity 76.5%; Pred. No. 4.8e+03;  
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 618 CCCACGCACACGCCCTG 634  
|||||  
Db 19 CCCACCCGCACCTCTG 3

RESULT 3697  
AZ828826

LOCUS  
DEFINITION  
AZ828826 2M0106O01F Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
clone UUGC2M0106O01 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Mus musculus (house mouse)

REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von



TITLE  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0106 row: 0 column: 01  
Seq primer: CGTTGTAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source

1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0106001"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 10.6; DB 1; Length 20;  
Best Local Similarity 76.5%; Pred. No. 4.5e+03;  
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1913 AACAAATACCTTTT 1929  
||| ||||| |||||  
Db 1 AATAATACCATTTAT 17

RESULT 3698  
AZ387816  
LOCUS  
DEFINITION  
IM0147B22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0147B22 R, genomic survey sequence.  
ACCESSION  
AZ387816  
VERSION  
GSS.  
KEYWORDS  
Mus musculus (house mouse)  
SOURCE  
Mus musculus  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0147 row: B column: 22  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
source

1. .20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0147B22"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.4%; Score 10.6; DB 1; Length 20;  
Best Local Similarity 76.5%; Pred. No. 4.5e+03;  
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1784 ACCCCATTCTTCTTC 1800  
||| ||||| |||||  
Db 4 ACTCCATTCTCTCTCC 20

RESULT 3699  
BQ591425/c  
LOCUS  
DEFINITION  
E012712-024-017-C11-T7 MP1Z-ADIS-024-storage root Beta vulgaris  
cDNA clone 024-017-C11 3-PRIME, mRNA sequence.  
ACCESSION  
BQ591425  
VERSION  
BQ591425.1 GI:26121008  
KEYWORDS  
EST.  
SOURCE  
Beta vulgaris  
ORGANISM  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
REFERENCE  
1 (bases 1 to 16)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
TITLE  
Construction of a 'unigene' cDNA clone set by oligonucleotide

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698

Contact: Weisshaar B  
ADIS DNA core facility at MPiZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 16 Std Error: 0.00  
Plate: 17 row: C column: 11  
Seq primer: T7; GTAATACGACTCACTATAGGGC.

FEATURES  
source

1. .16  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:188698"  
/db\_xref="taxon:161934"  
/clone="024-017-C11"  
/tissue\_type="storage root"  
/lab\_host="EMDH10B"  
/clone\_lib="MPiZ-ADIS-024-storage root"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; CDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:  
SP6-Sali-CCACGGTCCG-5prime-CDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

Query Match 0.4%; Score 10.4; DB 1; Length 16;  
Best Local Similarity 91.7%; Pred. No. 5.5e+03;  
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2467 TTTTAAATATTAA 2478  
|||||  
Db 14 TTTTAAATAGTAA 3

Search completed: June 10, 2004, 13:03:18  
Job time : 93 secs





Db 16 GAAAAAAAAA 5

RESULT 3696

US-10-362-262-2/c  
; Sequence 2, Application US/10362262  
; Publication No. US20040014636A1  
; GENERAL INFORMATION:  
; APPLICANT: Brodin et al.  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING A MODULATOR OF ADAMTS-1  
; FILE REFERENCE: ASZD-P01-138  
; CURRENT APPLICATION NUMBER: US/10/362,262  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: PCT/GB01/03650  
; PRIOR FILING DATE: 2001-08-16  
; PRIOR APPLICATION NUMBER: SE 0002973-6  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:PCR primer  
US-10-362-262-2

Query Match 0.4%; Score 12; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAA 2796  
Db 16 GAAAAAAAAA 5

RESULT 3697

US-10-362-607-4/c  
; Sequence 4, Application US/10362607  
; Publication No. US20040096842A1  
; GENERAL INFORMATION:  
; APPLICANT: Brodin , Peter  
; APPLICANT: Thelin, Anders Lars  
; TITLE OF INVENTION: MOLECULES INVOLVED IN THE REGULATION OF  
; TITLE OF INVENTION: INSULIN RESISTANCE SYNDROME (IRS)  
; FILE REFERENCE: 06275-339US1  
; CURRENT APPLICATION NUMBER: US/10/362,607  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: PCT/GB01/03828  
; PRIOR FILING DATE: 2001-08-23  
; PRIOR APPLICATION NUMBER: US 60/228,117  
; PRIOR FILING DATE: 2000-08-28  
; PRIOR APPLICATION NUMBER: US 60/282,496  
; PRIOR FILING DATE: 2000-04-10  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: H-T11-C primer  
US-10-362-607-4

Query Match 0.4%; Score 12; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAA 2796  
Db 16 GAAAAAAAAA 5

RESULT 3698

US-10-432-803-4/c  
; Sequence 4, Application US/10432803  
; Publication No. US20040029199A1  
; GENERAL INFORMATION:  
; APPLICANT: KIM, Jin Woo  
; TITLE OF INVENTION: HUMAN CERVICAL CANCER 2 PROTOONCOGENE AND PROTEIN ENCODED THEREIN  
; FILE REFERENCE: KJW-0613  
; CURRENT APPLICATION NUMBER: US/10/432,803  
; CURRENT FILING DATE: 2003-05-23  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: KOPATIN 1.5  
; SEQ ID NO 4  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: H-T11G anchored oligo-dT primer  
US-10-432-803-4

Query Match 0.4%; Score 12; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAA 2797  
Db 15 AAAAAAAAAA 4

RESULT 3699

US-10-338-777-262/c  
; Sequence 262, Application US/10338777  
; Publication No. US20030188343A1  
; GENERAL INFORMATION:  
; APPLICANT: Lynx Therapeutics, Inc.  
; APPLICANT: United States Department of Agriculture  
; APPLICANT: Bowen, Benjamin A  
; APPLICANT: Haudenschild, Christian D  
; APPLICANT: Buckler, Edward S  
; TITLE OF INVENTION: Identification of Genes Associated with Growth in Plants  
; FILE REFERENCE: 37-000510US  
; CURRENT APPLICATION NUMBER: US/10/338,777  
; CURRENT FILING DATE: 2003-01-07  
; NUMBER OF SEQ ID NOS: 405  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 262  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-338-777-262

Query Match 0.4%; Score 12; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAA 2797  
Db 17 AAAAAAAAAA 6

Search completed: June 10, 2004, 12:49:50  
Job time : 100 secs

schultz782-3.rnpb

Thu Jun 10 13:10:21 2004

US-10-291-808-84/c  
; Sequence 84, Application US/10291808  
; Publication No. US20030224382A1  
; GENERAL INFORMATION:  
; APPLICANT: McClelland, Michael  
; APPLICANT: Welsh, John  
; APPLICANT: Trenkle, Thomas  
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of  
; TITLE OF INVENTION: Using Same  
; FILE REFERENCE: P-PH 3457  
; CURRENT APPLICATION NUMBER: US/10/291,808  
; CURRENT FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US/09/300,958  
; PRIOR FILING DATE: 1999-04-27  
; PRIOR APPLICATION NUMBER: 60/083,331  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/098,070  
; PRIOR FILING DATE: 1998-08-27  
; PRIOR APPLICATION NUMBER: 60/118,624  
; PRIOR FILING DATE: 1999-02-04  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-10-291-808-84

Query Match 0.4%; Score 12; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAA 2796  
|||  
Db 16 GAAAAAAAAAAAAA 5

RESULT 3695  
US-10-431-304-17/c  
; Sequence 17, Application US/10431304  
; Publication No. US20030182690A1  
; GENERAL INFORMATION:  
; APPLICANT: Clendennen, Stephanie K.  
; APPLICANT: Kellogg, Jill A.  
; APPLICANT: Phan, Chau B.  
; APPLICANT: Mathews, Helena V.  
; APPLICANT: Webb, Nancy M.  
; TITLE OF INVENTION: Banana and Melon Promoters for  
; TITLE OF INVENTION: Expression of Transgenes in Plants  
; FILE REFERENCE: 4257-0019.30  
; CURRENT APPLICATION NUMBER: US/10/431,304  
; CURRENT FILING DATE: 2003-05-06  
; PRIOR APPLICATION NUMBER: US/09/527,972  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/125,310  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide primer  
US-10-431-304-17

Query Match 0.4%; Score 12; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAA 2796

US-10-432-803-5/c  
; Sequence 5, Application US/10432803  
; Publication No. US20040029199A1  
; GENERAL INFORMATION:  
; APPLICANT: KIM, Jin Woo  
; TITLE OF INVENTION: HUMAN CERVICAL CANCER 2 PROTOONCOGENE AND PROTEIN ENCODED THEREIN  
; FILE REFERENCE: KJW-0613  
; CURRENT APPLICATION NUMBER: US/10/432,803  
; CURRENT FILING DATE: 2003-05-23  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: KOPATIN 1.5  
; SEQ ID NO 5  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: H-T11C anchored oligo-dT primer  
US-10-432-803-5

Query Match 0.4%; Score 12; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAA 2796  
|||  
Db 16 GAAAAAAAAAAAAA 5

RESULT 3693  
US-10-291-808-58/c  
; Sequence 58, Application US/10291808  
; Publication No. US20030224382A1  
; GENERAL INFORMATION:  
; APPLICANT: McClelland, Michael  
; APPLICANT: Welsh, John  
; APPLICANT: Trenkle, Thomas  
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of  
; TITLE OF INVENTION: Using Same  
; FILE REFERENCE: P-PH 3457  
; CURRENT APPLICATION NUMBER: US/10/291,808  
; CURRENT FILING DATE: 2002-11-07  
; PRIOR APPLICATION NUMBER: US/09/300,958  
; PRIOR FILING DATE: 1999-04-27  
; PRIOR APPLICATION NUMBER: 60/083,331  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/098,070  
; PRIOR FILING DATE: 1998-08-27  
; PRIOR APPLICATION NUMBER: 60/118,624  
; PRIOR FILING DATE: 1999-02-04  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 58  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-10-291-808-58

Query Match 0.4%; Score 12; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAA 2796  
|||  
Db 16 GAAAAAAAAAAAAA 5

RESULT 3694

RESULT 3688  
US-09-924-946-8/c  
; Sequence 8, Application US/09924946  
; Patent No. US20020102645A1  
; GENERAL INFORMATION:  
; APPLICANT: American Home Products Corporation  
; APPLICANT: Evans, Mark  
; APPLICANT: Scicchitano, Marshall  
; APPLICANT: Bapat, Ashok  
; APPLICANT: Beer, Eric  
; APPLICANT: Bhat, Ramesh  
; APPLICANT: Ferris, Elissa  
; APPLICANT: Mastroeni, Rob  
; APPLICANT: Zhang, Jianxiong  
; APPLICANT: Karathanasis, Sotirios K.  
; TITLE OF INVENTION: A No. US20020102645A1 Member of the Lysyl Oxidase Gene Family  
; FILE REFERENCE: 0630/1G703-US2  
; CURRENT APPLICATION NUMBER: US/09/924,946  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: 60/223,763  
; PRIOR FILING DATE: 2000-08-08  
; PRIOR APPLICATION NUMBER: 60/255,838  
; PRIOR FILING DATE: 2000-12-15  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-924-946-8

Query Match 0.4%; Score 12; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAA 2796  
Db 15 GAAAAAAAAA 4

RESULT 3689  
US-09-811-093-22/c  
; Sequence 22, Application US/09811093  
; Patent No. US20020133850A1  
; GENERAL INFORMATION:  
; APPLICANT: Clendennen, Stephanie K.  
; APPLICANT: Kellogg, Jill A.  
; TITLE OF INVENTION: MELON PROMOTERS FOR EXPRESSION OF  
; FILE REFERENCE: 4257-0025.30  
; CURRENT APPLICATION NUMBER: US/09/811,093  
; CURRENT FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: US 60/190,414  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer  
US-09-811-093-22

Query Match 0.4%; Score 12; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAA 2796

Db 16 GAAAAAAAAA 5  
RESULT 3690  
US-09-997-672-31/c  
; Sequence 31, Application US/09997672  
; Publication No. US20030061632A1  
; GENERAL INFORMATION:  
; APPLICANT: Weterings, Koen  
; APPLICANT: Apuya, Nestor R.  
; APPLICANT: Tatarinova, Tatiana  
; APPLICANT: Goldberg, Robert B.  
; APPLICANT: The Regents of the University of California  
; APPLICANT: Ceres, Inc.  
; TITLE OF INVENTION: Polynucleotides Useful for Modulating Transcription  
; FILE REFERENCE: 023070-115810US  
; CURRENT APPLICATION NUMBER: US/09/997,672  
; CURRENT FILING DATE: 2001-11-28  
; PRIOR APPLICATION NUMBER: US 60/253,672  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: anchor/reverse  
; OTHER INFORMATION: primer C primer  
US-09-997-672-31

Query Match 0.4%; Score 12; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAA 2796  
Db 16, GAAAAAAAAA 5

RESULT 3691  
US-10-362-711-8/c  
; Sequence 8, Application US/10362711  
; Publication No. US20040029141A1  
; GENERAL INFORMATION:  
; APPLICANT: Brodin, Peter  
; APPLICANT: Thelin, Anders Lars  
; TITLE OF INVENTION: HUMAN AND MOUSE E2-PROTEIN, NUCLEIC  
; FILE REFERENCE: 06275-340US1  
; CURRENT APPLICATION NUMBER: US/10/362,711  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: PCT/GB01/03807  
; PRIOR FILING DATE: 2001-08-23  
; PRIOR APPLICATION NUMBER: US 60/228,118  
; PRIOR FILING DATE: 2000-08-28  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: H-T11-C primer  
US-10-362-711-8

Query Match 0.4%; Score 12; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAA 2796

EXT GENE FAMILY AND DIAGNOSTIC AND THERAPEUTIC USES  
THEREOF  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/809,920  
FILING DATE: 16-Mar-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/156,191  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/51902  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 35:  
US-09-809-920-35  
Query Match 0.4%; Score 12.2; DB 1; Length 22;  
Best Local Similarity 82.4%; Pred. No. 4.3e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 790 CTGTCAGAAGGAGCTGG 806  
Db 5 CTGTCAGTATTAGCTGG 21  
RESULT 3686  
US-10-127-890-58  
Sequence 58, Application US/10127890  
Publication No. US20030166196A1  
GENERAL INFORMATION:  
APPLICANT: Better, Marc D.  
Carroll, Stephen F.  
Studnika, Gary M.  
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins  
NUMBER OF SEQUENCES: 173  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAndrews, Held & Malloy, Ltd.  
STREET: 500 West Madison Street, 34th floor  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60661  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/127,890

FILING DATE: 23-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/646,360  
FILING DATE: 13-MAY-1996  
APPLICATION NUMBER: PCT/US94/05348  
FILING DATE: 12-MAY-1994  
APPLICATION NUMBER: US 08/064,691  
FILING DATE: 12-MAY-1993  
APPLICATION NUMBER: US 07/988,430  
FILING DATE: 09-DEC-1992  
APPLICATION NUMBER: US 07/901,707  
FILING DATE: 19-JUN-1992  
APPLICATION NUMBER: US 07/787,567  
FILING DATE: 04-NOV-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: McNicholas, Janet M.  
REGISTRATION NUMBER: 32,918  
REFERENCE/DOCKET NUMBER: 200-70.P4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/707-8889  
TELEFAX: 312/707-9155  
TELEX: 650 388-1248  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 58:  
US-10-127-890-58  
Query Match 0.4%; Score 12.2; DB 1; Length 22;  
Best Local Similarity 82.4%; Pred. No. 4.3e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2452 AGACATGGGATCCCAATT 2468  
Db 2 AGCCATGGAATCCCAATT 18  
RESULT 3687  
US-09-964-261-301  
Sequence 301, Application US/09964261  
Publication No. US20020197613A1  
GENERAL INFORMATION:  
APPLICANT: De Canck, Ilse  
APPLICANT: Rombout, Annelles  
APPLICANT: Rossau, Rudi  
TITLE OF INVENTION: METHOD FOR THE AMPLIFICATION OF HLA CLASS I ALLELES  
FILE REFERENCE: IGJ-002  
CURRENT APPLICATION NUMBER: US/09/964,261  
PRIOR FILING DATE: 2001-09-25  
PRIOR APPLICATION NUMBER: EP 99870068.6  
PRIOR FILING DATE: 1999-04-09  
PRIOR APPLICATION NUMBER: US 60/138,614  
PRIOR FILING DATE: 1999-06-11  
NUMBER OF SEQ ID NOS: 446  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 301  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-964-261-301  
Query Match 0.4%; Score 12.2; DB 1; Length 23;  
Best Local Similarity 66.7%; Pred. No. 4.2e+03;  
Matches 14; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 959 GTTCTCAGAAGAGCCAAATCG 979  
Db 1 RTTCTCAGGATRGTCACATGG 21



; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: mouse origin  
US-10-056-790-67

Query Match 0.4%; Score 12.2; DB 1; Length 20;  
Best Local Similarity 82.4%; Pred. No. 4.2e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1036 GGCCGGGAGGCGGAAAG 1052  
||| ||||| |||||  
Db 4 GGAAGGAGGCTGAAAG 20

RESULT 3681  
US-10-728-509-34/c  
; Sequence 34, Application US/10728509  
; Publication No. US20040077583A1  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION  
; FILE REFERENCE: RTS-0185  
; CURRENT APPLICATION NUMBER: US/10/728,509  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: US/09/908,147  
; PRIOR FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 168  
; SEQ ID NO 34  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-728-509-34

Query Match 0.4%; Score 12.2; DB 1; Length 20;  
Best Local Similarity 82.4%; Pred. No. 4.2e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1920 CCTTTTTCAGTGTT 1936  
||||| ||||| |||  
Db 18 CCTTTGCTTCAGGGTT 2

RESULT 3682  
US-10-728-509-35/c  
; Sequence 35, Application US/10728509  
; Publication No. US20040077583A1  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION  
; FILE REFERENCE: RTS-0185  
; CURRENT APPLICATION NUMBER: US/10/728,509  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: US/09/908,147  
; PRIOR FILING DATE: 2001-07-17  
; NUMBER OF SEQ ID NOS: 168  
; SEQ ID NO 35  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-728-509-35

Query Match 0.4%; Score 12.2; DB 1; Length 20;  
Best Local Similarity 82.4%; Pred. No. 4.2e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1920 CCTTTTTCAGTGTT 1936  
||||| ||||| |||

Db 19 CCTTTTGCTTCAGGGTT 3

RESULT 3683  
US-10-303-635-44/c  
; Sequence 44, Application US/10303635  
; Publication No. US20040102621A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX C2 EXPRESSION  
; FILE REFERENCE: RTS-0418  
; CURRENT APPLICATION NUMBER: US/10/303,635  
; CURRENT FILING DATE: 2002-11-21  
; NUMBER OF SEQ ID NOS: 257  
; SEQ ID NO 44  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-303-635-44

Query Match 0.4%; Score 12.2; DB 1; Length 20;  
Best Local Similarity 82.4%; Pred. No. 4.2e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 500 GCGGGGCTGCCCTCGCA 516  
||| ||||| ||||| |||||  
Db 17 GCAGGGCAGCCCGCGCA 1

RESULT 3684  
US-10-227-001-16  
; Sequence 16, Application US/10227001  
; Publication No. US20030113765A1  
; GENERAL INFORMATION:  
; APPLICANT: Dempcy, Robert O.  
; APPLICANT: Afonina, Irina Aleksandrovna  
; APPLICANT: Vermeulen, Nicolaas M.J.  
; APPLICANT: Epoch Biosciences, Inc.  
; TITLE OF INVENTION: Hybridization-Triggered Fluorescent  
; TITLE OF INVENTION: Detection of Nucleic Acids  
; FILE REFERENCE: 17682A-004210US  
; CURRENT APPLICATION NUMBER: US/10/227,001  
; CURRENT FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: US 09/428,236  
; PRIOR FILING DATE: 1999-10-26  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: mismatched target sequence  
US-10-227-001-16

Query Match 0.4%; Score 12.2; DB 1; Length 21;  
Best Local Similarity 82.4%; Pred. No. 4.3e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2157 TTTTCTCCTTTTCTTTT 2173  
||| ||||| ||||| |||||  
Db 1 TCTTCTCCTTTTCTTTT 17

RESULT 3685  
US-09-809-920-35  
; Sequence 35, Application US/09809920  
; Publication No. US20030139584A1  
; GENERAL INFORMATION:  
; APPLICANT: Sato, Takaaki  
; TITLE OF INVENTION: TREX, A NOVEL GENE OF TRAF-INTERACTING

```

; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 228
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-949-428-228

Query Match      0.4%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      683 CAGATGGACGAGGTGCA 699
Db      20 CAAATGGAAGAAGTGCA 4

RESULT 3677
US-09-824-322B-54/c
; Sequence 54, Application US/09824322B
; Publication No. US20030022848A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-ALPHA
; TITLE OF INVENTION: ALPHA) EXPRESSION
; FILE REFERENCE: ISPH-0501
; CURRENT APPLICATION NUMBER: US/09/824,322B
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 09/313,932
; PRIOR FILING DATE: 1999-05-18
; PRIOR APPLICATION NUMBER: US 09/166,186
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 503
; SEQ ID NO 54
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-824-322B-54

Query Match      0.4%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1494 AGAAATGGAGAAACAC 1510
Db      18 AAAACATGGAGAAAGAC 2

RESULT 3678
US-09-908-147-34/c
; Sequence 34, Application US/09908147
; Publication No. US2003014221A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/09/908,147
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
```

```

US-09-908-147-34

Query Match      0.4%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1920 CCTTTTTCAGTGTT 1936
Db      18 CCTTTTCAGTGTT 2

RESULT 3679
US-09-908-147-35/c
; Sequence 35, Application US/09908147
; Publication No. US20030144221A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/09/908,147
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-908-147-35

Query Match      0.4%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1920 CCTTTTTCAGTGTT 1936
Db      19 CCTTTTCAGTGTT 3

RESULT 3680
US-10-056-790-67
; Sequence 67, Application US/10056790
; Publication No. US20030165497A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: RRP SEQUENCES AND KNOCKOUT MICE AND USES THEREOF
; FILE REFERENCE: RRP2002
; CURRENT APPLICATION NUMBER: US/10/056,790
; CURRENT FILING DATE: 2002-01-23
; PRIOR APPLICATION NUMBER: US 09/908,419
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/219,289
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 60/277,487
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/277,471
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/304,863
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/305,017
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/328,491
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
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; SEQ ID NO 15
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide
US-10-265-689-15

Query Match      0.4%; Score 12.2; DB 1; Length 19;
Best Local Similarity 82.4%; Pred. No. 4.1e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1787 CCATTCTTTCCTTCTCT 1803
Db 19 CCCTCCTTCCTTCTCT 3

RESULT 3673
US-10-023-782A-24
; Sequence 24, Application US/10023782A
; Publication No. US20030147863A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF TFAP2C EXPRESSION
; FILE REFERENCE: RTS-0343
; CURRENT APPLICATION NUMBER: US/10/023,782A
; CURRENT FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 24
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-023-782A-24

Query Match      0.4%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 59 GCGCGCGCGCAGCGCCT 75
Db 1 GCGCGCGCGCTACGCTT 17

RESULT 3674
US-10-349-143-5201
; Sequence 5201, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5201
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
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; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-22490 for SEQ 1267,
US-10-349-143-5201

Query Match      0.4%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1626 TACCTACCTTACTATT 1642
Db 2 TTCCTTCCTTCCTATT 18

RESULT 3675
US-09-949-427-228/c
; Sequence 228, Application US/09949427
; Publication No. US20030054418A1
; GENERAL INFORMATION:
; APPLICANT: Bodnar, Jackie S.
; APPLICANT: Castellani, Lawrence W.
; APPLICANT: Chatterjee, Aurobindo
; APPLICANT: de Jong, Pieter
; APPLICANT: Lusi, Aldons J.
; APPLICANT: Ohmen, Jeff
; APPLICANT: Ross, David
; APPLICANT: Tafuri, Sherrie
; APPLICANT: Wu, Chenyan
; TITLE OF INVENTION: Gene and Sequence Variation Associated with Cancer
; FILE REFERENCE: 02810.0014.NPUS02
; CURRENT APPLICATION NUMBER: US/09/949,427
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/231,322
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 228
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-949-427-228

Query Match      0.4%; Score 12.2; DB 1; Length 20;
Best Local Similarity 82.4%; Pred. No. 4.2e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 683 CAGATGACGAGGTGCA 699
Db 20 CAATGGAAGAAGTGCA 4

RESULT 3676
US-09-949-428-228/c
; Sequence 228, Application US/09949428
; Publication No. US20030064372A1
; GENERAL INFORMATION:
; APPLICANT: Bodnar, Jackie S.
; APPLICANT: Castellani, Lawrence W.
; APPLICANT: Chatterjee, Aurobindo
; APPLICANT: de Jong, Pieter
; APPLICANT: Lusi, Aldons J.
; APPLICANT: Ohmen, Jeff
; APPLICANT: Ross, David
; APPLICANT: Tafuri, Sherrie
; APPLICANT: Wu, Chenyan
; TITLE OF INVENTION: Gene and Sequence Variation Associated with Lipid Disorder
; FILE REFERENCE: 02810.0014.NPUS01
; CURRENT APPLICATION NUMBER: US/09/949,428
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/231,322
; PRIOR FILING DATE: 2000-09-08
```

```

; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 0163-0758-OX
; CURRENT APPLICATION NUMBER: US/10/683,386
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US/09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-47
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Query Match 0.4%; Score 12.2; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1979 AAAAAAGAAAAGTGTG 1995
    ||||| |||||
Db 1 AAAAAAGAAAAGGGG 17
```

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RESULT 3670
US-10-209-608-43/c
; Sequence 43, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 19953USOXDIV
; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/725,265
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-43
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Query Match 0.4%; Score 12.2; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 4e+03;

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Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1979 AAAAAAGAAAAGTGTG 1995
    ||||| |||||
Db 18 AAAAAAGAAAAGGGG 2

RESULT 3671
US-10-209-608-47
; Sequence 47, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 19953USOXDIV
; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/725,265
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-47
```

Query Match 0.4%; Score 12.2; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 4e+03;  
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1979 AAAAAAGAAAAGTGTG 1995
    ||||| |||||
Db 1 AAAAAAGAAAAGGGG 17
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RESULT 3672
US-10-265-689-15/c
; Sequence 15, Application US/10265689
; Publication No. US20030119775A1
; GENERAL INFORMATION:
; APPLICANT: SURWIT, RICHARD S.
; APPLICANT: COLLINS, SHEILA A.
; APPLICANT: WARDEN, CRAIG H.
; APPLICANT: SELDIN, MICHAEL F.
; APPLICANT: RICQUIER, DANIEL
; APPLICANT: BOULLAUD, FREDERIC
; TITLE OF INVENTION: RESPIRATION UNCOUPLING PROTEIN
; FILE REFERENCE: 1579-376
; CURRENT APPLICATION NUMBER: US/10/265,689
; CURRENT FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: US/09/353,645
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: PCT/US97/06864
; PRIOR FILING DATE: 1997-04-22
; PRIOR APPLICATION NUMBER: 60/034,960
; PRIOR FILING DATE: 1997-01-15
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
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; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1448
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-1448

Query Match      0.4%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAA 2802
      ||||| | | | | |
Db      1 AAAAAAACUAGAAAAA 17

RESULT 3661
US-09-745-237A-284
; Sequence 284, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 284
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-284

Query Match      0.4%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAA 2802
      ||||| | | | | |
Db      1 AAAAAAACUAGAAAAA 17

RESULT 3662
US-09-745-237A-959
; Sequence 959, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 959
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-959

Query Match      0.4%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAA 2802
      ||||| | | | | |
Db      1 AAAAAAACUAGAAAAA 17

RESULT 3663
US-09-745-237A-1448
; Sequence 1448, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1448
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1448

Query Match      0.4%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAA 2802
      ||||| | | | | |
Db      1 AAAAAAACUAGAAAAA 17

RESULT 3664
US-10-238-700-3359/c
; Sequence 3359, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Levels
; FILE REFERENCE: 400/057 (MBHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3359
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-3359

Query Match      0.4%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1544 GAGTAGGGAAGGAACAG 1560
      |||| | | | | | |
Db      17 GAGTGGGGCAGAGCAG 1

RESULT 3665
US-10-138-674-1080
; Sequence 1080, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
```

```

QY      2786 AAAAAAAAAAAAAAAAAA 2802
      ||||| | | | | |
Db      1 AAAAAAACUAGAAAAA 17

RESULT 3663
US-09-745-237A-1448
; Sequence 1448, Application US/09745237A
; Publication No. US20030143708A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: 400/007 (MBHB00-918-A)
; CURRENT APPLICATION NUMBER: US/09/745,237A
; CURRENT FILING DATE: 2002-04-15
; NUMBER OF SEQ ID NOS: 4550
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1448
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-745-237A-1448

Query Match      0.4%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAA 2802
      ||||| | | | | |
Db      1 AAAAAAACUAGAAAAA 17

RESULT 3664
US-10-238-700-3359/c
; Sequence 3359, Application US/10238700
; Publication No. US20030153521A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Levels
; FILE REFERENCE: 400/057 (MBHB01-1158-A)
; CURRENT APPLICATION NUMBER: US/10/238,700
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: PCT/US 02/16840
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: US 60/318,471
; PRIOR FILING DATE: 2001-09-10
; NUMBER OF SEQ ID NOS: 4666
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3359
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-238-700-3359

Query Match      0.4%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1544 GAGTAGGGAAGGAACAG 1560
      |||| | | | | | |
Db      17 GAGTGGGGCAGAGCAG 1

RESULT 3665
US-10-138-674-1080
; Sequence 1080, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
```

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-144-140-14

Query Match      0.4%; Score 12.4; DB 1; Length 20;
Best Local Similarity 92.9%; Pred. No. 4.1e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 360 AGCAGCTGGCCTAC 373
Db 14 AGCAGCTGGCCTGC 1

RESULT 3656
US-09-780-533A-237
; Sequence 237, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 237
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-237

Query Match      0.4%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802
Db 1 AAAAAAUAGAGAAAAA 17

RESULT 3657
US-09-780-533A-2172
; Sequence 2172, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2172
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2172

Query Match      0.4%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802
Db 1 AAAAAAUAGAGAAAAA 17

RESULT 3658
US-09-930-423-284
; Sequence 284, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 284
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-284

Query Match      0.4%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802
Db 1 AAAAAACUAGAAAAAA 17

RESULT 3659
US-09-930-423-959
; Sequence 959, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 959
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-959

Query Match      0.4%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802
Db 1 AAAAAACUAGAAAAAA 17

RESULT 3660
US-09-930-423-1448
; Sequence 1448, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
```

```

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802
Db 1 AAAAAAAAUAGAGAA 17

RESULT 3658
US-09-930-423-284
; Sequence 284, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 284
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-284

Query Match      0.4%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802
Db 1 AAAAAACUAGAAAAAA 17

RESULT 3659
US-09-930-423-959
; Sequence 959, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
; FILE REFERENCE: MBHB00,918-A 400/027
; CURRENT APPLICATION NUMBER: US/09/930,423
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 4553
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 959
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo Sapiens
US-09-930-423-959

Query Match      0.4%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2802
Db 1 AAAAAACUAGAAAAAA 17

RESULT 3660
US-09-930-423-1448
; Sequence 1448, Application US/09930423
; Publication No. US20030092003A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
```

; APPLICANT: Fundytus, Marian E

TYPE: DNA



```

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 102
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-257-294-102

Query Match      0.4%; Score 12.6; DB 1; Length 21;
Best Local Similarity 78.9%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db      21 AAATAAATAAATAATAAA 3

RESULT 3647
US-10-344-093A-33/c
; Sequence 33, Application US/10344093A
; Publication No. US20040076969A1
; GENERAL INFORMATION:
; APPLICANT: CAILLOUX, Fabrice
; APPLICANT: GOBRON, Stephane
; TITLE OF INVENTION: Method for detecting known mutations in tube
; FILE REFERENCE: D19019 - 344 339
; CURRENT APPLICATION NUMBER: US/10/344,093A
; PRIOR FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: PCT/FR 01/02 574
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: FR 00/104 25
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Primer for the detection of the mutations associated
; OTHER INFORMATION: with mucoviscidosis.
US-10-344-093A-33

Query Match      0.4%; Score 12.6; DB 1; Length 24;
Best Local Similarity 78.9%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2785 GAAAAAAAAAAAAAAAAAAAAA 2803
Db      24 GCAAAAAGAAAGAAAGAA 6

RESULT 3648
US-10-309-775A-4/c
; Sequence 4, Application US/10309775A
; Publication No. US2004006032A1
; GENERAL INFORMATION:
; APPLICANT: LOPEZ, Ricardo A.
; TITLE OF INVENTION: IMMUNOSTIMULATORY OLIGONUCLEOTIDES AND USES THEREOF
; FILE REFERENCE: 2901/OM327
; CURRENT APPLICATION NUMBER: US/10/309,775A
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: CA 2,388,049
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-309-775A-4
```

```

Query Match      0.4%; Score 12.6; DB 1; Length 24;
Best Local Similarity 78.9%; Pred. No. 4e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db      24 AAAGACAAAGACACAAAA 6

RESULT 3649
US-10-343-710-146/c
; Sequence 146, Application US/10343710
; Publication No. US20040087478A1
; GENERAL INFORMATION:
; APPLICANT: GILLEN, Clemens
; APPLICANT: WETZELS, Ingrid
; APPLICANT: WENDT, Stephan
; APPLICANT: WEIHE, E.
; APPLICANT: SCHAEFER, M., K.-H.
; TITLE OF INVENTION: SCREENING METHOD
; FILE REFERENCE: 029310.52022US
; CURRENT APPLICATION NUMBER: US/10/343,710
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP01/09011
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 157
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 146
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
US-10-343-710-146

Query Match      0.4%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.7e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2783 TTGAAAAAAAAAAAA 2796
Db      14 TTAAAAAAAAAAAA 1

RESULT 3650
US-10-138-674-1070/c
; Sequence 1070, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1070
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1070

Query Match      0.4%; Score 12.4; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1979 AAAAAAAAAAGT 1992
Db      1979 AAAAAAAAAAGT 1992
```

; Sequence 11, Application US/10165216  
; Publication No. US20030228675A1  
; GENERAL INFORMATION:  
; APPLICANT: Otterness, Diane M.  
; APPLICANT: Abraham, Robert T.  
; TITLE OF INVENTION: ATM Related Kinase ATX, Nucleic Acids  
; TITLE OF INVENTION: Encoding Same and Methods of Use  
; FILE REFERENCE: P-LJ 5222  
; CURRENT APPLICATION NUMBER: US/10/165,216  
; CURRENT FILING DATE: 2002-06-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic oligonucleotide  
US-10-165-216-11

Query Match 0.4%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1292 AGCAGGCTCGCCCGCTCT 1310  
Db 1 AGCAAGCTCCCTCCTGTCT 19

RESULT 3643  
US-10-688-706-2086  
; Sequence 2086, Application US/10688706  
; Publication No. US20040102412A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corp.  
; APPLICANT: Broschat, Kay  
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION  
; FILE REFERENCE: 01393/1  
; CURRENT APPLICATION NUMBER: US/10/688,706  
; CURRENT FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: 60/419,268  
; PRIOR FILING DATE: 2002-10-17  
; NUMBER OF SEQ ID NOS: 3071  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2086  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: human GFAT antisense  
US-10-688-706-2086

Query Match 0.4%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2783 TTGAAAAA 2801  
Db 1 TTAAAAACAAACAGAAA 19

RESULT 3644  
US-10-117-955B-3/c  
; Sequence 3, Application US/10117955B  
; Publication No. US20030199453A1  
; GENERAL INFORMATION:  
; APPLICANT: Giordano, Tony  
; APPLICANT: Sturgess, Michael A.  
; TITLE OF INVENTION: Small Molecule Inhibitors of Secretion  
; TITLE OF INVENTION: of Proteins Encoded by ARE-mRNAs  
; FILE REFERENCE: 50093/018002  
; CURRENT APPLICATION NUMBER: US/10/117,955B  
; CURRENT FILING DATE: 2002-04-08

; PRIOR APPLICATION NUMBER: US 60/282,974  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 21  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: consensus motif  
US-10-117-955B-3

Query Match 0.4%; Score 12.6; DB 1; Length 21;  
Best Local Similarity 78.9%; Pred. No. 4e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2786 AAAAAA 2804  
Db 20 AAATAATAATAATAAA 2

RESULT 3645  
US-10-257-294-44/c  
; Sequence 44, Application US/10257294  
; Publication No. US20040023231A1  
; GENERAL INFORMATION:  
; APPLICANT: Abu-Khabar, Khalid  
; APPLICANT: Williams, Bryan  
; APPLICANT: Frevel, Mathias  
; APPLICANT: Silverman, Robert  
; TITLE OF INVENTION: System for Identifying and Analyzing Expression of ARE-Containing  
; FILE REFERENCE: 26473/04185  
; CURRENT APPLICATION NUMBER: US/10/257,294  
; CURRENT FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: PCT/US01/11993  
; PRIOR FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: US 60/198,870  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 109  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 44  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-257-294-44

Query Match 0.4%; Score 12.6; DB 1; Length 21;  
Best Local Similarity 78.9%; Pred. No. 4e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2786 AAAAAA 2804  
Db 20 AAATAATAATAATAAA 2

RESULT 3646  
US-10-257-294-102/c  
; Sequence 102, Application US/10257294  
; Publication No. US20040023231A1  
; GENERAL INFORMATION:  
; APPLICANT: Abu-Khabar, Khalid  
; APPLICANT: Williams, Bryan  
; APPLICANT: Frevel, Mathias  
; APPLICANT: Silverman, Robert  
; TITLE OF INVENTION: System for Identifying and Analyzing Expression of ARE-Containing  
; FILE REFERENCE: 26473/04185  
; CURRENT APPLICATION NUMBER: US/10/257,294  
; CURRENT FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: PCT/US01/11993  
; PRIOR FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: US 60/198,870  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 109

```

; CURRENT APPLICATION NUMBER: US/10/159,834
; CURRENT FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleo
US-10-159-834-58

```

```

Query Match      0.4%;      Score 12.6;  DB 1;      Length 20;
Best Local Similarity 78.9%;      Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

Qy	1339	TCATTTCAGCCTGATTACC	1357
Db	19	TCATTTCAAACTGTTTCC	1

RESULT 3638  
US-10-159-834-117  
; Sequence 117, Application US/10159834  
; Publication No. US2003022868A1

Query Match	0.4%;	Score 12.6;	DB 1;	Length 20;
Best Local Similarity	78.9%;	Pred. No. 3.9e+03;		
Matches 15;	Conservative.	0;	Mismatches 4;	Indels

QY	1339	TCATTTCAGCCTGATTACC	1357
Dδ	2	TCATTTCAAACTGTTTCC	20

RESULT 3639  
US-10-688-706-2467  
; Sequence 2467, Application US/10688706  
; Publication No. US20040102412A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corp.  
; APPLICANT: Broschat, Kay  
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION  
; FILE REFERENCE: 01393/1  
; CURRENT APPLICATION NUMBER: US/10/688,706  
; CURRENT FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: 60/419,268  
; PRIOR FILING DATE: 2002-10-17  
; NUMBER OF SEQ ID NOS: 3071  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2467  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: human GFAT antisense  
US-10-688-706-2467

Query Match	0.4%;	Score 12.6;	DB 1;	Length 20;
Best Local Similarity	78.9%;	Pred. No. 3.9e+03;		

```

Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAAAAAA 2804
      ||||| ||||| |||||
Db 2 AAAAAACAAAAACAGAAACAA 20

```

RESULT 3640  
US-10-688-706-2843  
; Sequence 2843, Application US/10688706  
; Publication No. US20040102412A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corp.  
; APPLICANT: Broschat, Kay  
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION  
; FILE REFERENCE: 01393/1  
; CURRENT APPLICATION NUMBER: US/10/688,706  
; CURRENT FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: 60/419,268  
; PRIOR FILING DATE: 2002-10-17  
; NUMBER OF SEQ ID NOS: 3071  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2843  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: human GFAT antisense  
US-10-688-706-2843

```
Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

Qy 2786 AAAAAAAAAAAAAAAAAA 2804  
 ||||| ||||| ||||| |||||  
 Db 1 AAAAAACAAACAGAAACAAA 19

```

RESULT 3641
US-10-688-706-2908
; Sequence 2908, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2908
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-2908

```

```

Query Match          0.4%;   Score 12.6;   DB 1;   Length 20;
Best Local Similarity 78.9%;   Pred. NO. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

QY	2786	AAAAAAAAAAAAAAAAAAAA	2804
Db	2	AAACAAACAGAAACAA	20

RESULT 3642  
US-10-165-216-11

```
; Publication No. US20030165963A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide AGT02014
US-10-367-470-11
```

```
Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      2786 AAAAAAAAAAAAAAAAAAAAAA 2804
      |||||
Db      20 AAAAAAAAAAATTTTAAAAAA 2
```

```
RESULT 3634
US-10-367-470-12
; Sequence 12, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Complement DNA oligo AGT02009
US-10-367-470-12
```

```
Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      2786 AAAAAAAAAAAAAAAAAAAAAA 2804
      |||||
Db      1 AAAAAAAAAAATTTTAAAAAA 19
```

```
RESULT 3635
US-10-367-470-14
; Sequence 14, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
```

```
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02021
US-10-367-470-14
```

```
Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      2786 AAAAAAAAAAAAAAAAAAAAAA 2804
      |||||
Db      1 AAAAAAAAAAATTTTAAAAAA 19
```

```
RESULT 3636
US-10-367-470-17
; Sequence 17, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02024
US-10-367-470-17
```

```
Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      2786 AAAAAAAAAAAAAAAAAAAAAA 2804
      |||||
Db      1 AAAAAAAAAAATTTCTAAAAAA 19
```

```
RESULT 3637
US-10-159-834-58/c
; Sequence 58, Application US/10159834
; Publication No. US20030228688A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF ISOPRENYLCYSTEINE CARBOXYL METHYLTRANSFERASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0299
```



```
Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1449 TGAACCCCTGGAGACCAGG 1467
Db      19 TGAATCTGGAGACCAGGG 1

RESULT 3629
US-09-984-637-7/c
; Sequence 7, Application US/09984637
; Publication No. US20040048246A1
; GENERAL INFORMATION:
; APPLICANT: Tosoh Corporation
; TITLE OF INVENTION: OLIGONUCLEOTIDE FOR DETECTION OF HIV-1 AND DETECTION METHOD
; FILE REFERENCE: PA211-0315
; CURRENT APPLICATION NUMBER: US/09/984,637
; CURRENT FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide hybridizable with a specific site of HIV-1 RNA
US-09-984-637-7

Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAAAAA 2804
Db      20 AAAAAAAGTAAGAAAAA 2

RESULT 3630
US-10-367-470-8/c
; Sequence 8, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide AGT02008
US-10-367-470-8

Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAAAAA 2804
Db      20 AAAAAAATTTTAAAAAA 2
```

```
RESULT 3631
US-10-367-470-9/c
; Sequence 9, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide AGT02012
US-10-367-470-9

Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAAAAA 2804
Db      20 AAAAAAATTTTAAAAAA 2

RESULT 3632
US-10-367-470-10/c
; Sequence 10, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide AGT02013
US-10-367-470-10

Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAAAAA 2804
Db      20 AAAAAAATTTTAAAAAA 2

RESULT 3633
US-10-367-470-11/c
; Sequence 11, Application US/10367470
```

;  
; PRIOR APPLICATION NUMBER: US 09/616,761  
; PRIOR FILING DATE: 2000-07-14  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide AGT02014  
US-09-823-647B-11

Query Match 0.4%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 20 AAAAAAAAAATTTTAAAAAA 2

RESULT 3625  
US-09-823-647B-12  
; Sequence 12, Application US/09823647B  
; Patent No. US20020142309A1  
; GENERAL INFORMATION:  
; APPLICANT: Applied Gene Technologies, Inc.  
; APPLICANT: Dattagupta, Nanibhushan  
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 47541-20004.20  
; CURRENT APPLICATION NUMBER: US/09/823,647B  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: US 09/616,761  
; PRIOR FILING DATE: 2000-07-14  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Complement DNA oligo AGT02009  
US-09-823-647B-12

Query Match 0.4%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAATTTTAAAAAA 19

RESULT 3626  
US-09-823-647B-14  
; Sequence 14, Application US/09823647B  
; Patent No. US20020142309A1  
; GENERAL INFORMATION:  
; APPLICANT: Applied Gene Technologies, Inc.  
; APPLICANT: Dattagupta, Nanibhushan  
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 47541-20004.20  
; CURRENT APPLICATION NUMBER: US/09/823,647B  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: US 09/616,761  
; PRIOR FILING DATE: 2000-07-14  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 20  
; TYPE: DNA

;  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligo AGT02021  
US-09-823-647B-14

Query Match 0.4%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAATTTTAAAAAA 19

RESULT 3627  
US-09-823-647B-17  
; Sequence 17, Application US/09823647B  
; Patent No. US20020142309A1  
; GENERAL INFORMATION:  
; APPLICANT: Applied Gene Technologies, Inc.  
; APPLICANT: Dattagupta, Nanibhushan  
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 47541-20004.20  
; CURRENT APPLICATION NUMBER: US/09/823,647B  
; CURRENT FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: US 09/616,761  
; PRIOR FILING DATE: 2000-07-14  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligo AGT02024  
US-09-823-647B-17

Query Match 0.4%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2804  
|||||  
Db 1 AAAAAAAAAATTTTAAAAAA 19

RESULT 3628  
US-09-824-322B-217/c  
; Sequence 217, Application US/09824322B  
; Publication No. US20030022848A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Brenda  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Butler, Madeline M.  
; APPLICANT: Shanahan, William R.  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-ALPHA  
; TITLE OF INVENTION: ALPHA) EXPRESSION  
; FILE REFERENCE: ISPH-0501  
; CURRENT APPLICATION NUMBER: US/09/824,322B  
; CURRENT FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: US 09/313,932  
; PRIOR FILING DATE: 1999-05-18  
; PRIOR APPLICATION NUMBER: US 09/166,186  
; PRIOR FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 503  
; SEQ ID NO 217  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-824-322B-217

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Db      1 AAAAAAAAAATTGTAAGAAA 19
|||||
RESULT 3620
US-09-823-634A-17
; Sequence 17, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; TITLE OF INVENTION: MISMATCHES USING RNASE H
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02024
US-09-823-634A-17

Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAAAAA 2804
      |||||
Db      1 AAAAAAAAAATTCTAAGAAA 19
|||||

RESULT 3621
US-09-823-647B-8/c
; Sequence 8, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide AGT02008
US-09-823-647B-8

Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAAAAA 2804
      |||||
Db      20 AAAAAAAAAATTCTAAGAAA 2

RESULT 3622
US-09-823-647B-9/c
; Sequence 9, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide AGT02012
US-09-823-647B-9

Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAAAAA 2804
      |||||
Db      20 AAAAAAAAAATTCTAAGAAA 2

RESULT 3623
US-09-823-647B-10/c
; Sequence 10, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide AGT02013
US-09-823-647B-10

Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAAAAA 2804
      |||||
Db      20 AAAAAAAAAATTCTAAGAAA 2

RESULT 3624
US-09-823-647B-11/c
; Sequence 11, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
```

```

; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide AGT02012
US-09-823-634A-9

Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAAAAAA 2804
      |||||
Db      20 AAAAAAAAAATTTTAAAAAA 2

RESULT 3616
US-09-823-634A-10/c
; Sequence 10, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide AGT02013
US-09-823-634A-10

Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAAAAAA 2804
      |||||
Db      20 AAAAAAAAAATTTTAAAAAA 2

RESULT 3617
US-09-823-634A-11/c
; Sequence 11, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 20

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```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide AGT02014
US-09-823-634A-11

Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAAAAAA 2804
      |||||
Db      20 AAAAAAAAAATTTTAAAAAA 2

RESULT 3618
US-09-823-634A-12
; Sequence 12, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Complement DNA oligo AGT02009
US-09-823-634A-12

Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAAAAAA 2804
      |||||
Db      1 AAAAAAAAAATTTTAAAAAA 19

RESULT 3619
US-09-823-634A-14
; Sequence 14, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02021
US-09-823-634A-14

Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAAAAAA 2804

```



COMPUTER: IBM PS/2  
OPERATING SYSTEM: WINDOWS 95  
SOFTWARE: WORDPERFECT 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/430,196  
FILING DATE: 05-May-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/923,517A  
FILING DATE: 07-Aug-2001  
APPLICATION NUMBER: 09/364,416  
FILING DATE: 1999-07-30  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0209  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 810-1515  
TELEFAX: (609) 810-1454  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-10-430-196-38

Query Match 0.4%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1000 GCGGAGAGAGTTGGACAAG 1018  
Db 19 GCGGCTGAAGTTGGCGGAG 1

RESULT 3612  
US-09-465-589-7/c  
; Sequence 7, Application US/09465589  
; Patent No. US20020031764A1  
; GENERAL INFORMATION:  
; APPLICANT: KOCH, Jorn Erland  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMPLIFYING MULTIPLE TANDEM REPETITION  
; TITLE OF INVENTION: OLIGONUCLEOTIDE UNIT (AS AMENDED)  
; FILE REFERENCE: 4305/1E293-US2  
; CURRENT APPLICATION NUMBER: US/09/465,589  
; CURRENT FILING DATE: 1999-12-17  
; PRIOR APPLICATION NUMBER: US 09/091,146  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: PCT/DK96/00513  
; PRIOR FILING DATE: 1996-12-05  
; PRIOR APPLICATION NUMBER: DK 1379/95  
; PRIOR FILING DATE: 1995-12-05  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide with internal repetitions  
US-09-465-589-7

Query Match 0.4%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2166 TTTTCTTTCTTTCTTTCTTT 2184  
Db 20 TTTCTTTCTTTCTTTCTTT 2

RESULT 3613  
US-09-465-589-8/c  
; Sequence 8, Application US/09465589  
; Patent No. US20020031764A1  
; GENERAL INFORMATION:  
; APPLICANT: KOCH, Jorn Erland  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMPLIFYING MULTIPLE TANDEM REPETITION  
; TITLE OF INVENTION: OLIGONUCLEOTIDE UNIT (AS AMENDED)  
; FILE REFERENCE: 4305/1E293-US2  
; CURRENT APPLICATION NUMBER: US/09/465,589  
; CURRENT FILING DATE: 1999-12-17  
; PRIOR APPLICATION NUMBER: US 09/091,146  
; PRIOR FILING DATE: 1998-06-04  
; PRIOR APPLICATION NUMBER: PCT/DK96/00513  
; PRIOR FILING DATE: 1996-12-05  
; PRIOR APPLICATION NUMBER: DK 1379/95  
; PRIOR FILING DATE: 1995-12-05  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide with internal repetitions  
US-09-465-589-8

Query Match 0.4%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 20 AAAGAAAGAAAGAAAGAAA 2

RESULT 3614  
US-09-823-634A-8/c  
; Sequence 8, Application US/09823634A  
; Patent No. US20020142308A1  
; GENERAL INFORMATION:  
; APPLICANT: Applied Gene Technologies, Inc.  
; APPLICANT: Dattagupta, Nanibhushan  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE  
; TITLE OF INVENTION: MISMATCHES USING RNASE H  
; FILE REFERENCE: 47541-20006.00  
; CURRENT APPLICATION NUMBER: US/09/823,634A  
; CURRENT FILING DATE: 2002-02-28  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide AGT02008  
US-09-823-634A-8

Query Match 0.4%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 20 AAAAAAAAAATTTTAAAAAA 2

RESULT 3615  
US-09-823-634A-9/c  
; Sequence 9, Application US/09823634A  
; Patent No. US20020142308A1  
; GENERAL INFORMATION:

Query Match 0.4%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
Db 1 AAAAAAAAAATTGAAAAA 19

RESULT 3609  
US-09-784-674-557/c  
; Sequence 557, Application US/09784674  
; Publication No. US20030054346A1  
; GENERAL INFORMATION:  
; APPLICANT: Shannon, Karen W.  
; Wolber, Paul K.  
; Delenstarr, Glenda C.  
; Webb, Peter G.  
; Kincaid, Robert H.  
; TITLE OF INVENTION: Methods for evaluating oligonucleotide  
; probe sequences  
; NUMBER OF SEQUENCES: 1165  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard  
; Company M/S 20BO  
; STREET: 3000 Hanover Street  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/784,674  
; FILING DATE: 15-Feb-2001  
; CLASSIFICATION: No. US20030054346A1 available  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/021,701  
; FILING DATE: 10-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Choi, Wendy A.  
; REGISTRATION NUMBER: 36,697  
; REFERENCE/DOCKET NUMBER: 10971464-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-236-2386  
; TELEFAX: 650-852-8063  
; INFORMATION FOR SEQ ID NO: 557:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 557:  
US-09-784-674-557

Query Match 0.4%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAAAAAA 2797  
Db 20 AGGGTTAAAAAAGAAAAA 2

RESULT 3610  
US-09-923-517-38/c  
; Sequence 38, Application US/09923517

; Publication No. US20020039741A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.  
; Miraglia; Brenda F. Baker  
; TITLE OF INVENTION: Antisense Oligonucleotide  
; Compositions and Methods for the Modulation of  
; Activating Protein 1  
; NUMBER OF SEQUENCES: 139  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Jane Massey Licata  
; STREET: 66 East Main Street  
; CITY: Marlton  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 08053  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: WINDOWS 95  
; SOFTWARE: WORDPERFECT 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/923,517  
; FILING DATE: 07-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/364,416  
; FILING DATE: 1999-07-30  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jane Massey Licata  
; REGISTRATION NUMBER: 32,257  
; REFERENCE/DOCKET NUMBER: ISPH-0209  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (609) 810-1515  
; TELEFAX: (609) 810-1454  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; ANTI-SENSE: Yes  
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
US-09-923-517-38

Query Match 0.4%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1000 GCGGAGAAAGTTGGACAAG 1018  
Db 19 GCGGCTGAAGTTGGCGGAG 1

RESULT 3611  
US-10-430-196-38/c  
; Sequence 38, Application US/10430196  
; Publication No. US20030194738A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.  
; Miraglia; Brenda F. Baker  
; TITLE OF INVENTION: Antisense Oligonucleotide  
; Compositions and Methods for the Modulation of  
; Activating Protein 1  
; NUMBER OF SEQUENCES: 139  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Jane Massey Licata  
; STREET: 66 East Main Street  
; CITY: Marlton  
; STATE: NJ  
; COUNTRY: USA  
; ZIP: 08053  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

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; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02020
US-09-823-634A-13

Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db      1 AAAAAAAAAATTGAAAAAA 19

RESULT 3606
US-09-823-647B-13
; Sequence 13, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US/09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02020
US-09-823-647B-13

Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAAAAAA 2804
Db      1 AAAAAAAAAATTGAAAAAA 19

RESULT 3607
US-09-784-674-558/c
; Sequence 558, Application US/09784674
; Publication No. US20030054346A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Karen W.
; APPLICANT: Wolber, Paul K.
; APPLICANT: Delenstarr, Glenda C.
; APPLICANT: Webb, Peter G.
; APPLICANT: Kincaid, Robert H.
; TITLE OF INVENTION: Methods for evaluating oligonucleotide
; NUMBER OF SEQUENCES: 1165
; CORRESPONDENCE ADDRESS:
```

```

; ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
; Company M/S 2080
; STREET: 3000 Hanover Street
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,674
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: No. US20030054346A1 available
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/021,701
; FILING DATE: 10-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Wendy A.
; REGISTRATION NUMBER: 36,697
; REFERENCE/DOCKET NUMBER: 10971464-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-236-2386
; TELEFAX: 650-852-8063
; INFORMATION FOR SEQ ID NO: 558:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 558:
US-09-784-674-558

Query Match      0.4%; Score 12.6; DB 1; Length 20;
Best Local Similarity 78.9%; Pred. No. 3.9e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2779 AGAATTGAAAAAAAAAAAAA 2797
Db      19 AGGTTAAAGAAAAAA 1

RESULT 3608
US-10-367-470-13
; Sequence 13, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02020
US-10-367-470-13
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QY 2179 TTTTAACTTTGAAAG 2197  
| | | | | | | | | | | | | | |  
Db 19 TTTTAAATATAAGAG 1

RESULT 3601  
US-10-126-704-105/c  
; Sequence 105, Application US/10126704  
; Publication No. US20030170647A1  
; GENERAL INFORMATION:  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)  
; TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.  
; FILE REFERENCE: 44.U.S.DIV  
; CURRENT APPLICATION NUMBER: US/10/126,704  
; CURRENT FILING DATE: 2002-04-20  
; PRIOR APPLICATION NUMBER: US 60/091,315  
; PRIOR FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/111,909  
; PRIOR FILING DATE: 1998-12-10  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: Patent.pm  
; SEQ ID NO 105  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: 1..19  
; OTHER INFORMATION: potential microsequencing oligo for 5-129-144.misl  
US-10-126-704-105

Query Match 0.4%; Score 12.6; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 3.8e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2179 TTTTAACTTTGAAAG 2197  
| | | | | | | | | | | | | | |  
Db 19 TTTTAAATATAAGAG 1

RESULT 3602  
US-09-823-634A-16  
; Sequence 16, Application US/09823634A  
; Patent No. US20020142308A1  
; GENERAL INFORMATION:  
; APPLICANT: Applied Gene Technologies, Inc.  
; APPLICANT: Dattagupta, Nanibhushan  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE  
; TITLE OF INVENTION: MISMATCHES USING RNASE H  
; FILE REFERENCE: 47541-20006.00  
; CURRENT APPLICATION NUMBER: US/09/823,634A  
; CURRENT FILING DATE: 2002-02-28  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligo AGT02023  
US-09-823-634A-16

Query Match 0.4%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
| | | | | | | | | | | | | | |  
Db 1 AAAAAAAAAATGTGAAAAAAAA 19

RESULT 3603  
US-09-823-647B-16  
; Sequence 16, Application US/09823647B  
; Patent No. US20020142309A1  
; GENERAL INFORMATION:  
; APPLICANT: Applied Gene Technologies, Inc.  
; APPLICANT: Dattagupta, Nanibhushan  
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 47541-20004.20  
; CURRENT APPLICATION NUMBER: US/09/823,647B  
; CURRENT FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: US 09/616,761  
; PRIOR FILING DATE: 2000-07-14  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligo AGT02023  
US-09-823-647B-16

Query Match 0.4%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
| | | | | | | | | | | | | | |  
Db 1 AAAAAAAAAATGTGAAAAAAAA 19

RESULT 3604  
US-10-367-470-16  
; Sequence 16, Application US/10367470  
; Publication No. US20030165963A1  
; GENERAL INFORMATION:  
; APPLICANT: Applied Gene Technologies, Inc.  
; APPLICANT: Dattagupta, Nanibhushan  
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 47541-20004.20  
; CURRENT APPLICATION NUMBER: US/10/367,470  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US/09/823,647B  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: US 09/616,761  
; PRIOR FILING DATE: 2000-07-14  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 16  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligo AGT02023  
US-10-367-470-16

Query Match 0.4%; Score 12.6; DB 1; Length 20;  
Best Local Similarity 78.9%; Pred. No. 3.9e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2804  
| | | | | | | | | | | | | | |  
Db 1 AAAAAAAAAATGTGAAAAAAAA 19

RESULT 3605  
US-09-823-634A-13  
; Sequence 13, Application US/09823634A  
; Patent No. US20020142308A1  
; GENERAL INFORMATION:



APPLICANT: Ellerman, Karen  
APPLICANT: Gangolli, Esha A.  
APPLICANT: Boldog, Ference L.  
APPLICANT: Colman, Steven D.  
APPLICANT: Eisen, Andrew J.  
APPLICANT: Liu, Xiaohong  
APPLICANT: Padigar, Muralidhara  
APPLICANT: Spaderna, Steven K.  
APPLICANT: Zerhusen, Bryan D.  
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
FILE REFERENCE: 21402-216  
CURRENT APPLICATION NUMBER: US/10/231,913  
CURRENT FILING DATE: 2002-08-30  
PRIOR APPLICATION NUMBER: 60/251,660  
PRIOR FILING DATE: 2000-12-06  
PRIOR APPLICATION NUMBER: 60/255,029  
PRIOR FILING DATE: 2000-12-12  
PRIOR APPLICATION NUMBER: 60/260,326  
PRIOR FILING DATE: 2001-01-08  
PRIOR APPLICATION NUMBER: 60/263,800  
PRIOR FILING DATE: 2001-01-24  
PRIOR APPLICATION NUMBER: 60/269,942  
PRIOR FILING DATE: 2001-02-20  
PRIOR APPLICATION NUMBER: 60/286,183  
PRIOR FILING DATE: 2001-04-24  
PRIOR APPLICATION NUMBER: 60/313,627  
PRIOR FILING DATE: 2001-08-20  
PRIOR APPLICATION NUMBER: 60/318,712  
PRIOR FILING DATE: 2001-09-12  
NUMBER OF SEQ ID NOS: 292  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 179  
LENGTH: 23  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: CHEMICALLY  
OTHER INFORMATION: SYNTHESIZED  
US-10-231-913-179

Query Match 0.5%; Score 12.8; DB 1; Length 23;  
Best Local Similarity 87.5%; Pred. No. 4e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1398 CCTGCAGAACTACAT 1413  
Db 5 CCTGCAGACCAACAT 20

RESULT 3598  
US-10-629-453-20/c  
Sequence 20, Application US/10629453  
Publication No. US20040096878A1  
GENERAL INFORMATION:  
APPLICANT: Keene, Jack D.  
APPLICANT: Carson, Craig C.  
APPLICANT: Tenenbaum, Scott A.  
TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein  
TITLE OF INVENTION: complexes  
FILE REFERENCE: RBN-001DV  
CURRENT APPLICATION NUMBER: US/10/629,453  
CURRENT FILING DATE: 2003-07-29  
PRIOR APPLICATION NUMBER: US 09/750,401  
PRIOR FILING DATE: 2000-12-28  
PRIOR APPLICATION NUMBER: US 60/173,338  
PRIOR FILING DATE: 1999-12-28  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 20  
LENGTH: 23  
TYPE: RNA  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: 3 -UTR sequence of Neuronal-Cadherin  
US-10-629-453-20

Query Match 0.5%; Score 12.8; DB 1; Length 23;  
Best Local Similarity 87.5%; Pred. No. 4e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAA 2801  
Db 23 AAAAAAAAAATTAATA 8

RESULT 3599  
US-10-098-263B-27520/c  
Sequence 27520, Application US/10098263B  
Publication No. US20030104410A1  
GENERAL INFORMATION:  
APPLICANT: Mittman, Michael  
TITLE OF INVENTION: Human Microarray  
FILE REFERENCE: 3118.1  
CURRENT APPLICATION NUMBER: US/10/098,263B  
CURRENT FILING DATE: 2003-01-08  
PRIOR APPLICATION NUMBER: 60/276,759  
PRIOR FILING DATE: 2001-03-16  
NUMBER OF SEQ ID NOS: 131066  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 27520  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-098-263B-27520

Query Match 0.5%; Score 12.8; DB 1; Length 25;  
Best Local Similarity 70.8%; Pred. No. 3.9e+03;  
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1882 GTCAATTGATGCGCCCTAGATCA 1905  
Db 25 GTCCTTTGATGTGCTTATATTA 2

RESULT 3600  
US-10-071-179-105/c  
Sequence 105, Application US/10071179  
Publication No. US2003010882A1  
GENERAL INFORMATION:

APPLICANT: Bougueleret, Lydie  
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)  
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.  
FILE REFERENCE: GENSET.031A  
CURRENT APPLICATION NUMBER: US/10/071,179  
CURRENT FILING DATE: 2002-02-07  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/345,882  
PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-30  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/091,315  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-30  
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/111,909  
PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10  
NUMBER OF SEQ ID NOS: 140  
SOFTWARE: Patent.pm  
SEQ ID NO 105  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: primer\_bind  
LOCATION: 1..19  
OTHER INFORMATION: potential microsequencing oligo for 5-129-144.misl  
US-10-071-179-105

Query Match 0.4%; Score 12.6; DB 1; Length 19;  
Best Local Similarity 78.9%; Pred. No. 3.8e+03;  
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-161-229-99

Query Match          0.5%; Score 12.8; DB 1; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2179 TTTTAACTTTGA 2194
      |||||
Db 20 TTTTCAACGTTGA 5

RESULT 3594
US-10-349-9728/c
; Sequence 9728, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9728
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..21
; OTHER INFORMATION: downstream amplification primer 99-6979 for SEQ 1863, in compleme
US-10-349-143-9728

Query Match          0.5%; Score 12.8; DB 1; Length 21;
Best Local Similarity 87.5%; Pred. No. 3.9e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2785 GAAAAA 2800
      |||
Db 21 GAAGGAAAAA 6

RESULT 3595
US-10-309-788-20/c
; Sequence 20, Application US/10309788
; Publication No. US20030211466A1
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Tenenbaum, Scott A.
; APPLICANT: Carson, Craig C.
; APPLICANT: Phelps, William C.
; TITLE OF INVENTION: Method for Identifying Functionally Related Genes and Drug Target
; FILE REFERENCE: RBN-001CP
; CURRENT APPLICATION NUMBER: US/10/309,788
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/750,401
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 38
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR consensus sequence of Neuronal-Cadherin
US-10-309-788-20

Query Match          0.5%; Score 12.8; DB 1; Length 23;
Best Local Similarity 87.5%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAA 2801
      |||||
Db 23 AAAAAAATTA 8

RESULT 3596
US-10-238-306B-20/c
; Sequence 20, Application US/10238306B
; Publication No. US20030235830A1
; GENERAL INFORMATION:
; APPLICANT: Keene, Jack D.
; APPLICANT: Tenenbaum, Scott A.
; APPLICANT: Carson, Craig C.
; TITLE OF INVENTION: Methods for isolating and characterizing endogenous mRNA-protein
; TITLE OF INVENTION: complexes
; FILE REFERENCE: RBN-001CN
; CURRENT APPLICATION NUMBER: US/10/238,306B
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: US 09/750,401
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 60/173,338
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 3'-UTR sequence of Neuronal-Cadherin
US-10-238-306B-20

Query Match          0.5%; Score 12.8; DB 1; Length 23;
Best Local Similarity 87.5%; Pred. No. 4e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAA 2801
      |||||
Db 23 AAAAAAATTA 8

RESULT 3597
US-10-231-913-179
; Sequence 179, Application US/10231913
; Publication No. US20040005576A1
; GENERAL INFORMATION:
; APPLICANT: Guo, Xiaojia S.
; APPLICANT: Li, Li
; APPLICANT: Patturajan, Meera
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Edinger, Schlomit
; APPLICANT: Peyman, John A.
; APPLICANT: Stone, David J.
```

; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 776  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-776

Query Match 0.5%; Score 12.8; DB 1; Length 20;  
Best Local Similarity 87.5%; Pred. No. 3.8e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2179 TTTTAACTTTGA 2194  
|||||  
Db 20 TTTTCAACGTTGA 5

RESULT 3590  
US-10-314-578-776/c  
; Sequence 776, Application US/10314578  
; Publication No. US20030212026A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Schetter, Christian  
; APPLICANT: Vollmer, Jorg  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids  
; FILE REFERENCE: C1039/7035 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/314,578  
; CURRENT FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US 60/156,113  
; PRIOR FILING DATE: 1999-09-25  
; PRIOR APPLICATION NUMBER: US 60/156,135  
; PRIOR FILING DATE: 1999-09-27  
; PRIOR APPLICATION NUMBER: US 60/227,436  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 1145  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 776  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-314-578-776

Query Match 0.5%; Score 12.8; DB 1; Length 20;  
Best Local Similarity 87.5%; Pred. No. 3.8e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2179 TTTTAACTTTGA 2194  
|||||  
Db 20 TTTTCAACGTTGA 5

RESULT 3591  
US-10-112-653-749/c  
; Sequence 749, Application US/10112653  
; Publication No. US20030050268A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Berg, Daniel J.  
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR  
; TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES  
; FILE REFERENCE: C01039/70060(AWS)  
; CURRENT APPLICATION NUMBER: US/10/112,653  
; CURRENT FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/279,642  
; PRIOR FILING DATE: 2001-03-29  
; NUMBER OF SEQ ID NOS: 1040  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 749

; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide  
US-10-112-653-749

Query Match 0.5%; Score 12.8; DB 1; Length 20;  
Best Local Similarity 87.5%; Pred. No. 3.8e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2179 TTTTAACTTTGA 2194  
|||||  
Db 20 TTTTCAACGTTGA 5

RESULT 3592  
US-10-017-995-776/c  
; Sequence 776, Application US/10017995  
; Publication No. US20030055014A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids  
; FILE REFERENCE: C1037/7025 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/017,995  
; CURRENT FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: US 60/255,534  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 776  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-017-995-776

Query Match 0.5%; Score 12.8; DB 1; Length 20;  
Best Local Similarity 87.5%; Pred. No. 3.8e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2179 TTTTAACTTTGA 2194  
|||||  
Db 20 TTTTCAACGTTGA 5

RESULT 3593  
US-10-161-229-99/c  
; Sequence 99, Application US/10161229  
; Publication No. US20030100527A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Hartmann, Gunther  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules for  
; Activating Dendritic Cells  
; FILE REFERENCE: C01039/70061  
; CURRENT APPLICATION NUMBER: US/10/161,229  
; CURRENT FILING DATE: 2002-06-03  
; PRIOR APPLICATION NUMBER: US 09/191,170  
; PRIOR FILING DATE: 1998-11-13  
; PRIOR APPLICATION NUMBER: US 08/960,774  
; PRIOR FILING DATE: 1997-10-30  
; PRIOR APPLICATION NUMBER: US 08/738,652  
; PRIOR FILING DATE: 1996-10-30  
; PRIOR APPLICATION NUMBER: US 08/386,063  
; PRIOR FILING DATE: 1995-02-07  
; PRIOR APPLICATION NUMBER: US 08/276,358  
; PRIOR FILING DATE: 1994-07-15  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 99  
; LENGTH: 20

```
US-10-206-839-28
; Sequence 28, Application US/10206839
; Publication No. US2003009977A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Kurth, Janice
; TITLE OF INVENTION: Genotyping Human Phenol Sulfotransferase
; TITLE OF INVENTION: (STP2)
; FILE REFERENCE: 4389-6 (formerly SEQ-16P)
; CURRENT APPLICATION NUMBER: US/10/206,839
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 09/328,174
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 19
; TYPE: DNA
; ORGANISM: H. sapiens
US-10-206-839-28

Query Match      0.5%; Score 12.8; DB 1; Length 19;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2785 GAAAAAATAAAAAA 2800
Db      3 GAAAAAATAAAGGAA 18

RESULT 3586
US-10-007-814-29/c
; Sequence 29, Application US/10007814
; Publication No. US20020160479A1
; GENERAL INFORMATION:
; APPLICANT: Wojnowski, Leszek
; APPLICANT: Gellner, Klaus
; APPLICANT: Eiselt, Regina
; TITLE OF INVENTION: IDENTIFICATION OF A NEW MEMBER OF THE CYTOCHROME P450 3A
; TITLE OF INVENTION: (CYP3A) GENE FAMILY: CYP3AX
; FILE REFERENCE: 310115.401D1
; CURRENT APPLICATION NUMBER: US/10/007,814
; CURRENT FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-007-814-29

Query Match      0.5%; Score 12.8; DB 1; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      757 CATTTCATGACCAAG 772
Db      20 CATTTCATGGCAAAG 5

RESULT 3587
US-09-888-326-9/c
; Sequence 9, Application US/09888326
; Publication No. US20030026801A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Methods for Enhancing Antibody-Induced
; TITLE OF INVENTION: Cell Lysis and Treating Cancer
; FILE REFERENCE: C1039/7052 (AWS)
; CURRENT APPLICATION NUMBER: US/09/888,326
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,346
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US-09-888-326-9
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 848
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: chimeric phosphorothioate/phosphodiester backbone
; OTHER INFORMATION: with phosphorothioate at 5' and 3' ends
US-09-888-326-9

Query Match      0.5%; Score 12.8; DB 1; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2179 TTTTAACTTTGA 2194
Db      20 TTTTCAACGTTGA 5

RESULT 3588
US-09-776-479-776/c
; Sequence 776, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 776
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-776

Query Match      0.5%; Score 12.8; DB 1; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.8e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2179 TTTTAACTTTGA 2194
Db      20 TTTTCAACGTTGA 5

RESULT 3589
US-09-776-479-776/c
; Sequence 776, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; TITLE OF INVENTION: Treatment of Asthma and Allergy
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
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; PRIOR FILING DATE: 1999-12-29  
; PRIOR APPLICATION NUMBER: 09/301,511  
; PRIOR FILING DATE: 1999-04-28  
; PRIOR APPLICATION NUMBER: 09/186,675  
; PRIOR FILING DATE: 1998-11-04  
; PRIOR APPLICATION NUMBER: 60/083,727  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/064,866  
; PRIOR FILING DATE: 1997-11-05  
; NUMBER OF SEQ ID NOS: 1558  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 558  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-09-825-805-558

Query Match 0.5%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 3.2e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2801  
||||| |||||  
Db 16 AAAAAAAAAACAA 1

RESULT 3581  
US-10-675-685-483/c  
; Sequence 483, Application US/10675685  
; Publication No. US20040063134A1  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E  
; FILE REFERENCE: PB0114  
; CURRENT APPLICATION NUMBER: US/10/675,685  
; CURRENT FILING DATE: 2003-09-30  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 1881  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 483  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-675-685-483

Query Match 0.5%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 3.2e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2163 TCCTTTTTCCTTTT 2178  
||||| |||||  
Db 17 TTCTTCTTTTTCCTTT 2

RESULT 3582  
US-10-163-552-984/c  
; Sequence 984, Application US/10163552  
; Publication No. US20030105051A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Nucleic acid treatment of diseases related to level  
; TITLE OF INVENTION: HER2  
; FILE REFERENCE: MBHB01-1653-A (400/014)  
; CURRENT APPLICATION NUMBER: US/10/163,552  
; CURRENT FILING DATE: 2002-06-06  
; NUMBER OF SEQ ID NOS: 1997  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 984

; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-163-552-984

Query Match 0.5%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 3.2e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2801  
||||| |||||  
Db 17 AAACAAACAAACAAA 2

RESULT 3583  
US-10-163-552-985/c  
; Sequence 985, Application US/10163552  
; Publication No. US20030105051A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level  
; TITLE OF INVENTION: HER2  
; FILE REFERENCE: MBHB01-1653-A (400/014)  
; CURRENT APPLICATION NUMBER: US/10/163,552  
; CURRENT FILING DATE: 2002-06-06  
; NUMBER OF SEQ ID NOS: 1997  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 985  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-163-552-985

Query Match 0.5%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 3.2e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2801  
||||| |||||  
Db 16 AAAAAAAAAACAA 1

RESULT 3584  
US-10-156-306-1646/c  
; Sequence 1646, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR  
; FILE REFERENCE: MBHB01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1646  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-1646

Query Match 0.5%; Score 12.8; DB 1; Length 17;  
Best Local Similarity 87.5%; Pred. No. 3.2e+03;  
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2801  
||||| |||||  
Db 17 AAAAAAAAAAGATAAA 2

RESULT 3585

```

; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1079

Query Match          0.5%; Score 12.8; DB 1; Length 17;
Best Local Similarity 12.5%; Pred. No. 3.2e+03;
Matches 2; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

Qy 2173 TTTTCTTTTCTTTTAA 2188
Db 1 UUUUUUUUUUUUCCAA 16

RESULT 3577
US-10-287-949A-1079
; Sequence 1079, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1079
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1079

Query Match          0.5%; Score 12.8; DB 1; Length 17;
Best Local Similarity 12.5%; Pred. No. 3.2e+03;
Matches 2; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

Qy 2173 TTTTCTTTTCTTTTAA 2188
Db 1 UUUUUUUUUUUUCCAA 16

RESULT 3578
US-09-827-998-483/c
; Sequence 483, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDhMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 483
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-998-483

Query Match          0.5%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2173 TTTTCTTTTCTTTTAA 2188
Db 1 UUUUUUUUUUUUCCAA 16

RESULT 3579
US-09-825-805-557/c
; Sequence 557, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleoti
; FILE REFERENCE: MBHB00-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 09/476,387
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1558
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 557
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-825-805-557

Query Match          0.5%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 3.2e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2786 AAAAAAAAAAAAAAAAAA 2801
Db 17 AAACAAACAAACAAACAA 2

RESULT 3580
US-09-825-805-558/c
; Sequence 558, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleoti
; FILE REFERENCE: MBHB00-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 09/476,387
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/474,432
```

; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953US0XDIV
; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/725,265
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-48

Query Match 0.5%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAA 2797
|||||
Db 13 GAAAAAAAAAAAAA 1

RESULT 3574
US-10-349-143-8908/c
; Sequence 8908, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 8908
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer\_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-1997 for SEQ 1043, in compleme
US-10-349-143-8908

Query Match 0.5%; Score 13; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1096 TGTTCAATTGGCT 1108
|||||
Db 13 TGTTCAATTGGCT 1

RESULT 3575

US-10-173-509-1/c
; Sequence 1, Application US/10173509
; Publication No. US20030017490A1
; GENERAL INFORMATION:
; APPLICANT: Belyavsky et al.
; TITLE OF INVENTION: Method Of Identification And
Cloning Differentially Expressed
Messenger RNAs
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: USA
; ZIP: 11753
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/173,509
; FILING DATE: 18-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/664,534
; FILING DATE: 18-Sep-2000
; APPLICATION NUMBER: US/08/499,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: O'Dea, Sean W.
; REGISTRATION NUMBER: 37690
; REFERENCE/DOCKET NUMBER: 454-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-173-509-1

Query Match 0.5%; Score 13; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798
|||||
Db 22 AAAAAAAAAAAAAA 10

RESULT 3576
US-10-138-674-1079
; Sequence 1079, Application US/10138674
; Publication No. US2004007565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1079

; TITLE OF INVENTION: METHOD OF INTRODUCING WATER-STRESS TOLERANCE
; FILE REFERENCE: 3097-4009
; CURRENT APPLICATION NUMBER: US/10/109,363
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Camellia sinensis
US-10-109-363-16

Query Match 0.5%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798
| | | | | | | | | | | | | | | |
Db 17 AAAAAAAAAAAAAA 5

RESULT 3570
US-10-109-363-18/c
; Sequence 18, Application US/10109363
; Publication No. US20030196214A1
; GENERAL INFORMATION:
; APPLICANT: SHARMA, PRITI
; APPLICANT: KUMAR, SANJAY
; APPLICANT: AHUJA, PARAMVIR SINGH
; TITLE OF INVENTION: NOVEL GENES FROM DROUGHT STRESS TOLERANT TEA PLANT AND A
; TITLE OF INVENTION: METHOD OF INTRODUCING WATER-STRESS TOLERANCE
; FILE REFERENCE: 3097-4009
; CURRENT APPLICATION NUMBER: US/10/109,363
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Camellia sinensis
US-10-109-363-18

Query Match 0.5%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798
| | | | | | | | | | | | | | | |
Db 17 AAAAAAAAAAAAAA 5

RESULT 3571
US-09-891-517-44
; Sequence 44, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: TORIMURA, MASAKI
; APPLICANT: KURATA, SHINYA
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS
; TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA
; TITLE OF INVENTION: METHOD
; FILE REFERENCE: 210352US-1994-163-0-X
; CURRENT APPLICATION NUMBER: US/09/891,517
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: JP2000-193133
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: JP2000-236115
; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: JP2000-292483
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-891-517-44

Query Match 0.5%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 AAAAAAAAAAAAAA 2797
| | | | | | | | | | | | | | | |
Db 6 AAAAAAAAAAAAAA 18

RESULT 3572
US-10-683-386-48/c
; Sequence 48, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOLE
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/10/683,386
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US/09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-48

Query Match 0.5%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2785 AAAAAAAAAAAAAA 2797
| | | | | | | | | | | | | | | |
Db 13 AAAAAAAAAAAAAA 1

RESULT 3573
US-10-209-608-48/c
; Sequence 48, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU



```

; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1071

Query Match      0.5%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2798
Db      17 AAAAAAAAAAAAAA 5

RESULT 3565
US-09-823-887C-5/c
; Sequence 5, Application US/09823887C
; Publication No. US20030180723A1
; GENERAL INFORMATION:
; APPLICANT: Kumar, Sanjay
; APPLICANT: Lal, Lakhvir
; APPLICANT: Ahuja, Paramvir
; TITLE OF INVENTION: Cloning of No. US20030180723A1e1 Gene Sequences Expressed and Rep
; TITLE OF INVENTION: Dormancy in the Apical Buds of Tea (Camellia Sinensis L. (O.) Ku
; FILE REFERENCE: HO53916.0001US0
; CURRENT APPLICATION NUMBER: US/09/823,887C
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer_bind
US-09-823-887C-5

Query Match      0.5%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2798
Db      17 AAAAAAAAAAAAAA 5

RESULT 3566
US-09-823-887C-7/c
; Sequence 7, Application US/09823887C
; Publication No. US20030180723A1
; GENERAL INFORMATION:
; APPLICANT: Kumar, Sanjay
; APPLICANT: Lal, Lakhvir
; APPLICANT: Ahuja, Paramvir
; TITLE OF INVENTION: Cloning of No. US20030180723A1e1 Gene Sequences Expressed and Rep
; TITLE OF INVENTION: Dormancy in the Apical Buds of Tea (Camellia Sinensis L. (O.) Ku
; FILE REFERENCE: HO53916.0001US0
; CURRENT APPLICATION NUMBER: US/09/823,887C
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer_bind
US-09-823-887C-7

Query Match      0.5%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2798
```

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; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1071

Query Match      0.5%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2798
Db      17 AAAAAAAAAAAAAA 5

RESULT 3567
US-10-106-799-1/c
; Sequence 1, Application US/10106799
; Publication No. US20030140379A1
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: No. US20030140379A1e1 DNA sequence in plants Caragana jubata with
; TITLE OF INVENTION: method thereof
; FILE REFERENCE: US 673
; CURRENT APPLICATION NUMBER: US/10/106,799
; CURRENT FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T11A anchored primers for differential display
US-10-106-799-1

Query Match      0.5%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2798
Db      17 AAAAAAAAAAAAAA 5

RESULT 3568
US-10-106-799-3/c
; Sequence 3, Application US/10106799
; Publication No. US20030140379A1
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: No. US20030140379A1e1 DNA sequence in plants Caragana jubata with
; TITLE OF INVENTION: method thereof
; FILE REFERENCE: US 673
; CURRENT APPLICATION NUMBER: US/10/106,799
; CURRENT FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T11G (anchored) primer for differential display
US-10-106-799-3

Query Match      0.5%; Score 13; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAA 2798
Db      17 AAAAAAAAAAAAAA 5

RESULT 3569
US-10-109-363-16/c
; Sequence 16, Application US/10109363
; Publication No. US20030196214A1
; GENERAL INFORMATION:
; APPLICANT: SHARMA, PRITI
; APPLICANT: KUMAR, SANJAY
; APPLICANT: AHUJA, PARAMVIR SINGH
; TITLE OF INVENTION: NOVEL GENES FROM DROUGHT STRESS TOLERANT TEA PLANT AND A
```

```
;
;
; Best Local Similarity 83.3%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1970 TTTACCTTGAAAAAAGA 1987
Db 18 TTTACACTGAAAAAAGA 1

RESULT 3561
US-10-080-797-17/c
; Sequence 17, Application US/10080797
; Publication No. US20020183253A1
; GENERAL INFORMATION:
; APPLICANT: Campochiaro, Peter A.
; APPLICANT: Dixon, Katharine H.
; APPLICANT: Brazzell, Romulus K.
; TITLE OF INVENTION: METHOD FOR TREATING OCULAR
; TITLE OF INVENTION: NEOVASCULARIZATION
; FILE REFERENCE: 4-31891A
; CURRENT APPLICATION NUMBER: US/10/080,797
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-080-797-17

Query Match 0.5%; Score 13.2; DB 1; Length 23;
Best Local Similarity 83.3%; Pred. No. 3.7e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1970 TTTACCTTGAAAAAAGA 1987
Db 18 TTTACACTGAAAAAAGA 1

RESULT 3562
US-10-301-844-23/c
; Sequence 23, Application US/10301844
; Publication No. US20030100747A1
; GENERAL INFORMATION:
; APPLICANT: Ruddy, David A.
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: POLYMORPHISMS IN THE REGION OF THE HUMAN
; HEMOCHROMATOSIS GENE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds, LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/301,844
; FILING DATE: 20-No. US20030100747A1-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,495C
; FILING DATE: 07-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0057-999
```

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;
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-301-844-23

Query Match 0.5%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798
Db 14 AAAAAAAAAAAAAA 2

RESULT 3563
US-10-138-674-1071/c
; Sequence 1071, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1071
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-1071

Query Match 0.5%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2798
Db 17 AAAAAAAAAAAAAA 5

RESULT 3564
US-10-287-949A-1071/c
; Sequence 1071, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions ReJ
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1071
; LENGTH: 17
```

; APPLICANT: Batra, Surinder K.  
; APPLICANT: Brandt, Randall E.  
; APPLICANT: Ringel, J"erg  
; APPLICANT: Faulmann, Grit  
; APPLICANT: L"hr, Matthias  
; APPLICANT: Varshney, Grish C.  
; APPLICANT: University of Nebraska Board of Regents  
; TITLE OF INVENTION: Specific Mucin Expression as a Marker  
; FILE REFERENCE: UNMC 63155  
; CURRENT APPLICATION NUMBER: US/10/279,454  
; CURRENT FILING DATE: 2002-10-24  
; PRIOR APPLICATION NUMBER: US/09/733,444  
; PRIOR FILING DATE: 2000-12-08  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-10-279-454-13

Query Match 0.5%; Score 13.2; DB 1; Length 21;  
Best Local Similarity 83.3%; Pred. No. 3.6e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 718 CCTGTTGCTGCACGATCA 735  
|||||  
Db 18 CCTGCTGCTGGATGATCA 1

RESULT 3558  
US-10-213-329-3/c  
; Sequence 3, Application US/10213329  
; Publication No. US20030083465A1  
; GENERAL INFORMATION:  
; APPLICANT: Zimin, Ann B.  
; APPLICANT: Maciag, Thomas  
; APPLICANT: Wong, Michael K.K.  
; APPLICANT: Pepper, Michael S.  
; APPLICANT: Montesano, Roberto  
; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC METHODS AND COMPOSITIONS  
; TITLE OF INVENTION: BASED ON JAGGED/NOTCH PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE: 0036-101  
; CURRENT APPLICATION NUMBER: US/10/213,329  
; CURRENT FILING DATE: 2002-08-06  
; PRIOR APPLICATION NUMBER: US/09/199,865  
; PRIOR FILING DATE: 1998-11-25  
; PRIOR APPLICATION NUMBER: 60/018,841  
; PRIOR FILING DATE: 1996-05-31  
; PRIOR APPLICATION NUMBER: PCT/US97/09407  
; PRIOR FILING DATE: 1997-05-30  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: 3' reverse  
; OTHER INFORMATION: transcription primer  
US-10-213-329-3

Query Match 0.5%; Score 13.2; DB 1; Length 22;  
Best Local Similarity 83.3%; Pred. No. 3.7e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1978 GAAAAAAGAAAAAGTGTG 1995  
|||||  
Db 21 GAAAAAAGAAAAAGCTTG 4

RESULT 3559  
US-09-263-959-614/c  
; Sequence 614, Application US/09263959  
; Patent No. US20020150891A1  
; GENERAL INFORMATION:  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Rowen, Lee  
; APPLICANT: Koop, Ben F.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
; NUMBER OF SEQUENCES: 1279  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/263,959  
; FILING DATE: 05-MAR-1999  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 920010.426C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 614:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-263-959-614

Query Match 0.5%; Score 13.2; DB 1; Length 22;  
Best Local Similarity 83.3%; Pred. No. 3.7e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAA 2803  
|||||  
Db 22 AAAAAAAAAACAAACAAAA 5

RESULT 3560  
US-09-373-938-13/c  
; Sequence 13, Application US/09373938  
; Publication No. US20020115202A1  
; GENERAL INFORMATION:  
; APPLICANT: Hallenbeck, Paul  
; APPLICANT: Chen, Cheauyun Theresa  
; TITLE OF INVENTION: ADENO VIRAL VECTORS INCLUDING DNA SEQUENCES ENCODING ANGIOGENIC IN  
; FILE REFERENCE: 4-30899P1  
; CURRENT APPLICATION NUMBER: US/09/373,938  
; CURRENT FILING DATE: 1999-08-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-373-938-13

Query Match 0.5%; Score 13.2; DB 1; Length 23;

RESULT 3553  
US-10-085-906-446  
; Sequence 446, Application US/10085906  
; Publication No. US20030054371A1  
; GENERAL INFORMATION:  
; APPLICANT: Ying, Vincent  
; APPLICANT: Wu, Paul  
; APPLICANT: Gray, Gary S.  
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE  
; FILE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF  
; FILE REFERENCE: GNN-5343CP2  
; CURRENT APPLICATION NUMBER: US/10/085,906  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: US 60/126,215  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: US 09/534,061  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: PCT/US00/07938  
; NUMBER OF SEQ ID NOS: 545  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 446  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-085-906-446

Query Match 0.5%; Score 13.2; DB 1; Length 21;  
Best Local Similarity 83.3%; Pred. No. 3.6e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2803  
|||||  
Db 1 AAAAAAAAAATAAGGAA 18

RESULT 3554  
US-10-380-584-123/c  
; Sequence 123, Application US/10380584  
; Publication No. US20040014088A1  
; GENERAL INFORMATION:  
; APPLICANT: Utermohlen, Joseph  
; APPLICANT: Connaughton, John  
; TITLE OF INVENTION: Oligonucleotide Sequence Formula for Labeling Oligonucleotide Pro  
; TITLE OF INVENTION: Proteins for In Situ Analysis  
; FILE REFERENCE: 355/001/PCT  
; CURRENT APPLICATION NUMBER: US/10/380,584  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 60/233,177  
; PRIOR FILING DATE: 2000-09-15  
; NUMBER OF SEQ ID NOS: 126  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 123  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide probe  
US-10-380-584-123

Query Match 0.5%; Score 13.2; DB 1; Length 21;  
Best Local Similarity 83.3%; Pred. No. 3.6e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2803  
|||||  
Db 21 AAAAGAAAAATAGAAAAA 4

RESULT 3555  
US-10-085-906-465  
; Sequence 465, Application US/10085906  
; Publication No. US20030054371A1

; GENERAL INFORMATION:  
; APPLICANT: Ying, Vincent  
; APPLICANT: Wu, Paul  
; APPLICANT: Gray, Gary S.  
; TITLE OF INVENTION: POLYMORPHIC ELEMENTS IN THE  
; FILE OF INVENTION: COSTIMULATORY RECEPTOR LOCUS AND USES THEREOF  
; FILE REFERENCE: GNN-5343CP2  
; CURRENT APPLICATION NUMBER: US/10/085,906  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: US 60/126,215  
; PRIOR FILING DATE: 1999-03-25  
; PRIOR APPLICATION NUMBER: US 09/534,061  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: PCT/US00/07938  
; NUMBER OF SEQ ID NOS: 545  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 465  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-085-906-465

Query Match 0.5%; Score 13.2; DB 1; Length 21;  
Best Local Similarity 83.3%; Pred. No. 3.6e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAAAAAAAAAA 2803  
|||||  
Db 2 AAAAAATTAAAAAAAAAA 19

RESULT 3556  
US-09-733-444-13/c  
; Sequence 13, Application US/09733444  
; Patent No. US20020150894A1  
; GENERAL INFORMATION:  
; APPLICANT: Batra, Surinder K.  
; APPLICANT: Brandt, Randall E.  
; APPLICANT: Ringel, J"erg  
; APPLICANT: Faulmann, Grit  
; APPLICANT: L"hr, Matthias  
; APPLICANT: Varshney, Grish C.  
; APPLICANT: University of Nebraska Board of Regents  
; TITLE OF INVENTION: Specific Mucin Expression as a Marker  
; TITLE OF INVENTION: for Pancreatic Cancer  
; FILE REFERENCE: UNMC 63155  
; CURRENT APPLICATION NUMBER: US/09/733,444  
; CURRENT FILING DATE: 2000-12-08  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-733-444-13

Query Match 0.5%; Score 13.2; DB 1; Length 21;  
Best Local Similarity 83.3%; Pred. No. 3.6e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 718 CCTGTTGCTGCACGATCA 735  
|||||  
Db 18 CCTGCTGCTGGATGATCA 1

RESULT 3557  
US-10-279-454-13/c  
; Sequence 13, Application US/10279454  
; Publication No. US20030134343A1  
; GENERAL INFORMATION:



; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1724  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: human GFAT antisense  
US-10-688-706-1724

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 894 CAGTGGCTGAAGTACAGA 911  
||| | ||| |||||  
Db 18 CAGAGACTGGAGTACAGA 1

RESULT 3549  
US-10-688-706-1855  
; Sequence 1855, Application US/10688706  
; Publication No. US20040102412A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corp.  
; APPLICANT: Broschat, Kay  
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION  
; FILE REFERENCE: 01393/1  
; CURRENT APPLICATION NUMBER: US/10/688,706  
; CURRENT FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: 60/419,268  
; PRIOR FILING DATE: 2002-10-17  
; NUMBER OF SEQ ID NOS: 3071  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1855  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: human GFAT antisense  
US-10-688-706-1855

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1824 TAGAATCTTTTAAATACA 1841  
||||| |||||  
Db 3 TAGAATCTTCTGATACA 20

RESULT 3550  
US-10-688-706-2086/c  
; Sequence 2086, Application US/10688706  
; Publication No. US20040102412A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corp.  
; APPLICANT: Broschat, Kay  
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION  
; FILE REFERENCE: 01393/1  
; CURRENT APPLICATION NUMBER: US/10/688,706  
; CURRENT FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: 60/419,268  
; PRIOR FILING DATE: 2002-10-17  
; NUMBER OF SEQ ID NOS: 3071  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2086  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: human GFAT antisense  
US-10-688-706-2086

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2171 TTTTCTTTTGTGTTTAA 2188  
||| | ||| |||||  
Db 19 TTTCTGTTTGTGTTTAA 2

RESULT 3551  
US-10-688-706-2139  
; Sequence 2139, Application US/10688706  
; Publication No. US20040102412A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corp.  
; APPLICANT: Broschat, Kay  
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION  
; FILE REFERENCE: 01393/1  
; CURRENT APPLICATION NUMBER: US/10/688,706  
; CURRENT FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: 60/419,268  
; PRIOR FILING DATE: 2002-10-17  
; NUMBER OF SEQ ID NOS: 3071  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2139  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: human GFAT antisense  
US-10-688-706-2139

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1824 TAGAATCTTTTAAATACA 1841  
||||| |||||  
Db 2 TAGAATCTTCTGATACA 19

RESULT 3552  
US-10-688-706-2365  
; Sequence 2365, Application US/10688706  
; Publication No. US20040102412A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corp.  
; APPLICANT: Broschat, Kay  
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION  
; FILE REFERENCE: 01393/1  
; CURRENT APPLICATION NUMBER: US/10/688,706  
; CURRENT FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: 60/419,268  
; PRIOR FILING DATE: 2002-10-17  
; NUMBER OF SEQ ID NOS: 3071  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2365  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: human GFAT antisense  
US-10-688-706-2365

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1824 TAGAATCTTTTAAATACA 1841  
||||| |||||  
Db 1 TAGAATCTTCTGATACA 18

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Db      18 AAGCCAGTGGCAGTGTAT 1
      || |||||
RESULT 3544
US-10-688-706-441/c
; Sequence 441, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 441
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-441

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      896 GTGGCTGAAGTACAGAGG 913
      || |||||
Db      20 GAGACTGGAGTACAGAGG 3

RESULT 3545
US-10-688-706-475/c
; Sequence 475, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 475
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-475

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1148 AAACCAAGTGGCAGATAT 1165
      || |||||
Db      20 AAGCCAGTGGCAGTGTAT 3

RESULT 3546
US-10-688-706-1639
; Sequence 1639, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1639
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-1639

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2226 AATGACATGTTCCCTTAA 2243
      ||| ||||| ||| |||||
Db      1 AATCACATCTTCTCTTAA 18

RESULT 3547
US-10-688-706-1698
; Sequence 1698, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1698
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-1698

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2225 AAATGACATGTTCCCTTA 2242
      |||| ||||| ||| |||||
Db      3 AAATCACATCTTCTCTTA 20

RESULT 3548
US-10-688-706-1724/c
; Sequence 1724, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
```

```
; APPLICANT: Susan M. Freier
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF SQUALENE SYNTHASE EXPRESSION
; FILE REFERENCE: PTS-0056
; CURRENT APPLICATION NUMBER: US/10/304,125
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-125-68

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1059 ATGTGACTCTCCTGACAT 1076
Db      18 ATGTGACTGTTCATGAGAT 1

RESULT 3540
US-10-304-125-126
; Sequence 126, Application US/10304125
; Publication No. US20040102405A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF SQUALENE SYNTHASE EXPRESSION
; FILE REFERENCE: PTS-0056
; CURRENT APPLICATION NUMBER: US/10/304,125
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 126
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-304-125-126

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1740 GTGACAAGTACTGGCTCT 1757
Db      3 GGGACAAGTACTGCCACT 20

RESULT 3541
US-10-304-125-135
; Sequence 135, Application US/10304125
; Publication No. US20040102405A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF SQUALENE SYNTHASE EXPRESSION
; FILE REFERENCE: PTS-0056
; CURRENT APPLICATION NUMBER: US/10/304,125
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 135
; LENGTH: 20
; TYPE: DNA
```

```
; ORGANISM: H. sapiens
; FEATURE:
US-10-304-125-135

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1059 ATGTGACTCTCCTGACAT 1076
Db      3 ATGTGACTGTTCATGAGAT 20

RESULT 3542
US-10-688-706-331/c
; Sequence 331, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 331
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-331

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1148 AAACCAGTGGCAGAAATAT 1165
Db      19 AAGCCAGTGGCAGTGTAT 2

RESULT 3543
US-10-688-706-341/c
; Sequence 341, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 341
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-341

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1148 AAACCAGTGGCAGAAATAT 1165
```

```

; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF HEPATOCYTE GROWTH FACTOR RECEPTOR EXPRESSION
; FILE REFERENCE: PTS-0043
; CURRENT APPLICATION NUMBER: US/10/304,019
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 147
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-019-38

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1139 TTTCTAGTAAACCAAGTG 1156
      ||||| ||||| |||||
Db      2 TGTCTATTAAAGCAGTG 19

RESULT 3535
US-10-304-019-109/c
; Sequence 109, Application US/10304019
; Publication No. US20040102622A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF HEPATOCYTE GROWTH FACTOR RECEPTOR EXPRESSION
; FILE REFERENCE: PTS-0043
; CURRENT APPLICATION NUMBER: US/10/304,019
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 147
; SEQ ID NO 109
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-304-019-109

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1139 TTTCTAGTAAACCAAGTG 1156
      ||||| ||||| |||||
Db      19 TGTCTATTAAAGCAGTG 2

RESULT 3536
US-10-304-113-71/c
; Sequence 71, Application US/10304113
; Publication No. US20040102623A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF PAK1 EXPRESSION
; FILE REFERENCE: RTS-0415
; CURRENT APPLICATION NUMBER: US/10/304,113
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 167
; SEQ ID NO 71
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-113-71
```

```

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 701 AATGTCGACGACCAAGCAC 718
      ||||| ||||| |||||
Db 20 AATGTCAAATACCAGCAC 3

RESULT 3537
US-10-304-113-145
; Sequence 145, Application US/10304113
; Publication No. US20040102623A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF PAK1 EXPRESSION
; FILE REFERENCE: RTS-0415
; CURRENT APPLICATION NUMBER: US/10/304,113
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 167
; SEQ ID NO 145
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-304-113-145

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 701 AATGTCGACGACCAAGCAC 718
      ||||| ||||| |||||
Db 1 AATGTCAAATACCAGCAC 18

RESULT 3538
US-10-304-125-59/c
; Sequence 59, Application US/10304125
; Publication No. US20040102405A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF SQUALENE SYNTHASE EXPRESSION
; FILE REFERENCE: PTS-0056
; CURRENT APPLICATION NUMBER: US/10/304,125
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-125-59

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1740 GTGACAAGTACTGGCTCT 1757
      ||||| ||||| |||||
Db 18 GGGACAAGTACTGCCACT 1

RESULT 3539
US-10-304-125-68/c
; Sequence 68, Application US/10304125
; Publication No. US20040102405A1
; GENERAL INFORMATION:
```



```

; APPLICANT: Donna T. Ward
; APPLICANT: Alexander H. Borchers
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF GLUCOSE TRANSPORTER-4 EXPRESSION
; FILE REFERENCE: RTS-0426
; CURRENT APPLICATION NUMBER: US/10/303,266
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 157
; SEQ ID NO 103
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-303-266-103

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1165 TTTAACCAGACCTCATCT 1182
Db 1 TTGACCAGATCTCAGCT 18

RESULT 3530
US-10-303-327-44
; Sequence 44, Application US/10303327
; Publication No. US20040102396A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF BCL2-ASSOCIATED ATHANOGENE 5 EXPRESSION
; FILE REFERENCE: HTS-0004
; CURRENT APPLICATION NUMBER: US/10/303,327
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 77
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-327-44

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1086 AAGGTGAAGCTGTTTCATT 1103
Db 3 AAGGTCAATCTGATCATT 20

RESULT 3531
US-10-303-327-75/c
; Sequence 75, Application US/10303327
; Publication No. US20040102396A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF BCL2-ASSOCIATED ATHANOGENE 5 EXPRESSION
; FILE REFERENCE: HTS-0004
; CURRENT APPLICATION NUMBER: US/10/303,327
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 77
; SEQ ID NO 75
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-303-327-75
```

```

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1086 AAGGTGAAGCTGTTTCATT 1103
Db 18 AAGGTCAATCTGATCATT 1

RESULT 3532
US-10-303-420-167/c
; Sequence 167, Application US/10303420
; Publication No. US20040102398A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF B7H EXPRESSION
; FILE REFERENCE: RTS-0417
; CURRENT APPLICATION NUMBER: US/10/303,420
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 271
; SEQ ID NO 167
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-420-167

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 794 CAGAAGGAGCTGGTGGG 811
Db 19 CACAAGGAGCAGTTGGG 2

RESULT 3533
US-10-303-635-44
; Sequence 44, Application US/10303635
; Publication No. US20040102621A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF FORKHEAD BOX C2 EXPRESSION
; FILE REFERENCE: RTS-0418
; CURRENT APPLICATION NUMBER: US/10/303,635
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 257
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-635-44

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1388 GCGGTGTCTGCCCTGCAG 1405
Db 2 GCGGGGCTGCCCTGCAG 19

RESULT 3534
US-10-304-019-38
; Sequence 38, Application US/10304019
; Publication No. US20040102622A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
```



Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2704 TGAACCTCTCTGCCTGTAA 2721  
| | | | | | | | | | | | | | | |  
Db 18 TGAGATCTCTGGCTGTAA 1

RESULT 3519  
US-10-300-236-45/c  
; Sequence 45, Application US/10300236  
; Publication No. US20040097448A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: MODULATION OF CD24 EXPRESSION  
; FILE REFERENCE: RTS-0178  
; CURRENT APPLICATION NUMBER: US/10/300,236  
; CURRENT FILING DATE: 2002-11-19  
; NUMBER OF SEQ ID NOS: 148  
; SEQ ID NO 45  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-300-236-45

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2696 TTTGGAATTGAACTCTCT 2713  
| | | | | | | | | | | | | | | |  
Db 19 TTGGGAAGCTGAACTCACT 2

RESULT 3520  
US-10-300-236-116  
; Sequence 116, Application US/10300236  
; Publication No. US20040097448A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: MODULATION OF CD24 EXPRESSION  
; FILE REFERENCE: RTS-0178  
; CURRENT APPLICATION NUMBER: US/10/300,236  
; CURRENT FILING DATE: 2002-11-19  
; NUMBER OF SEQ ID NOS: 148  
; SEQ ID NO 116  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
US-10-300-236-116

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2696 TTTGGAATTGAACTCTCT 2713  
| | | | | | | | | | | | | | | |  
Db 2 TTGGGAAGCTGAACTCACT 19

RESULT 3521  
US-10-300-263-23  
; Sequence 23, Application US/10300263  
; Publication No. US20040096834A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: MODULATION OF HIP-1 PROTEIN INTERACTOR EXPRESSION  
; FILE REFERENCE: RTS-0431  
; CURRENT APPLICATION NUMBER: US/10/300,263  
; CURRENT FILING DATE: 2002-11-19  
; NUMBER OF SEQ ID NOS: 154

; SEQ ID NO 23  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-300-263-23

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1264 CAGCCAAGACCGGACACC 1281  
| | | | | | | | | | | | | | | |  
Db 1 CAGCCACGACCGGTTACC 18

RESULT 3522  
US-10-300-263-29/c  
; Sequence 29, Application US/10300263  
; Publication No. US20040096834A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: MODULATION OF HIP-1 PROTEIN INTERACTOR EXPRESSION  
; FILE REFERENCE: RTS-0431  
; CURRENT APPLICATION NUMBER: US/10/300,263  
; CURRENT FILING DATE: 2002-11-19  
; NUMBER OF SEQ ID NOS: 154  
; SEQ ID NO 29  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-300-263-29

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1082 GTAGAAGGTGAAGCTGTT 1099  
| | | | | | | | | | | | | | | |  
Db 18 GGAGAAGCTGAAGCTGCT 1

RESULT 3523  
US-10-300-263-104  
; Sequence 104, Application US/10300263  
; Publication No. US20040096834A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: MODULATION OF HIP-1 PROTEIN INTERACTOR EXPRESSION  
; FILE REFERENCE: RTS-0431  
; CURRENT APPLICATION NUMBER: US/10/300,263  
; CURRENT FILING DATE: 2002-11-19  
; NUMBER OF SEQ ID NOS: 154  
; SEQ ID NO 104  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
US-10-300-263-104

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1082 GTAGAAGGTGAAGCTGTT 1099  
| | | | | | | | | | | | | | | |  
Db 3 GGAGAAGCTGAAGCTGCT 20

RESULT 3524

```

; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-34

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1485 AAACCCTGGAGAAATGG 1502
Db 1 AAACCCTGAAGCAAAAGG 18

RESULT 3515
US-10-728-509-35
; Sequence 35, Application US/10728509
; Publication No. US20040077583A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
; CURRENT FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US/09/908,147
; PRIOR FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-728-509-35

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1485 AAACCCTGGAGAAATGG 1502
Db 2 AAACCCTGAAGCAAAAGG 19

RESULT 3516
US-10-280-183A-393/c
; Sequence 393, Application US/10280183A
; Publication No. US20040081964A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Bachmanov, Alexander A
; APPLICANT: Beauchamp, Gary K.
; APPLICANT: Chatterjee, Aurobindo
; APPLICANT: De Jong, Pieter J.
; APPLICANT: Li, Shanru
; APPLICANT: Li, Xia
; APPLICANT: Ohmen, Jeffrey D
; APPLICANT: Reed, Danielle R.
; APPLICANT: Ross, David
; APPLICANT: Tordoff, Michael G.
; TITLE OF INVENTION: GENE AND SEQUENCE VARIATION ASSOCIATED WITH SENSING
; FILE REFERENCE: PC18306A
; CURRENT APPLICATION NUMBER: US/10/280,183A
; CURRENT FILING DATE: 2002-10-25

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; PRIOR APPLICATION NUMBER: 60/200,794
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 393
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Mouse
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-280-183A-393

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1571 ATCCTTCTCCACCGCACA 1588
Db 20 ATCCTTTTCCACCCCAAA 3

RESULT 3517
US-10-643-432-75
; Sequence 75, Application US/10643432
; Publication No. US20040087536A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF KOX 1 EXPRESSION
; FILE REFERENCE: RTS-0359
; CURRENT APPLICATION NUMBER: US/10/643,432
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US/10/173,817
; PRIOR FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 131
; SEQ ID NO 75
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-432-75

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2704 TGAACCTCTGCGCTGTAA 2721
Db 3 TGAGATCTCTGGCTGTAA 20

RESULT 3518
US-10-643-432-127/c
; Sequence 127, Application US/10643432
; Publication No. US20040087536A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF KOX 1 EXPRESSION
; FILE REFERENCE: RTS-0359
; CURRENT APPLICATION NUMBER: US/10/643,432
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US/10/173,817
; PRIOR FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 131
; SEQ ID NO 127
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-643-432-127

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;

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; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-628-841-87

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1063 GACTCTCCTGACATCCTT 1080
Db 19 GACTCTGCTGACAGCCCT 2

RESULT 3510
US-10-272-461-49/c
; Sequence 49, Application US/10272461
; Publication No. US20040076959A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasan, Subha
; APPLICANT: Bingham, Jonathan
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR POLYNUCLEOTIDE DETECTION
; FILE REFERENCE: 37087-8002 US 01
; CURRENT APPLICATION NUMBER: US/10/272,461
; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/343,298
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-461-49

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2679 TGTGGTGAATGAGAT 2696
Db 20 TGTGGTTGAATGGTGCT 3

RESULT 3511
US-10-272-810-29
; Sequence 29, Application US/10272810
; Publication No. US20040077568A1
; GENERAL INFORMATION:
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF NOTCH (DROSOPHILA) HOMOLOG 4 EXPRESSION
; FILE REFERENCE: RTS-0263
; CURRENT APPLICATION NUMBER: US/10/272,810
; CURRENT FILING DATE: 2002-10-16
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-272-810-29

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 722 TTGCTGCACGATCAGACA 739
Db 3 TTGCTGGGCCATCAGACA 20
```

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RESULT 3512
US-10-273-070-29
; Sequence 29, Application US/10273070
; Publication No. US20040077569A1
; GENERAL INFORMATION:
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF NOTCH (DROSOPHILA) HOMOLOG 4 EXPRESSION
; FILE REFERENCE: RTS-0231
; CURRENT APPLICATION NUMBER: US/10/273,070
; CURRENT FILING DATE: 2002-10-16
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-273-070-29

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 722 TTGCTGCACGATCAGACA 739
Db 3 TTGCTGGGCCATCAGACA 20

RESULT 3513
US-10-703-864-62/c
; Sequence 62, Application US/10703864
; Publication No. US20040077580A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: Susan Murray
; APPLICANT: Madeline M. Butler
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE MODULATION OF PI3K P85 EXPRESSION
; FILE REFERENCE: ISIS0057-102 (ISPH-0519)
; CURRENT APPLICATION NUMBER: US/10/703,864
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US/09/715,983
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-703-864-62

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 452 ACAGGCAGCCGACGACGAG 469
Db 20 AGAGACAGCCGACGACCCAG 3

RESULT 3514
US-10-728-509-34
; Sequence 34, Application US/10728509
; Publication No. US20040077583A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/10/728,509
```

US-10-210-723-116

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1675 CCTGGACTTCTTAGTTGT 1692  
| | | | | | | | | | | | | | | | | | | | | |  
Db 19 CCTGGAGCTCTGAGTTGT 2

RESULT 3505

US-10-210-723-121/c  
; Sequence 121, Application US/10210723  
; Publication No. US20040023382A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPP3CB EXPRESSION  
; FILE REFERENCE: PTS-0028  
; CURRENT APPLICATION NUMBER: US/10/210,723  
; CURRENT FILING DATE: 2002-07-31  
; NUMBER OF SEQ ID NOS: 141  
; SEQ ID NO 121  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-210-723-121

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2074 ATCTGACACACTCTAAAC 2091  
| | | | | | | | | | | | | | | | | | | | | |  
Db 20 ATAAGACACACTCTATAC 3

RESULT 3506

US-10-210-838-60  
; Sequence 60, Application US/10210838  
; Publication No. US20040023905A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Sanjay Bhanot  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF LAR EXPRESSION  
; FILE REFERENCE: PTS-0013  
; CURRENT APPLICATION NUMBER: US/10/210,838  
; CURRENT FILING DATE: 2002-07-31  
; NUMBER OF SEQ ID NOS: 198  
; SEQ ID NO 60  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-210-838-60

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1640 TTAAAGAGCCTTCACTG 1657  
| | | | | | | | | | | | | | | | | | | | | |  
Db 2 TTGAAGAGCTTTCACG 19

RESULT 3507

US-10-212-993-24  
; Sequence 24, Application US/10212993  
; Publication No. US20040023385A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF REQUIEM EXPRESSION  
; FILE REFERENCE: PTS-0031  
; CURRENT APPLICATION NUMBER: US/10/212,993  
; CURRENT FILING DATE: 2002-08-05  
; NUMBER OF SEQ ID NOS: 132  
; SEQ ID NO 24  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-212-993-24

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 460 CCAGCAGCAGCCTGGCC 477  
| | | | | | | | | | | | | | | | | | | | | |  
Db 3 CGAGCTGCTGGCCTGGCC 20

RESULT 3508

US-10-212-993-91/c  
; Sequence 91, Application US/10212993  
; Publication No. US20040023385A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF REQUIEM EXPRESSION  
; FILE REFERENCE: PTS-0031  
; CURRENT APPLICATION NUMBER: US/10/212,993  
; CURRENT FILING DATE: 2002-08-05  
; NUMBER OF SEQ ID NOS: 132  
; SEQ ID NO 91  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
US-10-212-993-91

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 460 CCAGCAGCAGCCTGGCC 477  
| | | | | | | | | | | | | | | | | | | | | |  
Db 18 CGAGCTGCTGGCCTGGCC 1

RESULT 3509

US-10-628-841-87/c  
; Sequence 87, Application US/10628841  
; Publication No. US20040023918A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-GAMMA EXPRESSION  
; FILE REFERENCE: RTS-0191  
; CURRENT APPLICATION NUMBER: US/10/628,841  
; CURRENT FILING DATE: 2003-07-28  
; PRIOR APPLICATION NUMBER: US/09/972,607  
; PRIOR FILING DATE: 2001-10-06  
; NUMBER OF SEQ ID NOS: 88  
; SEQ ID NO 87

US-10-179-940-533/c  
; Sequence 533, Application US/10179940  
; Publication No. US20040018618A1  
; GENERAL INFORMATION:  
; APPLICANT: Abrams, Mark A.  
; Bauer, S. C.  
; Braford-Goldberg, Sarah R.  
; Caparon, Mairé H.  
; Easton, Alan M.  
; Klein, Barbara K.  
; McKearn, John P.  
; Olin, Peter O.  
; Paik, Kuman  
; Polazzi, Joseph O.  
; TITLE OF INVENTION: Interleukin-3 (IL-3) Mutant Polypeptides  
; NUMBER OF SEQUENCES: 549  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Carol M. Nielsen, Gardere Wynne Sewell LLP,  
; STREET: 1601 Elm Street, Suite 3000  
; CITY: Dallas  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 75201-4761  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/179,940  
; FILING DATE: 19-Jun-2002  
; CLASSIFICATION: Unknown  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/981044  
; FILING DATE: 24-NOV-1992  
; APPLICATION NUMBER: PCT/US93/11198  
; FILING DATE: 22-NOV-1993  
; APPLICATION NUMBER: US 08/411796  
; FILING DATE: 09-APR-1995  
; APPLICATION NUMBER: US 08/559390  
; FILING DATE: 15-NOV-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Carol M. Nielsen  
; REGISTRATION NUMBER: 37,676  
; REFERENCE/DOCKET NUMBER: 126181-1056 (C2713/1)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (713)276-5383  
; TELEFAX: (713)276-5555  
; INFORMATION FOR SEQ ID NO: 533:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (synthetic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 533:  
US-10-179-940-533  
  
Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1241 TGTAAGAATTTCACAGAA 1258  
||| ||| ||| ||| |||  
Db 18 TGTCAGAGCTTACAGAA 1  
  
RESULT 3502  
US-10-210-723-47  
; Sequence 47, Application US/10210723  
; Publication No. US20040023382A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean

; APPLICANT: C. Frank Bennett  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPP3CB EXPRESSION  
; FILE REFERENCE: PTS-0028  
; CURRENT APPLICATION NUMBER: US/10/210,723  
; CURRENT FILING DATE: 2002-07-31  
; NUMBER OF SEQ ID NOS: 141  
; SEQ ID NO 47  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-210-723-47  
  
Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1675 CCTGGACTTCTTAGTTGT 1692  
||||| ||| |||||  
Db 2 CCTGGAGCTCTGAGTTGT 19  
  
RESULT 3503  
US-10-210-723-53  
; Sequence 53, Application US/10210723  
; Publication No. US20040023382A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPP3CB EXPRESSION  
; FILE REFERENCE: PTS-0028  
; CURRENT APPLICATION NUMBER: US/10/210,723  
; CURRENT FILING DATE: 2002-07-31  
; NUMBER OF SEQ ID NOS: 141  
; SEQ ID NO 53  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-210-723-53  
  
Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2074 ATCTGACACACTCTAAAC 2091  
|| ||||| ||||| |||  
Db 1 ATAAGACACACTCTATAC 18  
  
RESULT 3504  
US-10-210-723-116/c  
; Sequence 116, Application US/10210723  
; Publication No. US20040023382A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PPP3CB EXPRESSION  
; FILE REFERENCE: PTS-0028  
; CURRENT APPLICATION NUMBER: US/10/210,723  
; CURRENT FILING DATE: 2002-07-31  
; NUMBER OF SEQ ID NOS: 141  
; SEQ ID NO 116  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-131-827-8899

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 455 GGCAGCCAGCAGCAGGCC 472
Db 20 GACAGACAGCAGCAGACC 3

RESULT 3497
US-10-131-827-8991/c
; Sequence 8991, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8991
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-131-827-8991

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2131 GTAGAAACGAAGCCTGCT 2148
Db 19 GTAGAAACCAACCCCTGCT 2

RESULT 3498
US-10-199-199-85
; Sequence 85, Application US/10199199
; Publication No. US20040014047A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIM DOMAIN KINASE 1 EXPRESSION
; FILE REFERENCE: RTS-0375
; CURRENT APPLICATION NUMBER: US/10/199,199
; CURRENT FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 148
; SEQ ID NO 85
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-199-199-85

Query Match      0.5%; Score 13.2; DB 1; Length 20;
```

```

Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2656 AGGTGAGTGTGCAGTACA 2673
Db 3 AGGTGAGTGTGCAAGGCA 20

RESULT 3499
US-10-199-199-143/c
; Sequence 143, Application US/10199199
; Publication No. US20040014047A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIM DOMAIN KINASE 1 EXPRESSION
; FILE REFERENCE: RTS-0375
; CURRENT APPLICATION NUMBER: US/10/199,199
; CURRENT FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 148
; SEQ ID NO 143
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION:
US-10-199-199-143

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2656 AGGTGAGTGTGCAGTACA 2673
Db 18 AGGTGAGTGTGCAAGGCA 1

RESULT 3500
US-10-435-696-204
; Sequence 204, Application US/10435696
; Publication No. US20040018525A1
; GENERAL INFORMATION:
; APPLICANT: Wirtz, Ralph
; APPLICANT: Munnes, Marc
; APPLICANT: Kallabis, Harald
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSIS,
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
; FILE REFERENCE: Lea 36 108
; CURRENT APPLICATION NUMBER: US/10/435,696
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: EP03003112.4
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: EP02010291.9
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 314
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 204
; LENGTH: 20
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: ORMDL3
US-10-435-696-204

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 505 GCTGCCCTCGCACCACGG 522
Db 2 GCTGCCCCAGCTCCACGG 19

RESULT 3501
```



```
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-5130

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      625 ACACGCCCTGGATGCCGC 642
      |||||
Db      18 ACACGCCCTGAATATCGC 1

RESULT 3492
US-10-289-762-6118
; Sequence 6118, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6118
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-6118

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1318 GAACATACAGAACTGCTT 1335
      |||||
Db      2 GAACATAGAGAACTCCAT 19

RESULT 3493
US-10-289-762-6292
; Sequence 6292, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6292
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-6292

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      762 CCATGACCAAGAACCCCTC 779
      |||||
Db      1 CCATCACAAGACCCCTC 18

RESULT 3494
US-10-289-762-6579/c
; Sequence 6579, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6579
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-6579

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      495 AGGAGCGGGGCTGCCCT 512
      |||||
Db      20 ATGTGCGGGGCTGCCCT 3

RESULT 3495
US-10-289-762-6757/c
; Sequence 6757, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6757
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-6757

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1068 TCCTGACATCCTTAGTAG 1085
      |||||
Db      20 TCCTGGCAATCTTAGTAG 3

RESULT 3496
US-10-131-827-8899/c
; Sequence 8899, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8899
; LENGTH: 20
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; CURRENT APPLICATION NUMBER: US/10/289,762  
; CURRENT FILING DATE: 2003-03-27  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 2313  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Chlamydia pneumoniae  
US-10-289-762-2313

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2046 TCTGCTTAGCAACTAGTT 2063  
| | | | | | | | | | | | | | | |  
Db 3 TCTGCTTAGGAAGTGTCT 20

RESULT 3487  
US-10-289-762-2530/c  
; Sequence 2530, Application US/10289762  
; Publication No. US20040006218A1  
; GENERAL INFORMATION:  
; APPLICANT: Griffais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/10/289,762  
; CURRENT FILING DATE: 2003-03-27  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 2530  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Chlamydia pneumoniae  
US-10-289-762-2530

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2551 TAAGAGGATGCTGGGCTC 2568  
| | | | | | | | | | | | | | | |  
Db 20 TATGAGGAGGCTGGGCC 3

RESULT 3488  
US-10-289-762-2581/c  
; Sequence 2581, Application US/10289762  
; Publication No. US20040006218A1  
; GENERAL INFORMATION:  
; APPLICANT: Griffais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/10/289,762  
; CURRENT FILING DATE: 2003-03-27  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 2581  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Chlamydia pneumoniae  
US-10-289-762-2581

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 686 ATGGACGAGGTGCAGAAAT 703  
| | | | | | | | | | | | | | | |  
Db 20 ATGTACGAGGTGCTGACT 3

RESULT 3489  
US-10-289-762-4019  
; Sequence 4019, Application US/10289762  
; Publication No. US20040006218A1  
; GENERAL INFORMATION:  
; APPLICANT: Griffais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/10/289,762  
; CURRENT FILING DATE: 2003-03-27  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 4019  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Chlamydia pneumoniae  
US-10-289-762-4019

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1479 CTAACAAAACCTGGAGA 1496  
| | | | | | | | | | | | | | | |  
Db 1 CCACCAAAAACCTGGAGA 18

RESULT 3490  
US-10-289-762-5039/c  
; Sequence 5039, Application US/10289762  
; Publication No. US20040006218A1  
; GENERAL INFORMATION:  
; APPLICANT: Griffais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/10/289,762  
; CURRENT FILING DATE: 2003-03-27  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 5039  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Chlamydia pneumoniae  
US-10-289-762-5039

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2127 ACTTGTAAGAACGAAGCC 2144  
| | | | | | | | | | | | | | | |  
Db 18 ACTTCTAAGACGAAGCC 1

RESULT 3491  
US-10-289-762-5130/c  
; Sequence 5130, Application US/10289762  
; Publication No. US20040006218A1  
; GENERAL INFORMATION:  
; APPLICANT: Griffais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/10/289,762  
; CURRENT FILING DATE: 2003-03-27  
; NUMBER OF SEQ ID NOS: 6849  
; SEQ ID NO 5130  
; LENGTH: 20  
; TYPE: DNA  
US-10-289-762-5130

; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10558
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer\_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-14228 for SEQ 2693, in complem
US-10-349-143-10558

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2688 AATGGAGATTGGAAATG 2705
||| ||| ||| ||| ||| ||| |||
Db 19 AAGGAAATTGAAATG 2

RESULT 3482
US-10-188-883-84
; Sequence 84, Application US/10188883
; Publication No. US20040006005A1
; GENERAL INFORMATION:

; APPLICANT: Bhanot, Sanjay
; TITLE OF INVENTION: USE OF INTEGRIN-LINKED KINASE INHIBITORS FOR TREATING INSULIN RES
; TITLE OF INVENTION: HYPERGLYCEMIA AND DIABETES
; FILE REFERENCE: ISPH-0687
; CURRENT APPLICATION NUMBER: US/10/188,883
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide.
US-10-188-883-84

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1461 ACCAGAGTCGAGTGATT 1478
||| ||| ||| ||| ||| ||| |||
Db 3 ACCAGAGGCCTGCTGCTT 20

RESULT 3483
US-10-189-267-101/c
; Sequence 101, Application US/10189267
; Publication No. US20040006030A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION
; FILE REFERENCE: PTS-0038
; CURRENT APPLICATION NUMBER: US/10/189,267
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 284

; SEQ ID NO 101
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-267-101

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1830 CTTTAAATACATTCCT 1847
||||| ||| |||
Db 18 CTTTAAACATGCACT 1

RESULT 3484
US-10-289-762-1828/c
; Sequence 1828, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1828
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-1828

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2658 GTGAGTGTGCAGTACAGT 2675
||| ||| ||| ||| ||| ||| |||
Db 20 GAGAGTGTGCTGTAAGT 3

RESULT 3485
US-10-289-762-2037
; Sequence 2037, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2037
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-2037

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 750 AAGTCCCATTTCCATGA 767
||||| ||| ||| ||| |||
Db 3 AAGTCTCATATCCAGGA 20

RESULT 3486
US-10-289-762-2313
; Sequence 2313, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999

```
QY      1681 CTTCTTAGTTGTTTCTCT 1698
      ||||| ||||| ||||| |||||
Db      20 CTTCCAAGTTGTTTCTCT 3

RESULT 3478
US-10-349-143-4188/c
; Sequence 4188, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4188
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-13861 for SEQ 254,
US-10-349-143-4188

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1240 GTGTAAGAATTCACAGA 1257
      ||||| ||||| ||||| |||||
Db      19 GTGTAAAAACTCAAAGA 2

RESULT 3479
US-10-349-143-4995/c
; Sequence 4995, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4995
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
```

```
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-20074 for SEQ 1061,
US-10-349-143-4995

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      424 CATCAACCCCTGCACCA 441
      ||||| ||||| ||||| |||||
Db      20 CTTCAACCCCTGCCCAA 3

RESULT 3480
US-10-349-143-7152
; Sequence 7152, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7152
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-24966 for SEQ 3218,
US-10-349-143-7152

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      770 AAGAACCCTCTGAACCTC 787
      ||||| ||||| ||||| |||||
Db      1 AGGAACCCCTGAACCTC 18

RESULT 3481
US-10-349-143-10558/c
; Sequence 10558, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
```



; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
; FILE REFERENCE: RTS-0373
; CURRENT APPLICATION NUMBER: US/10/188,646
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 138
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-188-646-138

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2561 CTGGGCTCTGTTCTTGGC 2578
||||| ||| ||||| |||
Db 2 CTGGACTGTGTTCTTGGC 19

RESULT 3474
US-10-188-779A-111/c
; Sequence 111, Application US/10188779A
; Publication No. US20040005567A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF CYCLIN-DEPENDENT KINASE 4 EXPRESSION
; FILE REFERENCE: PTS-0042
; CURRENT APPLICATION NUMBER: US/10/188,779A
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 282
; SEQ ID NO 111
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-188-779A-111

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 799 GGAGCTGGTGGGGCCGT 816
| ||||| ||||| |||
Db 20 GCAGCTGGAGGGGCCCTT 3

RESULT 3475
US-10-188-779A-240
; Sequence 240, Application US/10188779A
; Publication No. US20040005567A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF CYCLIN-DEPENDENT KINASE 4 EXPRESSION
; FILE REFERENCE: PTS-0042
; CURRENT APPLICATION NUMBER: US/10/188,779A
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 282
; SEQ ID NO 240
; LENGTH: 20
; TYPE: DNA
; ORGANISM: M. musculus
US-10-188-779A-240

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 799 GGAGCTGGTGGGGCCGT 816
| ||||| ||||| |||
Db 1 GCAGCTGGAGGGGCCCTT 18

RESULT 3476
US-10-189-268-47/c
; Sequence 47, Application US/10189268
; Publication No. US20040005570A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF GERANYLGERANYL DIPHOSPHATE SYNTHASE 1 EXPRESSION
; FILE REFERENCE: PTS-0021
; CURRENT APPLICATION NUMBER: US/10/189,268
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 131
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-189-268-47

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1824 TAGAATCTTTTAAATACA 1841
||| ||||| |||||
Db 19 TAGGTTCTTTTGAATACA 2

RESULT 3477
US-10-349-143-4087/c
; Sequence 4087, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4087
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer\_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-13229 for SEQ 153,
US-10-349-143-4087

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
; Sequence 61, Application US/10177554
; Publication No. US20030235911A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF PRL-3 EXPRESSION
; FILE REFERENCE: RTS-0370
; CURRENT APPLICATION NUMBER: US/10/177,554
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 239
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-177-554-61
```

```
Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      470 GCCTGGCCCGGCCGACG 487
      ||||| ||||| |||||
Db      20 GCCTGGCCCGGGCTCCAG 3
```

```
RESULT 3469
US-10-177-554-188
; Sequence 188, Application US/10177554
; Publication No. US20030235911A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Hong Zhang
; TITLE OF INVENTION: ANTISENSE MODULATION OF PRL-3 EXPRESSION
; FILE REFERENCE: RTS-0370
; CURRENT APPLICATION NUMBER: US/10/177,554
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 239
; SEQ ID NO 188
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-177-554-188
```

```
Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2674 GTGTGTGGGTGAATG 2691
      ||| ||||| ||||| ||
Db      1 GTGCGTGTGTGTGAGTG 18
```

```
RESULT 3470
US-10-177-798-25/c
; Sequence 25, Application US/10177798
; Publication No. US20030235912A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF ORPHAN G-PROTEIN COUPLED RECEPTOR GPRC5B
; FILE REFERENCE: PTS-0047
; CURRENT APPLICATION NUMBER: US/10/177,798
; CURRENT FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 70
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-177-798-25
```

```
Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1175 CCTCATCTTGGAGGACGA 1192
      ||||| ||||| |||||
Db      19 CATCATCCAGGAGGACGA 2
```

```
RESULT 3471
US-10-187-659A-143/c
; Sequence 143, Application US/10187659A
; Publication No. US20040002152A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF P2X4 EXPRESSION
; FILE REFERENCE: RTS-0379
; CURRENT APPLICATION NUMBER: US/10/187,659A
; CURRENT FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 143
; SEQ ID NO 143
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-187-659A-143
```

```
Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1026 TGAATCTTCCGGCCGCGGA 1043
      ||||| ||||| ||||| ||
Db      19 TGAATCGTCCAGCCGCGGA 2
```

```
RESULT 3472
US-10-188-646-74/c
; Sequence 74, Application US/10188646
; Publication No. US20040005565A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
; FILE REFERENCE: RTS-0373
; CURRENT APPLICATION NUMBER: US/10/188,646
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 74
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-188-646-74
```

```
Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2561 CTGGGCTCTGTTCTTGGC 2578
      ||||| ||||| ||||| ||
Db      19 CTGGACTGTGTTCTGGGC 2
```

```
RESULT 3473
US-10-188-646-138
; Sequence 138, Application US/10188646
; Publication No. US20040005565A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Freier, Susan M.
; TITLE OF INVENTION: Phosphatidylinositol-4 Phosphate 5-Kinase, Type 11 Beta
; TITLE OF INVENTION: Inhibitors For Inhibiting Angiogenesis
; FILE REFERENCE: ISPH-0727
; CURRENT APPLICATION NUMBER: US/10/348,073A
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 10/175,627
; PRIOR FILING DATE: 2002-06-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-348-073A-62

```

Query Match	0.5%	Score 13.2;	DB 1;	Length 20;
Best Local Similarity	83.3%	Pred. No. 3.5e+03;		
Matches 15; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy	2686	GAAATCGAGATT	TGGAAT	2703
Dy	1	GAACTGGGGATT	TGGGAT	18

```

RESULT 3465
US-10-448-914A-162
; Sequence 162, Application US/10448914A
; Publication No. US20030235856A1
; GENERAL INFORMATION:
; APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
; APPLICANT: KIM, Cheol Min
; APPLICANT: PARK, Hee Kyung
; TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria
; FILE REFERENCE: PP05020/PCT
; CURRENT APPLICATION NUMBER: US/10/448,914A
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: KR 10-1999-0019631
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019632
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019633
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019634
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019635
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-2000-0018189
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 243
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 162
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium smegmatis
US-10-448-914A-162

```

Query Match	0.5%	Score 13.2;	DB 1;	Length 20;
Best Local Similarity	83.3%	Pred. No. 3.5e+03;		
Matches 15;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps 0;

QY 104 CCGCTTGGGGGCTGGGGG 121  
||| ||| ||| ||| |||  
Db 2 CCGGTGGGGGCGGGGG 19

RESULT 3466  
US-10--448-914A-239

```

; Sequence 239, Application US/10448914A
; Publication No. US20030235856A1
; GENERAL INFORMATION:
; APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
; APPLICANT: KIM, Cheol Min
; APPLICANT: PARK, Hee Kyung
; TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacterium
; FILE REFERENCE: PP05020/PCT
; CURRENT APPLICATION NUMBER: US/10/448,914A
; CURRENT FILING DATE, 2003-05-30
; PRIOR APPLICATION NUMBER: KR 10-1999-0019631
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019632
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019633
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019634
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-1999-0019635
; PRIOR FILING DATE: 1999-05-29
; PRIOR APPLICATION NUMBER: KR 10-2000-0018189
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 243
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 239
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium
; OTHER INFORMATION: paratuberculosis
US-10-448-914A-239

```

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 71 CGCCTGGTCACCGTGACC 88  
Db 2 CGCATGGTCTCCGTGGCC 19

RESULT 3467  
US-10-177-554-52/c  
; Sequence 52, Application US/10177554  
; Publication No. US20030235911A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Hong Zhang  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PRL-3 EXPRESSION  
; FILE REFERENCE: RTS-0370  
; CURRENT APPLICATION NUMBER: US/10/177,554  
; CURRENT FILING DATE: 2002-06-20  
; NUMBER OF SEQ ID NOS: 239  
; SEQ ID NO 52  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-177-554-52

```
Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. NO. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Qy 2674 GTGTGTGTGGTGAATG 2691  
||| ||| ||| ||| ||| |||  
Db 20 GTCCGTGTGTGTGAATG 3

RESULT 3468  
US-10-177-554-61/c

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-174-460-28

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1381 CTGTGCCGCGGTGCTGC 1398
Db 20 CTGTGCTGCGGAGGCTGC 3

RESULT 3460
US-10-174-460-88
; Sequence 88, Application US/10174460
; Publication No. US20030232441A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 4 EXPRESSION
; FILE REFERENCE: PTS-0014
; CURRENT APPLICATION NUMBER: US/10/174,460
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 88
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-174-460-88

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1381 CTGTGCCGCGGTGCTGC 1398
Db 1 CTGTGCTGCGGAGGCTGC 18

RESULT 3461
US-10-175-627-27/c
; Sequence 27, Application US/10175627
; Publication No. US20030232775A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan M. Freier
; APPLICANT: Edward A. Dennis
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE
; FILE REFERENCE: PTS-0005
; CURRENT APPLICATION NUMBER: US/10/175,627
; CURRENT FILING DATE: 2002-06-18
; NUMBER OF SEQ ID NOS: 75
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-175-627-27

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2686 GAAATGGAGATTGGAAT 2703
```

```
Db 20 GAACTGGGGATTGGGAT 3

RESULT 3462
US-10-175-627-61
; Sequence 61, Application US/10175627
; Publication No. US20030232775A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan M. Freier
; APPLICANT: Edward A. Dennis
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE,
; FILE REFERENCE: PTS-0005
; CURRENT APPLICATION NUMBER: US/10/175,627
; CURRENT FILING DATE: 2002-06-18
; NUMBER OF SEQ ID NOS: 75
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-175-627-61

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2686 GAAATGGAGATTGGAAT 2703
Db 1 GAACTGGGGATTGGGAT 18

RESULT 3463
US-10-348-073A-28/c
; Sequence 28, Application US/10348073A
; Publication No. US20030232777A1
; GENERAL INFORMATION:
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Freier, Susan M.
; TITLE OF INVENTION: Phosphatidylinositol-4 Phosphate 5-Kinase, Type 11 Beta
; TITLE OF INVENTION: Inhibitors For Inhibiting Angiogenesis
; FILE REFERENCE: ISPH-0727
; CURRENT APPLICATION NUMBER: US/10/348,073A
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 10/175,627
; PRIOR FILING DATE: 2002-06-18
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-348-073A-28

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2686 GAAATGGAGATTGGAAT 2703
Db 20 GAACTGGGGATTGGGAT 3

RESULT 3464
US-10-348-073A-62
; Sequence 62, Application US/10348073A
; Publication No. US20030232777A1
```



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; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 947
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 513
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-513

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2681 TGGGTGAAATGGAGATT 2698
      ||| ||| ||| ||| ||| |||
Db      19 TGGCTGAGATGGAGTTT 2

RESULT 3455
US-10-173-208-25/c
; Sequence 25, Application US/10173208
; Publication No. US20030232435A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF AMYLOID BETA PROTEIN PRECURSOR EXPRESSION
; FILE REFERENCE: HTS-0023
; CURRENT APPLICATION NUMBER: US/10/173,208
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-173-208-25

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1608 CCTGGGGGAAGAGTTTGT 1625
      || ||| ||| ||| ||| |||
Db      20 CCGAGGGGTAGAGTTTGT 3

RESULT 3456
US-10-173-208-61
; Sequence 61, Application US/10173208
; Publication No. US20030232435A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF AMYLOID BETA PROTEIN PRECURSOR EXPRESSION
; FILE REFERENCE: HTS-0023
; CURRENT APPLICATION NUMBER: US/10/173,208
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-173-208-61

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1608 CCTGGGGGAAGAGTTTGT 1625
      || ||| ||| ||| ||| |||
Db      1 CCGAGGGGTAGAGTTTGT 18
```

```

RESULT 3457
US-10-173-817-75
; Sequence 75, Application US/10173817
; Publication No. US20030232438A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF KOX 1 EXPRESSION
; FILE REFERENCE: RTS-0359
; CURRENT APPLICATION NUMBER: US/10/173,817
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 131
; SEQ ID NO 75
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-173-817-75

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2704 TGAATCTCTGCCTGTAA 2721
      ||| ||| ||| ||| ||| |||
Db      3 TGAGATCTCTGGCTGTAA 20

RESULT 3458
US-10-173-817-127/c
; Sequence 127, Application US/10173817
; Publication No. US20030232438A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF KOX 1 EXPRESSION
; FILE REFERENCE: RTS-0359
; CURRENT APPLICATION NUMBER: US/10/173,817
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 131
; SEQ ID NO 127
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-173-817-127

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2704 TGAATCTCTGCCTGTAA 2721
      ||| ||| ||| ||| ||| |||
Db      18 TGAGATCTCTGGCTGTAA 1

RESULT 3459
US-10-174-460-28/c
; Sequence 28, Application US/10174460
; Publication No. US20030232441A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 4 EXPRESSION
; FILE REFERENCE: PTS-0014
; CURRENT APPLICATION NUMBER: US/10/174,460
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 28
```

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Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2692 GAGATTGGGAATTGAACT 2709
Db 18 GAGAGTTGGGAATTCATCT 1

RESULT 3451
US-10-360-510-102
; Sequence 102, Application US/10360510
; Publication No. US20030220282A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/10/360,510
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US/09/854,883
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 102
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-360-510-102

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1133 GCCGAATTTCCTAGTAAA 1150
Db 2 GTCGAATATCCTGGTAAA 19

RESULT 3452
US-10-360-510-224/c
; Sequence 224, Application US/10360510
; Publication No. US20030220282A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/10/360,510
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US/09/854,883
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 224
; LENGTH: 20
```

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-360-510-224

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1287 GGACCAGCAGCGCTGCCC 1304
Db 19 GGGCAAGCAGGCGCGCCC 2

RESULT 3453
US-10-360-522-25/c
; Sequence 25, Application US/10360522
; Publication No. US20030221215A1
; GENERAL INFORMATION:
; APPLICANT: Allefs, Josephus J.H.M.
; APPLICANT: Vossen v.d., Edwin A.G.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING PRODUCT THAT PROVIDES PLANTS WITH
; FILE REFERENCE: U 014413-9
; CURRENT APPLICATION NUMBER: US/10/360,522
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02075565.8
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: PCT/NL03/00091
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: reverse primer
US-10-360-522-25

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2566 CTCTGTTCTTGGCTTGA 2583
Db 20 CTCGGTTCCTGGCTGAA 3

RESULT 3454
US-10-388-263-513/c
; Sequence 513, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
; APPLICANT: Cowser, Lex M.
; APPLICANT: Baker, Brenda F.
; APPLICANT: McNeil, John
; APPLICANT: Freier, Susan M.
; APPLICANT: Sasnor, Henri M.
; APPLICANT: Brooks, Douglas G.
; APPLICANT: Ohashi, Cara
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Borchers, Alexander
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
; FILE REFERENCE: ISIS-4503
; CURRENT APPLICATION NUMBER: US/10/388,263
```

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; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 139
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Designed
; OTHER INFORMATION: oligonucleotide probe for Southern hybridization
US-10-148-835-139

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      466 GCAGGCCTGGCCCGCGC 483
Db      3 GCAGGCCTGACCCCTGCAG 20

RESULT 3447
US-10-148-355A-64/c
; Sequence 64, Application US/10148355A
; Publication No. US20030207831A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: ISIS PHARMACEUTICALS, INC.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TELOMERIC REPEAT BINDING FACTOR 2
; FILE REFERENCE: RTSP-0082
; CURRENT APPLICATION NUMBER: US/10/148,355A
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: 09/467,642
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-148-355A-64

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      898 GGCTGAAGTACAGAGCG 915
Db      20 GGCTGGAGTGCAGTGGCG 3

RESULT 3448
US-10-114-279-29
; Sequence 29, Application US/10114279
; Publication No. US20030219742A1
; GENERAL INFORMATION:
; APPLICANT: Sanjay Bhanot
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF HMGI-C EXPRESSION
; FILE REFERENCE: RTS-0296
; CURRENT APPLICATION NUMBER: US/10/114,279
; CURRENT FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 29
; LENGTH: 20
; TYPE: DNA
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```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-114-279-29

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      416 GCCGCCGCCATCAACCC 433
Db      1 GCTGCCACCATCAACACC 18

RESULT 3449
US-10-310-677-126
; Sequence 126, Application US/10310677
; Publication No. US20030219772A1
; GENERAL INFORMATION:
; APPLICANT: Kuyi v.d., Antoinette C.
; APPLICANT: Cornelissen, Marion
; TITLE OF INVENTION: Means and methods for treatment evaluation
; FILE REFERENCE: P55190US10
; CURRENT APPLICATION NUMBER: US/10/310,677
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: EP 01200228.3
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: EP 01203703.2
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/325,722
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 126
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 3'TAG011GENE-2
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(20)
US-10-310-677-126

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2527 ATATATATACAGGGTATT 2544
Db      3 ATATATTTACAGGATAGT 20

RESULT 3450
US-10-146-860-88/c
; Sequence 88, Application US/10146860
; Publication No. US20030220273A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Mark P. Roach
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHODIESTERASE 4D EXPRESSION
; FILE REFERENCE: RTS-0351
; CURRENT APPLICATION NUMBER: US/10/146,860
; CURRENT FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 100
; SEQ ID NO 88
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-146-860-88
```

; APPLICANT: KIM, Cheol Min  
; APPLICANT: PARK, Hee Kyung  
; TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria  
; FILE REFERENCE: PP05020/PCT  
; CURRENT APPLICATION NUMBER: US/10/448,836  
; CURRENT FILING DATE: 2003-05-30  
; PRIOR APPLICATION NUMBER: KR 10-1999-0019631  
; PRIOR FILING DATE: 1999-05-29  
; PRIOR APPLICATION NUMBER: KR 10-1999-0019632  
; PRIOR FILING DATE: 1999-05-29  
; PRIOR APPLICATION NUMBER: KR 10-1999-0019633  
; PRIOR FILING DATE: 1999-05-29  
; PRIOR APPLICATION NUMBER: KR 10-1999-0019634  
; PRIOR FILING DATE: 1999-05-29  
; PRIOR APPLICATION NUMBER: KR 10-1999-0019635  
; PRIOR FILING DATE: 1999-05-29  
; PRIOR APPLICATION NUMBER: KR 10-2000-0018189  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 243  
; SOFTWARE: KopatentIn 1.71  
; SEQ ID NO 162  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium smegmatis  
US-10-448-836-162

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 104 CCGCTTGGGGCTGGGG 121  
|| |||||  
Db 2 CCCGTTGGGGCGGGGG 19

RESULT 3443  
US-10-448-836-239  
; Sequence 239, Application US/10448836  
; Publication No. US20030207313A1  
; GENERAL INFORMATION:  
; APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.  
; APPLICANT: KIM, Cheol Min  
; APPLICANT: PARK, Hee Kyung  
; TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria  
; FILE REFERENCE: PP05020/PCT  
; CURRENT APPLICATION NUMBER: US/10/448,836  
; CURRENT FILING DATE: 2003-05-30  
; PRIOR APPLICATION NUMBER: KR 10-1999-0019631  
; PRIOR FILING DATE: 1999-05-29  
; PRIOR APPLICATION NUMBER: KR 10-1999-0019632  
; PRIOR FILING DATE: 1999-05-29  
; PRIOR APPLICATION NUMBER: KR 10-1999-0019633  
; PRIOR FILING DATE: 1999-05-29  
; PRIOR APPLICATION NUMBER: KR 10-1999-0019634  
; PRIOR FILING DATE: 1999-05-29  
; PRIOR APPLICATION NUMBER: KR 10-1999-0019635  
; PRIOR FILING DATE: 1999-05-29  
; PRIOR APPLICATION NUMBER: KR 10-2000-0018189  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 243  
; SOFTWARE: KopatentIn 1.71  
; SEQ ID NO 239  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: sequence of probe or primer for detecting Mycobacterium  
; OTHER INFORMATION: paratuberculosis  
US-10-448-836-239

Query Match 0.5%; Score 13.2; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 71 CGCCTGGTCACCGTGACC 88  
||| |||||  
Db 2 CGCATGGTCTCCGTGGCC 19  
RESULT 3444  
US-10-148-835-58/c  
; Sequence 58, Application US/10148835  
; Publication No. US20030207380A1  
; GENERAL INFORMATION:  
; APPLICANT: SAITO et al.  
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION  
; FILE REFERENCE: 2185-0648P  
; CURRENT APPLICATION NUMBER: US/10/148,835  
; CURRENT FILING DATE: 2002-10-11  
; NUMBER OF SEQ ID NOS: 213  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 58  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Designed  
; OTHER INFORMATION: oligonucleotide primer for PCR  
US-10-148-835-58

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 601 CTCGACCTGCTGCTGCC 618  
|| |||||  
Db 19 CTCGACATGCTGCTGGC 2

RESULT 3445  
US-10-148-835-60/c  
; Sequence 60, Application US/10148835  
; Publication No. US20030207380A1  
; GENERAL INFORMATION:  
; APPLICANT: SAITO et al.  
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION  
; FILE REFERENCE: 2185-0648P  
; CURRENT APPLICATION NUMBER: US/10/148,835  
; CURRENT FILING DATE: 2002-10-11  
; NUMBER OF SEQ ID NOS: 213  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 60  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Designed  
; OTHER INFORMATION: oligonucleotide primer for PCR  
US-10-148-835-60

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1085 GAAGGTGAAGCTGTTTCAT 1102  
||| |||||  
Db 20 GAAGGTGGACCTGATCAT 3

RESULT 3446  
US-10-148-835-139  
; Sequence 139, Application US/10148835  
; Publication No. US20030207380A1  
; GENERAL INFORMATION:



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; SEQ ID NO 170
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-109-349A-170

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2723 TGTTCCCAATAATTGT 2740
Db      3 TGTGCCCAAGTAATTTT 20

RESULT 3439
US-10-165-099-145
; Sequence 145, Application US/10165099
; Publication No. US20030188326A1
; GENERAL INFORMATION:
; APPLICANT: D'Andrea, Alan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS OF CANCER SUSCEPTIBILITY
; TITLE OF INVENTION: DEFECTIVE DNA REPAIR MECHANISMS AND TREATMENT THEREOF
; FILE REFERENCE: 7032/2055
; CURRENT APPLICATION NUMBER: US/10/165,099
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 09/998,027
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US 60/245,756
; PRIOR FILING DATE: 2000-11-03
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 145
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-165-099-145

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1917 ATACCTTTTTCAGTG 1934
Db      2 ATACCTTCTTTGCTGTG 19

RESULT 3440
US-10-321-856-320
; Sequence 320, Application US/10321856
; Publication No. US20030194393A1
; GENERAL INFORMATION:
; APPLICANT: Milhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: TX-1-C2-1
; CURRENT APPLICATION NUMBER: US/10/321,856
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/216,393
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,825
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 320
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-10-321-856-320
```

```

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1485 AAACCTGGAGAAATGG 1502
Db      2 AAACCTGGGAAACGG 19

RESULT 3441
US-10-430-196-75/c
; Sequence 75, Application US/10430196
; Publication No. US20030194738A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; Miraglia; Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; Compositions and Methods for the Modulation of
; Activating Protein 1
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/430,196
; FILING DATE: 05-May-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/923,517A
; FILING DATE: 07-Aug-2001
; APPLICATION NUMBER: 09/364,416
; FILING DATE: 1999-07-30
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-10-430-196-75

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      52 CGCGGGGGCGCGGCAG 69
Db      20 CGCGGGCGCGGCTACAG 3

RESULT 3442
US-10-448-836-162
; Sequence 162, Application US/10448836
; Publication No. US20030207313A1
; GENERAL INFORMATION:
; APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
```

; APPLICANT: Skrzypczynski, Zbigniew  
; APPLICANT: Takova, Tsetska Y.  
; APPLICANT: Thompson, Lisa C.  
; APPLICANT: Vedvik, Kevin L.  
; TITLE OF INVENTION: RNA Detection Assays  
; FILE REFERENCE: FORS-06666  
; CURRENT APPLICATION NUMBER: US/10/084,839  
; CURRENT FILING DATE: 2002-02-26  
; NUMBER OF SEQ ID NOS: 4004  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 651  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-084-839-651

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 628 CGCCCTGGATGCCGCGG 645  
Db 18 CGCCGTGCATGCCTCGG 1

RESULT 3436  
US-10-084-839-1861/c  
; Sequence 1861, Application US/10084839  
; Publication No. US20030186238A1  
; GENERAL INFORMATION:  
; APPLICANT: Third Wave Technologies  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Argue, Brad T.  
; APPLICANT: Bartholomay, Christian T.  
; APPLICANT: Chehak, LuAnne  
; APPLICANT: Curtis, Michelle L.  
; APPLICANT: Eis, Peggy S.  
; APPLICANT: Hall, Jeff G.  
; APPLICANT: Ip, Hon S.  
; APPLICANT: Ji, Lin  
; APPLICANT: Kaiser, Michael  
; APPLICANT: Kwiatkowski, Jr., Robert W.  
; APPLICANT: Lukowiak, Andrew A.  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Lymaicheva, Natalie E.  
; APPLICANT: Ma, WuPo  
; APPLICANT: Neri, Bruce P.  
; APPLICANT: Olson, Sarah M.  
; APPLICANT: Olson-Munoz, Marilyn C.  
; APPLICANT: Schaefer, James J.  
; APPLICANT: Skrzypczynski, Zbigniew  
; APPLICANT: Takova, Tsetska Y.  
; APPLICANT: Thompson, Lisa C.  
; APPLICANT: Vedvik, Kevin L.  
; TITLE OF INVENTION: RNA Detection Assays  
; FILE REFERENCE: FORS-06666  
; CURRENT APPLICATION NUMBER: US/10/084,839  
; CURRENT FILING DATE: 2002-02-26  
; NUMBER OF SEQ ID NOS: 4004  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1861  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-084-839-1861

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 628 CGCCCTGGATGCCGCGG 645  
Db 18 CGCCGTGCATGCCTCGG 1

RESULT 3437  
US-10-084-839-1866/c  
; Sequence 1866, Application US/10084839  
; Publication No. US20030186238A1  
; GENERAL INFORMATION:  
; APPLICANT: Third Wave Technologies  
; APPLICANT: Allawi, Hatim  
; APPLICANT: Argue, Brad T.  
; APPLICANT: Bartholomay, Christian T.  
; APPLICANT: Chehak, LuAnne  
; APPLICANT: Curtis, Michelle L.  
; APPLICANT: Eis, Peggy S.  
; APPLICANT: Hall, Jeff G.  
; APPLICANT: Ip, Hon S.  
; APPLICANT: Ji, Lin  
; APPLICANT: Kaiser, Michael  
; APPLICANT: Kwiatkowski, Jr., Robert W.  
; APPLICANT: Lukowiak, Andrew A.  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Lymaicheva, Natalie E.  
; APPLICANT: Ma, WuPo  
; APPLICANT: Neri, Bruce P.  
; APPLICANT: Olson, Sarah M.  
; APPLICANT: Olson-Munoz, Marilyn C.  
; APPLICANT: Schaefer, James J.  
; APPLICANT: Skrzypczynski, Zbigniew  
; APPLICANT: Takova, Tsetska Y.  
; APPLICANT: Thompson, Lisa C.  
; APPLICANT: Vedvik, Kevin L.  
; TITLE OF INVENTION: RNA Detection Assays  
; FILE REFERENCE: FORS-06666  
; CURRENT APPLICATION NUMBER: US/10/084,839  
; CURRENT FILING DATE: 2002-02-26  
; NUMBER OF SEQ ID NOS: 4004  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1866  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-084-839-1866

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 628 CGCCCTGGATGCCGCGG 645  
Db 18 CGCCGTGCATGCCTCGG 1

RESULT 3438  
US-10-109-349A-170  
; Sequence 170, Application US/10109349A  
; Publication No. US20030186246A1  
; GENERAL INFORMATION:  
; APPLICANT: Medical College of Ohio  
; APPLICANT: Willey, James C.  
; APPLICANT: Crawford, Erin L.  
; TITLE OF INVENTION: MULTIPLEX STANDARDIZED REVERSE TRANSCRIPTASE-POLYMERASE CHAIN REAC  
; FILE REFERENCE: 01154/2001-203  
; CURRENT APPLICATION NUMBER: US/10/109,349A  
; CURRENT FILING DATE: 2002-06-12  
; NUMBER OF SEQ ID NOS: 282  
; SOFTWARE: PatentIn version 3.1

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; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:human herpes
US-10-165-410A-15

Query Match      0.5%;   Score 13.2;  DB 1;   Length 20;
Best Local Similarity 83.3%;   Pred. No. 3.5e+03;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      499 AGCGGGGCTGCCCTCGCA 516
Db      19 AGCGGGGCTGCGTTCGGA 2

RESULT 3432
US-10-364-360-1/c
; Sequence 1, Application US/10364360
; Publication No. US20030180324A1
; GENERAL INFORMATION:
; APPLICANT: GUERTLER, Lutz Gerhard
; APPLICANT: HAUSER, Hans Peter
; APPLICANT: DONGMO DELOKO, Yvette Beatrice
; APPLICANT: ZEKENG, Leopold
; APPLICANT: KAPTUE, Lazare
; TITLE OF INVENTION: LENTIVIRUS FROM THE GROUP OF IMMUNODEFICIENCY VIRUSES OF DRILL MO
; TITLE OF INVENTION: (MANDRILLUS LEUCOPHAUS) AND THEIR USE
; FILE REFERENCE: 067595/0106
; CURRENT APPLICATION NUMBER: US/10/364,360
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: US/09/625,972
; PRIOR FILING DATE: 2000-07-29
; PRIOR APPLICATION NUMBER: DE 199 36 003.0
; PRIOR FILING DATE: 1999-08-03
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ().()
; OTHER INFORMATION: primer, non-genomic DNA
US-10-364-360-1

Query Match      0.5%;   Score 13.2;  DB 1;   Length 20;
Best Local Similarity 83.3%;   Pred. No. 3.5e+03;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      2442 GACTTTTGTGACATGG 2459
Db      19 GACATTTTGGACACATGG 2

RESULT 3433
US-10-032-585-5682/c
; Sequence 5682, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
```

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; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5682
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-5682

Query Match      0.5%;   Score 13.2;  DB 1;   Length 20;
Best Local Similarity 83.3%;   Pred. No. 3.5e+03;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      1438 CAAATCCTACATGAACCC 1455
Db      19 CAAATCCAACACGAAGCC 2

RESULT 3434
US-10-032-585-5723
; Sequence 5723, Application US/10032585
; Publication No. US20030180953A1
; GENERAL INFORMATION:
; APPLICANT: Terry, Roemer D.
; APPLICANT: Bo, Jiang
; APPLICANT: Charles, Boone
; APPLICANT: Howard, Bussey
; TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
; FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5723
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-032-585-5723

Query Match      0.5%;   Score 13.2;  DB 1;   Length 20;
Best Local Similarity 83.3%;   Pred. No. 3.5e+03;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      244 TCCGCGGGTCCCCCACCT 261
Db      1 TCCGCTTGTCCTCCCATCT 18

RESULT 3435
US-10-084-839-651/c
; Sequence 651, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Eis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Ip, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lymaicheva, Natalie E.
; APPLICANT: Ma, WuPo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
```

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 891 TGACAGTGGCTGAAGTAC 908  
||||| ||||| ||||| |||||  
Db 3 TGACATTGGCTGATGAC 20

RESULT 3428  
US-10-056-790-67/c  
; Sequence 67, Application US/10056790  
; Publication No. US20030165497A1  
; GENERAL INFORMATION:  
; APPLICANT: EXELIXIS, INC.  
; TITLE OF INVENTION: RRP SEQUENCES AND KNOCKOUT MICE AND USES THEREOF  
; FILE REFERENCE: RRPCIP2002  
; CURRENT APPLICATION NUMBER: US/10/056,790  
; PRIOR APPLICATION NUMBER: US 09/908,419  
; PRIOR FILING DATE: 2002-01-23  
; PRIOR FILING DATE: 2001-07-18  
; PRIOR APPLICATION NUMBER: US 60/219,289  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: US 60/277,487  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: US 60/277,471  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: US 60/304,863  
; PRIOR FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: US 60/296,076  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/305,017  
; PRIOR FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: US 60/328,605  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/328,491  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 67  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: mouse origin  
US-10-056-790-67

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 343 CTTTCCCCCTCCCTACCA 360  
||||| ||||| ||||| |||||  
Db 20 CTTTCAGCCTCCCTTCCA 3

RESULT 3429  
US-10-055-728-126  
; Sequence 126, Application US/10055728  
; Publication No. US20030170720A1  
; GENERAL INFORMATION:  
; APPLICANT: van der Kuyl, Antoinette C.  
; APPLICANT: Cornelissen, Marion  
; TITLE OF INVENTION: MEANS AND METHODS FOR TREATMENT EVALUATION  
; FILE REFERENCE: 5244US (REN/P5190US00)  
; CURRENT APPLICATION NUMBER: US/10/055,728  
; CURRENT FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: 60/325,722  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: EP 0120373.2  
; PRIOR FILING DATE: 2001-09-28  
; PRIOR APPLICATION NUMBER: EP 01200228.3

; PRIOR FILING DATE: 2001-01-23  
; NUMBER OF SEQ ID NOS: 156  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 126  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 3'TAG011GENE-2  
US-10-055-728-126

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2527 ATATATATACAGGGTATT 2544  
||||| ||||| ||||| |||||  
Db 3 ATATATTACAGGATAGT 20

RESULT 3430  
US-10-113-901-11/c  
; Sequence 11, Application US/10113901  
; Publication No. US20030172065A1  
; GENERAL INFORMATION:  
; APPLICANT: Sorenson, James L.  
; APPLICANT: Woodward, Scott  
; APPLICANT: Myres, Joel  
; TITLE OF INVENTION: System and Method for Molecular Genealogy Research  
; FILE REFERENCE: 4722.1US  
; CURRENT APPLICATION NUMBER: US/10/113,901  
; CURRENT FILING DATE: 2002-03-29  
; PRIOR APPLICATION NUMBER: US 60/280,226  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: forward primer  
US-10-113-901-11

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1775 TTTTTTTGAACCCCATTC 1792  
||||| ||||| ||||| |||||  
Db 20 TTTTTTTATACCCCACTC 3

RESULT 3431  
US-10-165-410A-15/c  
; Sequence 15, Application US/10165410A  
; Publication No. US20030175728A1  
; GENERAL INFORMATION:  
; APPLICANT: Belousov, Yevgeniy S.  
; APPLICANT: Afonina, Irina A.  
; APPLICANT: Epoch Biosciences, Inc.  
; TITLE OF INVENTION: Real-Time Linear Detection Probes: Sensitive 5'-Minor  
; TITLE OF INVENTION: Groove Binder-Containing Probes for PCR Analysis  
; FILE REFERENCE: 17682A-007220US  
; CURRENT APPLICATION NUMBER: US/10/165,410A  
; CURRENT FILING DATE: 2003-03-17  
; PRIOR APPLICATION NUMBER: US 09/457,616  
; PRIOR FILING DATE: 1999-12-08  
; PRIOR APPLICATION NUMBER: US 09/876,830  
; PRIOR FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: US 60/302,137  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/351,637



```

; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: primer
US-10-319-221-6

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1932 GTGTTAAGGTAATGGTTG 1949
Db 1 GTGCTCAGGTAGTGGTTG 18

RESULT 3424
US-10-172-094-56
; Sequence 56, Application US/10172094
; Publication No. US20030161830A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, DONALD
; APPLICANT: LORENZI, MATTHEW
; APPLICANT: ATTAR, RICARDO
; APPLICANT: GOTTARDIS, MARCO
; TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
; FILE REFERENCE: 3053-4145US1
; CURRENT APPLICATION NUMBER: US/10/172,094
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,296
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-172-094-56

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2548 AATTAAGAGGATGCTGGG 2565
Db 3 AATGTACAGGATGCTGGG 20

RESULT 3425
US-10-172-094-58
; Sequence 58, Application US/10172094
; Publication No. US20030161830A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, DONALD
; APPLICANT: LORENZI, MATTHEW
; APPLICANT: ATTAR, RICARDO
; APPLICANT: GOTTARDIS, MARCO
; TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
; FILE REFERENCE: 3053-4145US1
; CURRENT APPLICATION NUMBER: US/10/172,094
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,296
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-172-094-58
```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-172-094-58

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2548 AATTAAGAGGATGCTGGG 2565
Db 3 AATGTACAGGATGCTGGG 20

RESULT 3426
US-10-172-094-59/c
; Sequence 59, Application US/10172094
; Publication No. US20030161830A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, DONALD
; APPLICANT: LORENZI, MATTHEW
; APPLICANT: ATTAR, RICARDO
; APPLICANT: GOTTARDIS, MARCO
; TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
; FILE REFERENCE: 3053-4145US1
; CURRENT APPLICATION NUMBER: US/10/172,094
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,296
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-172-094-59

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2548 AATTAAGAGGATGCTGGG 2565
Db 18 AATGTACAGGATGCTGGG 1

RESULT 3427
US-10-172-094-79
; Sequence 79, Application US/10172094
; Publication No. US20030161830A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, DONALD
; APPLICANT: LORENZI, MATTHEW
; APPLICANT: ATTAR, RICARDO
; APPLICANT: GOTTARDIS, MARCO
; TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
; FILE REFERENCE: 3053-4145US1
; CURRENT APPLICATION NUMBER: US/10/172,094
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,296
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-172-094-79
```

```

; APPLICANT: Chang, Bey-Dih
; TITLE OF INVENTION: REAGENTS AND METHODS FOR IDENTIFYING AND MODULATING
; TITLE OF INVENTION: EXPRESSION OF GENES REGULATED BY CDK INHIBITORS
; FILE REFERENCE: 01-1156-A
; CURRENT APPLICATION NUMBER: US/10/233,032A
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: US 09/861,925
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/265,840
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Antisense PCR primer for CC3 promoter (spec Table IIIa)
US-10-233-032A-22

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 536 CTACTGCCCCACCTCTCC 553
    ||||| ||||| ||||| ||
Db 20 CTACTAACCACCTCCCC 3

RESULT 3422
US-10-376-566-65
; Sequence 65, Application US/10376566
; Publication No. US20030158144A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Mark P. Roach
; APPLICANT: Erich Koller
; TITLE OF INVENTION: ANTISENSE MODULATION OF ESTROGEN RECEPTOR BETA EXPRESSION
; FILE REFERENCE: RTS-0347
; CURRENT APPLICATION NUMBER: US/10/376,566
; CURRENT FILING DATE: 2003-02-27
; PRIOR APPLICATION NUMBER: US/10/005,058
; PRIOR FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 65
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-376-566-65

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1173 GACCTCATCTTGGAGGAC 1190
    ||||| ||||| ||||| |
Db 3 GACATCATCATGGAGGCC 20

RESULT 3423
US-10-319-221-6
; Sequence 6, Application US/10319221
; Publication No. US20030159169A1
; GENERAL INFORMATION:
; APPLICANT: Collodi, Paul
; APPLICANT: Fan, Lianchun
; APPLICANT: Ma, Chunguang
; TITLE OF INVENTION: CELL CULTURE SYSTEM AND METHODS OF USE
; FILE REFERENCE: 290.00300101
; CURRENT APPLICATION NUMBER: US/10/319,221

```



RESULT 3410  
US-10-206-839-86/c  
; Sequence 86, Application US/10206839  
; Publication No. US20030099977A1  
; GENERAL INFORMATION:  
; APPLICANT: Guida, Marco  
; APPLICANT: Kurth, Janice  
; TITLE OF INVENTION: Genotyping Human Phenol Sulfotransferase  
; TITLE OF INVENTION: (STP2)  
; FILE REFERENCE: 4389-6 (formerly SEQ-16P)  
; CURRENT APPLICATION NUMBER: US/10/206,839  
; CURRENT FILING DATE: 2002-07-26  
; PRIOR APPLICATION NUMBER: 09/328,174  
; PRIOR FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 110  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 86  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: H. sapiens  
US-10-206-839-86

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2511 TCATAAGGTTTATTTCAT 2528  
|||||  
Db 18 TCATAGGTTCTTCTTCAT 1

RESULT 3411  
US-10-269-353-26  
; Sequence 26, Application US/10269353  
; Publication No. US2003010447A1  
; GENERAL INFORMATION:  
; APPLICANT: Holtzman, Douglas A.  
; APPLICANT: Goodearl, Andrew D.J.  
; APPLICANT: McCarthy, Sean A.  
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
; TITLE OF INVENTION: USES  
; FILE REFERENCE: MPI2000-5380MNIC1M  
; CURRENT APPLICATION NUMBER: US/10/269,353  
; CURRENT FILING DATE: 2002-10-11  
; PRIOR APPLICATION NUMBER: US 09/790,264  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: US 09/065,661  
; PRIOR FILING DATE: 1998-04-23  
; PRIOR APPLICATION NUMBER: US 09/298,531  
; PRIOR FILING DATE: 1999-04-23  
; PRIOR APPLICATION NUMBER: US 09/065,363  
; PRIOR FILING DATE: 1998-04-23  
; PRIOR APPLICATION NUMBER: US 09/337,930  
; PRIOR FILING DATE: 1999-06-22  
; PRIOR APPLICATION NUMBER: US 09/102,705  
; PRIOR FILING DATE: 1998-06-22  
; PRIOR APPLICATION NUMBER: US 09/363,630  
; PRIOR FILING DATE: 1999-07-29  
; PRIOR APPLICATION NUMBER: US 09/124,538  
; PRIOR FILING DATE: 1998-07-29  
; NUMBER OF SEQ ID NOS: 68  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide for PCR  
US-10-269-353-26

Query Match 0.5%; Score 13.2; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1596 AACCCCTCCTGGCCTGGG 1613  
|||||  
Db 1 AGCCCTCATGGCCTGTG 18

RESULT 3412  
US-10-035-485A-23/c  
; Sequence 23, Application US/10035485A  
; Publication No. US20030105044A1  
; GENERAL INFORMATION:  
; APPLICANT: Brenda F. Baker  
; APPLICANT: Lex M. Cowser  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MATRIX METALLOPROTEINASE 1 EXPRESSION  
; FILE REFERENCE: RTS-0139  
; CURRENT APPLICATION NUMBER: US/10/035,485A  
; CURRENT FILING DATE: 2001-10-17  
; NUMBER OF SEQ ID NOS: 89  
; SEQ ID NO 23  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-035-485A-23

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2237 CCCTTAAGGTACTGAAGC 2254  
|||||  
Db 19 CCCTGAAGGTGATGAAGC 2

RESULT 3413  
US-10-003-354-81  
; Sequence 81, Application US/10003354  
; Publication No. US20030114400A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE,  
; TITLE OF INVENTION: EXPRESSION  
; FILE REFERENCE: RTS-0348  
; CURRENT APPLICATION NUMBER: US/10/003,354  
; CURRENT FILING DATE: 2001-12-06  
; NUMBER OF SEQ ID NOS: 89  
; SEQ ID NO 81  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-003-354-81

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1556 AACAGGACTGCAAAATC 1573  
|||||  
Db 1 AACAGGAATTCAACAATC 18

RESULT 3414  
US-10-003-919-33  
; Sequence 33, Application US/10003919  
; Publication No. US20030114401A1  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett



```

; PRIOR APPLICATION NUMBER: US/09/659,845A
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 146
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-271-887-146

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1674 CCCTGGACTTCTTAGTTG 1691
Db      18 CCCTGGACTGCTTTGTGG 1

RESULT 3406
US-10-238-011-35/c
; Sequence 35, Application US/10238011
; Publication No. US20030091568A1
; GENERAL INFORMATION:
; APPLICANT: Frey Jurgen
; APPLICANT: Frey, Jurgan
; TITLE OF INVENTION: Inhibitors for the Formation of Soluble Human CD23
; FILE REFERENCE: 516326-2002
; CURRENT APPLICATION NUMBER: US/10/238,011
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: EP 00 107 515.9
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/827,406
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-238-011-35

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1743 ACAAGTACTGGCTCTTTA 1760
Db      20 ACAGGTACTGGCGCTTCA 3

RESULT 3407
US-10-001-076-43
; Sequence 43, Application US/10001076
; Publication No. US20030096775A1
; GENERAL INFORMATION:
; APPLICANT: Mark J. Graham
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF COMPLEMENT COMPONENT C3 EXPRESSION
; FILE REFERENCE: RTS-0329
; CURRENT APPLICATION NUMBER: US/10/001,076
; CURRENT FILING DATE: 2001-10-23
; NUMBER OF SEQ ID NOS: 179
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-001-076-43

Query Match      0.5%; Score 13.2; DB 1; Length 20;
```

```

Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2676 GTGTCTGGGTGAAATGGA 2693
Db      2 GTGTCTGGTGAAGTGA 19

RESULT 3408
US-10-145-493B-33/c
; Sequence 33, Application US/10145493B
; Publication No. US20030096777A1
; GENERAL INFORMATION:
; APPLICANT: Besterman, Jeffrey
; APPLICANT: Macleod, Robert
; APPLICANT: Siders, William
; TITLE OF INVENTION: Modulation of Gene Expression by Combination Therapy
; FILE REFERENCE: MET-015DV
; CURRENT APPLICATION NUMBER: US/10/145,493B
; CURRENT FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 09/420,692
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/104,804
; PRIOR FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-145-493B-33

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2661 AGTGTGCAGTACAGTGTG 2678
Db      19 ATTGTGCAGTACTTTGTG 2

RESULT 3409
US-10-206-839-85/c
; Sequence 85, Application US/10206839
; Publication No. US20030099977A1
; GENERAL INFORMATION:
; APPLICANT: Guida, Marco
; APPLICANT: Kurth, Janice
; TITLE OF INVENTION: Genotyping Human Phenol Sulfotransferase
; TITLE OF INVENTION: (STP2)
; FILE REFERENCE: 4389-6 (formerly SEQ-16P)
; CURRENT APPLICATION NUMBER: US/10/206,839
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 09/328,174
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 85
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
US-10-206-839-85

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2511 TCATAAGGTTTATTTCAT 2528
Db      18 TCATAGGGTCTTCTTCAT 1
```

```
; FILE REFERENCE: NIH-05043
; CURRENT APPLICATION NUMBER: US/10/116,949
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/470,443
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/114,359
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-116-949-102

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1257 AACTTCTCAGCCCAAGACC 1274
Db      1 AACTTCTCAGCCCAAGCC 18

RESULT 3402
US-10-067-125-56/c
; Sequence 56, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowser, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/10/067,125
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/167,109
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-067-125-56

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      683 CAGATGGACGAGGTGCAG 700
Db      20 CAGGAGCACGAGGTGCAG 3

RESULT 3403
US-10-209-608-33/c
; Sequence 33, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; FILE REFERENCE: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
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```
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953US0XDIV
; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/725,265
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-33

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2517 GGTTTTATTCATATATAT 2534
Db      18 GGTTTTATATATATAT 1

RESULT 3404
US-10-181-177-94/c
; Sequence 94, Application US/10181177
; Publication No. US20030083296A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 8 EXPRESSION
; FILE REFERENCE: RTSP-0334
; CURRENT APPLICATION NUMBER: US/10/181,177
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/00955
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 09/487,445
; PRIOR FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 94
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-181-177-94

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      898 GGCTGAAGTACAGAGCG 915
Db      19 GGCTGGAGTGCAGTGCG 2

RESULT 3405
US-10-271-887-146/c
; Sequence 146, Application US/10271887
; Publication No. US20030087871A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 9 EXPRESSION
; FILE REFERENCE: RTS-0183
; CURRENT APPLICATION NUMBER: US/10/271,887
; CURRENT FILING DATE: 2002-10-15
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```
; Publication No. US20030025538A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, DONALD
; APPLICANT: LORENZI, MATTHEW
; APPLICANT: ATTAR, RICARDO
; APPLICANT: GOTTARDIS, MARCO
; TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
; FILE REFERENCE: 3053-4145US1
; CURRENT APPLICATION NUMBER: US/10/072,094
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,296
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-072-094-58
```

```
Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2548 AATTAAAGAGGATGCTGGG 2565
      ||| | ||||| |||||
Db       3 AATGTACAGGATGCTGGG 20

RESULT 3398
US-10-072-094-59/c
; Sequence 59, Application US/10072094
; Publication No. US20030025538A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, DONALD
; APPLICANT: LORENZI, MATTHEW
; APPLICANT: ATTAR, RICARDO
; APPLICANT: GOTTARDIS, MARCO
; TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
; FILE REFERENCE: 3053-4145US1
; CURRENT APPLICATION NUMBER: US/10/072,094
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,296
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-072-094-59
```

```
Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2548 AATTAAAGAGGATGCTGGG 2565
      ||| | ||||| |||||
Db       18 AATGTACAGGATGCTGGG 1

RESULT 3399
US-10-072-094-79
; Sequence 79, Application US/10072094
; Publication No. US20030025538A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, DONALD
; APPLICANT: LORENZI, MATTHEW
; APPLICANT: ATTAR, RICARDO
```

```
; APPLICANT: GOTTARDIS, MARCO
; TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
; FILE REFERENCE: 3053-4145US1
; CURRENT APPLICATION NUMBER: US/10/072,094
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,296
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-072-094-79
```

```
Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      891 TGACAGTGGCTGAAGTAC 908
      ||||| ||||| ||||| |||
Db       3 TGACATTGGCTGATGGAC 20

RESULT 3400
US-10-156-424A-17/c
; Sequence 17, Application US/10156424A
; Publication No. US2003003999A1
; GENERAL INFORMATION:
; APPLICANT: Yoshinaga, Steve Kiyoshi
; APPLICANT: Suh, Woong-Kyung
; APPLICANT: Mak, Tak W.
; TITLE OF INVENTION: B7 Related Protein-2 Molecules and Uses Thereof
; FILE REFERENCE: 01-384-A
; CURRENT APPLICATION NUMBER: US/10/156,424A
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/293,629
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide; PCR primer 2245-71
US-10-156-424A-17
```

```
Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1414 CAAAGAAGCCCTGATTGT 1431
      ||||| ||||| ||||| |||
Db       20 CAAACAAGCCCTGCTCGT 3

RESULT 3401
US-10-116-949-102
; Sequence 102, Application US/10116949
; Publication No. US2003004911A1
; GENERAL INFORMATION:
; APPLICANT: Lerman, Michael I.
; APPLICANT: Minna, John D.
; APPLICANT: Latif, Farida
; APPLICANT: Wei, Ming-Hui
; APPLICANT: Sekido, Yoshitaka
; APPLICANT: Gao, Boning
; APPLICANT: Duh, Fuh-Mei
; TITLE OF INVENTION: Calcium Channel Compositions and Methods of Use Thereof
```

; TITLE OF INVENTION: ANTISENSE MODULATION OF BETA-SITE APP-CLEAVING ENZYME 2 EXPRESSION
; FILE REFERENCE: RTS-0378
; CURRENT APPLICATION NUMBER: US/10/163,272
; CURRENT FILING DATE: 2002-06-04
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 54
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-163-272-54

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 974 AAATCGAAATAATGGAGGC 991
||||| ||||| ||||| |||||
Db 18 AAATTGGAAATTGGAGGC 1

RESULT 3393
US-10-163-272-128
; Sequence 128, Application US/10163272
; Publication No. US20030224517A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF BETA-SITE APP-CLEAVING ENZYME 2 EXPRESSION
; FILE REFERENCE: RTS-0378
; CURRENT APPLICATION NUMBER: US/10/163,272
; CURRENT FILING DATE: 2002-06-04
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 128
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-163-272-128

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 974 AAATCGAAATAATGGAGGC 991
||||| ||||| ||||| |||||
Db 3 AAATTGGAAATTGGAGGC 20

RESULT 3394
US-10-348-750-15
; Sequence 15, Application US/10348750
; Publication No. US20030225019A1
; GENERAL INFORMATION:
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Erich Koller
; TITLE OF INVENTION: NOTCH1 INHIBITORS FOR INDUCING APOPTOSIS
; FILE REFERENCE: ISPH-0729
; CURRENT APPLICATION NUMBER: US/10/348,750
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 10/160,497
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 146
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-348-750-15

Query Match 0.5%; Score 13.2; DB 1; Length 20;

Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 464 CAGCAGGCCTGGCCCGGC 481
||||| ||||| ||||| |||||
Db 3 CAGCAGACCTGGCAGGC 20

RESULT 3395
US-10-364-748-54
; Sequence 54, Application US/10364748
; Publication No. US20030224968A1
; GENERAL INFORMATION:
; APPLICANT: Fink, John K.
; APPLICANT: Zhao, Xinpeng
; TITLE OF INVENTION: Atlastin
; FILE REFERENCE: UM-07745
; CURRENT APPLICATION NUMBER: US/10/364,748
; CURRENT FILING DATE: 2003-02-11
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-364-748-54

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2164 CCTTTTCTTTTCTTTTCTTTT 2181
||||| ||||| ||||| |||||
Db 1 CCTTCTTATTATTATTTT 18

RESULT 3396
US-10-072-094-56
; Sequence 56, Application US/10072094
; Publication No. US20030025538A1
; GENERAL INFORMATION:
; APPLICANT: JACKSON, DONALD
; APPLICANT: LORENZI, MATTHEW
; APPLICANT: ATTAR, RICARDO
; APPLICANT: GOTTARDIS, MARCO
; TITLE OF INVENTION: NOVEL HUMAN HISTONE PEPTIDES
; FILE REFERENCE: 3053-4145US1
; CURRENT APPLICATION NUMBER: US/10/072,094
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/298,296
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-072-094-56

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2548 AATTAAGAGGATGCTGGG 2565
||||| ||||| ||||| |||||
Db 3 AATGTACAGGATGCTGGG 20

RESULT 3397
US-10-072-094-58
; Sequence 58, Application US/10072094



; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PCTAIRE PROTEIN KINASE 2 EXPRESSION  
; FILE REFERENCE: RTS-0204  
; CURRENT APPLICATION NUMBER: US/10/160,787  
; CURRENT FILING DATE: 2002-05-31  
; NUMBER OF SEQ ID NOS: 141  
; SEQ ID NO 115  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
US-10-160-787-115

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2206 TCRAATGGGAGACTCTTT 2223  
Db 20 TCRAATGGTGGACTGTTT 3

RESULT 3388

US-10-161-983-29/c  
; Sequence 29, Application US/10161983  
; Publication No. US20030225015A1  
; GENERAL INFORMATION:  
; APPLICANT: Donna T. Ward  
; APPLICANT: Susan M. Freier

; TITLE OF INVENTION: ANTISENSE MODULATION OF RB2/PI30 EXPRESSION  
; FILE REFERENCE: HTS-0020  
; CURRENT APPLICATION NUMBER: US/10/161,983  
; CURRENT FILING DATE: 2002-05-31  
; NUMBER OF SEQ ID NOS: 74  
; SEQ ID NO 29  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-161-983-29

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1827 AATCTTTTAAATACATTC 1844  
Db 18 AATGTTTGAAATATATTC 1

RESULT 3389

US-10-161-983-61  
; Sequence 61, Application US/10161983  
; Publication No. US20030225015A1  
; GENERAL INFORMATION:  
; APPLICANT: Donna T. Ward  
; APPLICANT: Susan M. Freier

; TITLE OF INVENTION: ANTISENSE MODULATION OF RB2/PI30 EXPRESSION  
; FILE REFERENCE: HTS-0020  
; CURRENT APPLICATION NUMBER: US/10/161,983  
; CURRENT FILING DATE: 2002-05-31  
; NUMBER OF SEQ ID NOS: 74  
; SEQ ID NO 61  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
US-10-161-983-61

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1827 AATCTTTTAAATACATTC 1844  
Db 3 AATGTTTGAAATATATTC 20

RESULT 3390

US-10-161-996-64/c  
; Sequence 64, Application US/10161996  
; Publication No. US20030224515A1  
; GENERAL INFORMATION:  
; APPLICANT: Susan M. Freier  
; APPLICANT: Brenda F. Baker

; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEROL REGULATORY ELEMENT-BINDING PROTEIN  
; TITLE OF INVENTION: EXPRESSION  
; FILE REFERENCE: RTS-0395  
; CURRENT APPLICATION NUMBER: US/10/161,996  
; CURRENT FILING DATE: 2002-06-04  
; NUMBER OF SEQ ID NOS: 273  
; SEQ ID NO 64  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-161-996-64

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 797 AAGGAGCTGGTGGGGCC 814  
Db 19 AAGGATCTGGTGGTGGC 2

RESULT 3391

US-10-161-996-198  
; Sequence 198, Application US/10161996  
; Publication No. US20030224515A1  
; GENERAL INFORMATION:  
; APPLICANT: Susan M. Freier  
; APPLICANT: Brenda F. Baker

; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEROL REGULATORY ELEMENT-BINDING PROTEIN  
; TITLE OF INVENTION: EXPRESSION  
; FILE REFERENCE: RTS-0395  
; CURRENT APPLICATION NUMBER: US/10/161,996  
; CURRENT FILING DATE: 2002-06-04  
; NUMBER OF SEQ ID NOS: 273  
; SEQ ID NO 198  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
US-10-161-996-198

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 797 AAGGAGCTGGTGGGGCC 814  
Db 2 AAGGATCTGGTGGTGGC 19

RESULT 3392

US-10-163-272-54/c  
; Sequence 54, Application US/10163272  
; Publication No. US20030224517A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 546 ACCTCTCCGGGCTGGAGG 563  
| | | | | | | | | | | | | | | | | | | |  
Db 18 AACACTGCGGGCTGGAGG 1

RESULT 3383  
US-09-861-925-22/c  
; Sequence 22, Application US/09861925  
; Publication No. US20030064426A1  
; GENERAL INFORMATION:  
; APPLICANT: Roninson, Igor  
; APPLICANT: Chang, Bey-Dih  
; TITLE OF INVENTION: REAGENTS AND METHODS FOR IDENTIFYING AND MODULATING EXPRESSION OF  
; TITLE OF INVENTION: REGULATED BY CDK INHIBITORS  
; FILE REFERENCE: 99,216-F  
; CURRENT APPLICATION NUMBER: US/09/861,925  
; CURRENT FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: US 60/  
; PRIOR FILING DATE: 2001-02-01  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 22  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Antisense PCR primer for CC3 promoter (spec Table IIIa)  
US-09-861-925-22

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 536 CTACTGCCCCACCTCTCC 553  
| | | | | | | | | | | | | | | | | | | |  
Db 20 CTACTAACCCACCTCCCC 3

RESULT 3384  
US-09-949-428-222  
; Sequence 222, Application US/09949428  
; Publication No. US20030064372A1  
; GENERAL INFORMATION:  
; APPLICANT: Bodnar, Jackie S.  
; APPLICANT: Castellani, Lawrence W.  
; APPLICANT: Chatterjee, Aurobindo  
; APPLICANT: de Jong, Pieter  
; APPLICANT: Lulis, Aldons J.  
; APPLICANT: Ohmen, Jeff  
; APPLICANT: Ross, David  
; APPLICANT: Tafuri, Sherrie  
; APPLICANT: Wu, Chenyan  
; TITLE OF INVENTION: Gene and Sequence Variation Associated with Lipid Disorder  
; FILE REFERENCE: 02810.0014.NPUS01  
; CURRENT APPLICATION NUMBER: US/09/949,428  
; CURRENT FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: 60/231,322  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 405  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 222  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Primer  
US-09-949-428-222

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2251 AAGCTTTATTTCATATT 2268  
| | | | | | | | | | | | | | | | | | | |  
Db 1 AAGCCTCATTTCATGTT 18

RESULT 3385  
US-10-160-497-15  
; Sequence 15, Application US/10160497  
; Publication No. US20030224513A1  
; GENERAL INFORMATION:  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Erich Koller  
; TITLE OF INVENTION: ANTISENSE MODULATION OF NOTCH1 EXPRESSION  
; FILE REFERENCE: RTS-0386  
; CURRENT APPLICATION NUMBER: US/10/160,497  
; CURRENT FILING DATE: 2002-05-30  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 15  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-160-497-15

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 464 CAGCAGGCCTGGCCCGC 481  
| | | | | | | | | | | | | | | | | | | |  
Db 3 CAGCAGACCTGGGCAGGC 20

RESULT 3386  
US-10-160-787-49  
; Sequence 49, Application US/10160787  
; Publication No. US20030225256A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PCTAIRE PROTEIN KINASE 2 EXPRESSION  
; FILE REFERENCE: RTS-0204  
; CURRENT APPLICATION NUMBER: US/10/160,787  
; CURRENT FILING DATE: 2002-05-31  
; NUMBER OF SEQ ID NOS: 141  
; SEQ ID NO 49  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-160-787-49

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2206 TCAAATGGGAGACTCTTT 2223  
| | | | | | | | | | | | | | | | | | | |  
Db 1 TCAAATGGTGGACTGTTT 18

RESULT 3387  
US-10-160-787-115/c  
; Sequence 115, Application US/10160787  
; Publication No. US20030225256A1  
; GENERAL INFORMATION:

; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J.
; Miraglia; Brenda F. Baker
; TITLE OF INVENTION: Antisense Oligonucleotide
; Compositions and Methods for the Modulation of
; Activating Protein 1
;
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Jane Massey Licata
; STREET: 66 East Main Street
; CITY: Marlton
; STATE: NJ
; COUNTRY: USA
; ZIP: 08053
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: WORDPERFECT 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/923,517
; FILING DATE: 07-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/364,416
; FILING DATE: 1999-07-30
; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: ISPH-0209
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 810-1515
; TELEFAX: (609) 810-1454
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; ANTI-SENSE: Yes
; SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-09-923-517-75
Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 52 CGCGGGCGGCGGCGAG 69
Db 20 CGCGGGCGGCGGCTACAG 3
RESULT 3381
US-10-683-386-33/c
; Sequence 33, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: Koyama, Osamu
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/10/683,386
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US/09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601

; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 20
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-33
Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2517 GGTTTTATTCATATAT 2534
Db 18 GGTTTTATATATAT 1
RESULT 3382
US-09-991-681-16/c
; Sequence 16, Application US/09991681
; Publication No. US20020086316A1
; GENERAL INFORMATION:
; APPLICANT: BILLING-MEDEL, PATRICIA
; COHEN, MAURICE
; COLPITTS, TRACEY L.
; FRIEDMAN, PAULA N.
; GORDON, JULIAN
; GRANADOS, EDWARD N.
; HODGES, STEVEN C.
; KLASS, MICHAEL R.
; KRATOCHVIL, JON D.
; ROBERTS-RAPP, LISA
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE PROSTATE
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/991,681
; FILING DATE: 26-Nov-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/065,383
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6084.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-991-681-16

```
; NUMBER OF SEQ ID NOS: 31
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-10-264-958B-7

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      116 TGGGGGGATCCTGGATT 133
Db      3 TGTGGAGATCCTGGGTTT 20

RESULT 3376
US-10-642-802-43
; Sequence 43, Application US/10642802
; Publication No. US20040043956A1
; GENERAL INFORMATION:
; APPLICANT: Mark J. Graham
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF COMPLEMENT COMPONENT C3 EXPRESSION
; FILE REFERENCE: RTS-0329
; CURRENT APPLICATION NUMBER: US/10/642,802
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/10/001,076
; PRIOR FILING DATE: 2001-10-23
; NUMBER OF SEQ ID NOS: 179
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-642-802-43

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2676 GTGTGTGGTGAATGGA 2693
Db      2 GTGTCTGGTGAAGTGA 19

RESULT 3377
US-10-665-216-154
; Sequence 154, Application US/10665216
; Publication No. US20040043957A1
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Susan M. Freier
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF UROKINASE PLASMINOGEN ACTIVATOR EXPRESSION
; FILE REFERENCE: RTS-0188
; CURRENT APPLICATION NUMBER: US/10/665,216
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/821,972
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 154
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-665-216-154

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
```

```
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      875 ACGTCTAAATACAAAGTG 892
Db      3 ACATCTATATAAAAAAGTG 20

RESULT 3378
US-10-672-981-37
; Sequence 37, Application US/10672981
; Publication No. US20040048825A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CREB EXPRESSION
; FILE REFERENCE: RTS-0237
; CURRENT APPLICATION NUMBER: US/10/672,981
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/973,827
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 37
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-672-981-37

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1510 CAGGAATAAAATTGGAA 1527
Db      1 CAGGAATTAAATTATAA 18

RESULT 3379
US-09-736-271-9
; Sequence 9, Application US/09736271
; Publication No. US20010044937A1
; GENERAL INFORMATION:
; APPLICANT: OREGON HEALTH SCIENCES UNIVERSITY
; APPLICANT: Schatten, Gerald
; APPLICANT: Chan, Anthony W.S.
; TITLE OF INVENTION: METHODS FOR PRODUCING TRANSGENIC ANIMALS
; FILE REFERENCE: 899-58374
; CURRENT APPLICATION NUMBER: US/09/736,271
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
US-09-736-271-9

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1932 GTGTTAAGGTAATGGTTG 1949
Db      3 GTGCTCAGGTAGTGGTTG 20

RESULT 3380
US-09-923-517-75/c
; Sequence 75, Application US/09923517
; Publication No. US20020039741A1
```



RESULT 3372  
US-09-864-426A-1866/c  
; Sequence 1866, Application US/09864426A  
; Publication No. US20040018489A1  
; GENERAL INFORMATION:  
; APPLICANT: Third Wave Technologies  
; APPLICANT: Ma, Wu Po  
; APPLICANT: Lyamichev, Victor  
; APPLICANT: Saiser, Michael  
; TITLE OF INVENTION: Enzymes for the Detection of RNA Sequences  
; FILE REFERENCE: FORS-04946  
; CURRENT APPLICATION NUMBER: US/09/864,426A  
; CURRENT FILING DATE: 2001-05-24  
; NUMBER OF SEQ ID NOS: 2640  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1866  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-864-426A-1866

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 628 CGCCCTGGATCGCGGG 645  
||||| || ||||| |||||  
Db 18 CGCGTGCATGCCTCGGG 1

RESULT 3373  
US-10-215-448-44  
; Sequence 44, Application US/10215448  
; Publication No. US20040029273A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF EDG1 EXPRESSION  
; FILE REFERENCE: RTS-0179  
; CURRENT APPLICATION NUMBER: US/10/215,448  
; CURRENT FILING DATE: 2002-08-09  
; NUMBER OF SEQ ID NOS: 105  
; SEQ ID NO 44  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-215-448-44

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1012 GGACAAGATCGGGTTGAA 1029  
||||| ||||| || |||||  
Db 2 GGACATGATCCGGATGAA 19

RESULT 3374  
US-10-072-012-1009  
; Sequence 1009, Application US/10072012  
; Publication No. US20040033493A1  
; GENERAL INFORMATION:  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Li, Li  
; APPLICANT: Gangolli, Esha  
; APPLICANT: Padigar, Muralidhara

; APPLICANT: Anderson, David W.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Taupier Jr, Raymond J.  
; APPLICANT: Gusev, Vladimir Y.  
; APPLICANT: Colman, Steven D.  
; APPLICANT: Wolenc, Adam R.  
; APPLICANT: Pena, Carol E. A  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Grosse, William M.  
; APPLICANT: Alsobrook II, John P.  
; APPLICANT: Lepley, Denise M.  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Burgess, Catherine E.  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-258  
; CURRENT APPLICATION NUMBER: US/10/072,012  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: 60/265,102  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 60/265,514  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/265,517  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/265,412  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/265,395  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/266,406  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 60/266,767  
; PRIOR FILING DATE: 2001-02-05  
; PRIOR APPLICATION NUMBER: 60/267,057  
; PRIOR FILING DATE: 2001-02-07  
; PRIOR APPLICATION NUMBER: 60/266,975  
; PRIOR FILING DATE: 2001-02-07  
; PRIOR APPLICATION NUMBER: 60/267,459  
; PRIOR FILING DATE: 2001-02-08  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1391  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1009  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Ag2954 Forward  
US-10-072-012-1009

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 328 TCAGCGCCACCCCTACTT 345  
||||| ||||| ||||| |||||  
Db 3 TCAGCCACTACCCCTCCTT 20

RESULT 3375  
US-10-264-958B-7  
; Sequence 7, Application US/10264958B  
; Publication No. US20040038224A1  
; GENERAL INFORMATION:  
; APPLICANT: Hoffman, Hal  
; APPLICANT: Kolodner, Richard  
; TITLE OF INVENTION: Isolated Cryopyrins, Nucleic Acid Molecules Encoding These, and U  
; TITLE OF INVENTION: Thereof  
; FILE REFERENCE: LUD 5738.1 CIP (10209575)  
; CURRENT APPLICATION NUMBER: US/10/264,958B  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: US60/327,728  
; PRIOR FILING DATE: 2001-10-05

; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-908-147-35

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1485 AAACCTGGAGAAATGG 1502
Db 2 AAACCTGAAGCAAAAGG 19

RESULT 3368
US-09-793-807-17
; Sequence 17, Application US/09793807
; Publication No. US20030171310A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF RECQL EXPRESSION
; FILE REFERENCE: RTS-0206
; CURRENT APPLICATION NUMBER: US/09/793,807
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-793-807-17

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2677 TGTGTGGTGAATGGAG 2694
Db 2 TGTGTGGCGAAGGAAG 19

RESULT 3369
US-09-865-879-38/c
; Sequence 38, Application US/09865879
; Publication No. US20030180707A1
; GENERAL INFORMATION:
; APPLICANT: Roninson, Igor
; APPLICANT: Dokmanovic, Milos
; APPLICANT: Chang, Bey-Dih
; TITLE OF INVENTION: REAGENTS AND METHODS FOR IDENTIFYING AND MODULATING EXPRESSION OF
; TITLE OF INVENTION: REGULATED BY RETINOIDS
; FILE REFERENCE: 99,216-H
; CURRENT APPLICATION NUMBER: US/09/865,879
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/207,535
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Sense primer for ring finger protein RNF
US-09-865-879-38

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2635 TTCCTGTTGGGCTGAACC 2652
Db 20 TTCCTTTTGGACTGCACC 3

RESULT 3370
US-09-864-426A-651/c
; Sequence 651, Application US/09864426A
; Publication No. US20040018489A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Ma, Wu Po
; APPLICANT: Lyamichev, Victor
; APPLICANT: Saisier, Michael
; TITLE OF INVENTION: Enzymes for the Detection of RNA Sequences
; FILE REFERENCE: FORS-04946
; CURRENT APPLICATION NUMBER: US/09/864,426A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 2640
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 651
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-864-426A-651

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 628 CGCCCTGGATGCCGCGG 645
Db 18 CGCCGTGCATGCCTCGG 1

RESULT 3371
US-09-864-426A-1861/c
; Sequence 1861, Application US/09864426A
; Publication No. US20040018489A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Ma, Wu Po
; APPLICANT: Lyamichev, Victor
; APPLICANT: Saisier, Michael
; TITLE OF INVENTION: Enzymes for the Detection of RNA Sequences
; FILE REFERENCE: FORS-04946
; CURRENT APPLICATION NUMBER: US/09/864,426A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 2640
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1861
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-864-426A-1861

Query Match 0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 628 CGCCCTGGATGCCGCGG 645
Db 18 CGCCGTGCATGCCTCGG 1

```

; FILE REFERENCE: RTS-0191
; CURRENT APPLICATION NUMBER: US/09/972,607
; CURRENT FILING DATE: 2001-10-06
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 87
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-972-607-87

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1063 GACTCTCCTGACATCCTT 1080
          ||||| ||||| |||||
Db       19 GACTCTGCTGACAGCCCT 2

RESULT 3363
US-09-973-827-37
; Sequence 37, Application US/09973827
; Publication No. US20030105038A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CREB EXPRESSION
; FILE REFERENCE: RTS-0237
; CURRENT APPLICATION NUMBER: US/09/973,827
; CURRENT FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 37
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-973-827-37

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1510 CAGGAATAAAATTGGAA 1527
          ||||| ||||| |||||
Db       1 CAGGAATTAAATTATAA 18

RESULT 3364
US-09-920-868A-12
; Sequence 12, Application US/09920868A
; Publication No. US20030113300A1
; GENERAL INFORMATION:
; APPLICANT: Perfetti, Riccardo
; TITLE OF INVENTION: HUMAN GLUCOSE-DEPENDENT INSULIN-SECRETING CELL LINE
; FILE REFERENCE: 81476-0255389
; CURRENT APPLICATION NUMBER: US/09/920,868A
; CURRENT FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-09-920-868A-12

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      394 CTCGCATCTGGGGGAGC 411
```

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||| || |||| |||||
Db       1 CTCACACCTGGTGAAGC 18

RESULT 3365
US-09-998-716-27
; Sequence 27, Application US/09998716
; Publication No. US20030126628A1
; GENERAL INFORMATION:
; APPLICANT: Avigenics, Inc
; TITLE OF INVENTION: Chicken Ovomuroid
; FILE REFERENCE: A181 8170
; CURRENT APPLICATION NUMBER: US/09/998,716
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer OVMUa9
US-09-998-716-27

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2135 AAACGAAGCCTGCTGATT 2152
          ||||| ||||| |||||
Db       1 AAATGAAGCCGCGTGTTT 18

RESULT 3366
US-09-908-147-34
; Sequence 34, Application US/09908147
; Publication No. US20030144221A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/09/908,147
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-908-147-34

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1485 AAACCTGGAGAAAATGG 1502
          ||||| ||||| |||||
Db       1 AAACCTGAAGCAAAAGG 18

RESULT 3367
US-09-908-147-35
; Sequence 35, Application US/09908147
; Publication No. US20030144221A1
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF BCL2-ASSOCIATED X PROTEIN EXPRESSION
; FILE REFERENCE: RTS-0185
; CURRENT APPLICATION NUMBER: US/09/908,147
; CURRENT FILING DATE: 2001-07-17
```

US-09-915-814-95

Query Match	0.5%	Score 13.2;	DB 1;	Length 20;
Best Local Similarity	83.3%	Pred. No. 3.5e+03;		
Matches 15;	Conservative	0;	Mismatches 3;	Indels 0;
				Gaps 0;

QY  
547 CCTCTCCGGGCTGGAGGC 564

Dd  
20 CCTGGCCGAGCTGGAGGC 3

RESULT 3358

US-09-920-394-58/c  
; Sequence 58, Application US/09920394  
; Publication No. US20030096773A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosanne M. Crooke  
; APPLICANT: Mark J. Graham  
; APPLICANT: Kristina M. Lemonidis  
; TITLE OF INVENTION: ANTISENSE MODULATION OF ACYL COENZYME A CHOLESTEROL ACYLTRANSFERASE  
; TITLE OF INVENTION: EXPRESSION  
; FILE REFERENCE: ISPH-0589  
; CURRENT APPLICATION NUMBER: US/09/920,394  
; CURRENT FILING DATE: 2001-08-01  
; NUMBER OF SEQ ID NOS: 62  
; SEQ ID NO 58  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-920-394-58

Query Match	0.5%;	Score 13.2;	DB 1;	Length 20;
Best Local Similarity	83.3%;	Pred. No. 3.5e+03;		
Matches 15: Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY            2204 CTTCAAATGGGAGACTCT 2221  
               ||            |  
db            19 CTGTGAATGGGAGACTCT 2

RESULT 3359

```

US-09-864-636A-651/c
; Sequence 651, Application US/09864636A
; Publication No. US20030104378A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allwai, Hatim
; APPLICANT: Bartholomay, Christian
; APPLICANT: Chehak, LuAnne
; TITLE OF INVENTION: Detection of RNA Sequences
; FILE REFERENCE: FORS-04944
; CURRENT APPLICATION NUMBER: US/09/864,636A
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 2640
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 651
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-864-636A-651

```

Query Match	0.5%;	Score 13.2;	DB 1;	Length 20;
Best Local Similarity	83.3%;	Pred. No. 3.5e+03;		
Matches 15: Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy 628 CGCCTGGATGCCGCGG 645  
p6 18 CGCCTGGATGCCCTCGG 1

RESULT 3360

US-09-864-636A-1861/c  
; Sequence 1861, Application US/09864636A  
; Publication No. US20030104378A1

```

; GENCODE INFORMATION.
; APPLICANT: Third Wave Technologies
; APPLICANT: Allwai, Hatim
; APPLICANT: Bartholomay, Christian
; APPLICANT: Chehak, LuAnne
; TITLE OF INVENTION: Detection of RNA Sequences
; FILE REFERENCE: FORS-04944
; CURRENT APPLICATION NUMBER: US/09/864,636A
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 2640
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1861
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-864-636A-1861

```

Query Match	0.5%;	Score 13.2;	DB 1;	Length 20;
Best Local Similarity	83.3%;	Pred. No. 3.5e+03;		
Matches 15; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy 628 CGCCCTGGATGCCCGGG 645  
Db 18 CGCCGTGCATGCCCTCGG 1

RESULT 3361

US-09-864-636A-1866/c  
; Sequence 1866, Application US/09864636A  
: Publication No. US20030104378A1

```

/ GENERAL INFORMATION:
/ APPLICANT: Third Wave Technologies
/ APPLICANT: Allwai, Hatim
/ APPLICANT: Bartholomay, Christian
/ APPLICANT: Chehak, LuAnne
/ TITLE OF INVENTION: Detection of RNA Sequences
/ FILE REFERENCE: FORS-04944
/ CURRENT APPLICATION NUMBER: US/09/864,636A
/ CURRENT FILING DATE: 2002-10-15
/ NUMBER OF SEQ ID NOS: 2640
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 1866
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic
/ US-09-864-636A-1866

```

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15: Conservative 0; Mismatches 3; Indels 0; Gaps 0;

**Qy** 628 CGCCCTGGATGCCGCGG 645  
||| ||| ||| ||| |||  
**pB** 18 CGCCGTGCATGCCTCGG 1

RESULT 3362

US-09-972-607-87/c  
; Sequence 87, Application US/09972607  
; Publication No. US20030105037A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODUL

APPLICANT: Jacqueline Wyatt  
TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-GAMMA EXPRESSION



```
Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 256 CCACCTCTCTCCGCGG 273
Db 3 CCCCATCTCTCCGCGG 20

RESULT 3353
US-09-816-460C-44/c
; Sequence 44, Application US/09816460C
; Publication No. US20030087235A1
; GENERAL INFORMATION:
; APPLICANT: Dairkee, Shanaz H.
; APPLICANT: Li, Zheng
; TITLE OF INVENTION: PROGNOSTIC METHODS FOR BREAST CANCER
; FILE REFERENCE: CPMC-010/00US
; CURRENT APPLICATION NUMBER: US/09/816,460C
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic primer
US-09-816-460C-44

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2027 GTAGAGGCAAAGTTCT 2044
Db 20 GCAGGAGCGAAAGTTCT 3

RESULT 3354
US-09-967-669-13
; Sequence 13, Application US/09967669
; Publication No. US20030092650A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF SPHINGOSINE-1-PHOSPHATE LYASE EXPRESSION
; FILE REFERENCE: RTS-0259
; CURRENT APPLICATION NUMBER: US/09/967,669
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-967-669-13

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 477 CCGCGCGCCAGAGCCAGG 494
Db 1 CAGCGCGCGAGACCCAGG 18

RESULT 3355
US-09-967-669-20
; Sequence 20, Application US/09967669
; Publication No. US20030092650A1
; GENERAL INFORMATION:
```

```
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF SPHINGOSINE-1-PHOSPHATE LYASE EXPRESSION
; FILE REFERENCE: RTS-0259
; CURRENT APPLICATION NUMBER: US/09/967,669
; CURRENT FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-967-669-20

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2704 TGAACCTCTCTGCTGTAA 2721
Db 1 TAAACTCTCTGGCTGGAA 18

RESULT 3356
US-09-998-027-145
; Sequence 145, Application US/09998027
; Publication No. US20030093819A1
; GENERAL INFORMATION:
; APPLICANT: D'Andrea et al.
; TITLE OF INVENTION: Methods and Compositions for the
; TITLE OF INVENTION: Diagnosis and Treatment of Cancers Associated with Defective
; TITLE OF INVENTION: DNA Repair Mechanisms
; FILE REFERENCE: 2486/101
; CURRENT APPLICATION NUMBER: US/09/998,027
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 20
; TYPE: DNA
; ORGANISM: MG779
US-09-998-027-145

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1917 ATACCTTTTTCAGTG 1934
Db 2 ATACCTTTTTCAGTG 19

RESULT 3357
US-09-915-814-95/c
; Sequence 95, Application US/09915814
; Publication No. US20030096771A1
; GENERAL INFORMATION:
; APPLICANT: Madeline M. Butler
; APPLICANT: Andrew T. Watt
; APPLICANT: Susan M. Freier
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF HORMONE-SENSITIVE LIPASE EXPRESSION
; FILE REFERENCE: ISPH-0587
; CURRENT APPLICATION NUMBER: US/09/915,814
; CURRENT FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 230
; SEQ ID NO 95
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
```

```

; Publication No. US20030082152A1
; GENERAL INFORMATION:
; APPLICANT: Mark J. Graham
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF SERUM AMYLOID A4 EXPRESSION
; FILE REFERENCE: RTS-0251
; CURRENT APPLICATION NUMBER: US/09/915,485
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 80
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-915-485-80

Query Match      0.5%;   Score 13.2;   DB 1;   Length 20;
Best Local Similarity 83.3%;   Pred. No. 3.5e+03;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      1181  CTTGGAGGACGAAATGAG 1198
Db      3      CCTGGTGGACTAAATGAG 20

RESULT 3351
US-09-922-146-43/c
; Sequence 43, Application US/09922146
; Publication No. US20030083285A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 9 EXPRESSION
; FILE REFERENCE: RTS-0252
; CURRENT APPLICATION NUMBER: US/09/922,146
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-922-146-43

Query Match      0.5%;   Score 13.2;   DB 1;   Length 20;
Best Local Similarity 83.3%;   Pred. No. 3.5e+03;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      547  CCTCTCCGGGCTGGAGGC 564
Db      19  CCTCTCCGGGCTGGGGCC 2

RESULT 3352
US-09-922-146-46
; Sequence 46, Application US/09922146
; Publication No. US20030083285A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Brett P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 9 EXPRESSION
; FILE REFERENCE: RTS-0252
; CURRENT APPLICATION NUMBER: US/09/922,146
; CURRENT FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 46
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-922-146-46

; Publication No. US20030082152A1
; GENERAL INFORMATION:
; APPLICANT: Lull, Ramon
; APPLICANT: Futrell, J. William
; APPLICANT: Hedrick, Marc H.
; APPLICANT: Benhaim, Prosper
; APPLICANT: Lorenz, Hermann Peter
; APPLICANT: Zhu, Min
; TITLE OF INVENTION: ADIPOSE-DERIVED STEM CELLS AND LATTICES
; FILE REFERENCE: 30448.77US11
; CURRENT APPLICATION NUMBER: US/09/952,522B
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: PCT/US00/06232
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 60/123,711
; PRIOR FILING DATE: 1999-03-10
; PRIOR APPLICATION NUMBER: 60/162,462
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Chat reverse
; OTHER INFORMATION: primer
; US-09-952-522B-50

Query Match      0.5%;   Score 13.2;   DB 1;   Length 20;
Best Local Similarity 83.3%;   Pred. No. 3.5e+03;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      825  CCACGTGAGTCTCTGCT 842
Db      18  CCACGGAGATGTTCTGCT 1

RESULT 3349
US-09-912-724-55
; Sequence 55, Application US/09912724
; Publication No. US20030083280A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF C-REACTIVE PROTEIN EXPRESSION
; FILE REFERENCE: ISPH-0584
; CURRENT APPLICATION NUMBER: US/09/912,724
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 63
; SEQ ID NO 55
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
; US-09-912-724-55

Query Match      0.5%;   Score 13.2;   DB 1;   Length 20;
Best Local Similarity 83.3%;   Pred. No. 3.5e+03;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      1239  TGTGTAAGAATTTCACAG 1256
Db      1      TGAAGAAAGAATTTCACAG 18

RESULT 3350
US-09-915-485-80
; Sequence 80, Application US/09915485
; Publication No. US20030083281A1
; GENERAL INFORMATION:

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; PRIOR APPLICATION NUMBER: 08/843,704
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: 08/842,898
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: 60/071,589
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: 09/009,802
; PRIOR FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-972-473-30

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1576 TCTCCACCGCAGACTG 1593
Db      18 TCTCCACGACTCACTG 1

RESULT 3344
US-09-972-469-49
; Sequence 49, Application US/09972469
; Publication No. US20030073085A1
; GENERAL INFORMATION:
; APPLICANT: Lai, Fang
; APPLICANT: Zhou, Daixing
; TITLE OF INVENTION: AMPLIFYING EXPRESSED SEQUENCES FROM GENOMIC DNA OF HIGHER-ORDER
; TITLE OF INVENTION: EUKARYOTIC ORGANISMS FOR DNA ARRAYS
; FILE REFERENCE: SP01-290
; CURRENT APPLICATION NUMBER: US/09/972,469
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-972-469-49

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1571 ATCCTTCTCCACGCACA 1588
Db      3 ATCCTTCTCCACCAAGA 20

RESULT 3345
US-09-972-469-166
; Sequence 166, Application US/09972469
; Publication No. US20030073085A1
; GENERAL INFORMATION:
; APPLICANT: Lai, Fang
; APPLICANT: Zhou, Daixing
; TITLE OF INVENTION: AMPLIFYING EXPRESSED SEQUENCES FROM GENOMIC DNA OF HIGHER-ORDER
; TITLE OF INVENTION: EUKARYOTIC ORGANISMS FOR DNA ARRAYS
; FILE REFERENCE: SP01-290
; CURRENT APPLICATION NUMBER: US/09/972,469
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
; LENGTH: 20
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-09-972-469-166

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      881 AAATACAAAGTGACAGTG 898
Db      3 AACTCCAAAGCGACAGTG 20

RESULT 3346
US-09-972-469-186/c
; Sequence 186, Application US/09972469
; Publication No. US20030073085A1
; GENERAL INFORMATION:
; APPLICANT: Lai, Fang
; APPLICANT: Zhou, Daixing
; TITLE OF INVENTION: AMPLIFYING EXPRESSED SEQUENCES FROM GENOMIC DNA OF HIGHER-ORDER
; TITLE OF INVENTION: EUKARYOTIC ORGANISMS FOR DNA ARRAYS
; FILE REFERENCE: SP01-290
; CURRENT APPLICATION NUMBER: US/09/972,469
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 186
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-972-469-186

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1793 TTTCCTTCTCTGAAAGTG 1810
Db      20 TGTCTTCTCTGGAATG 3

RESULT 3347
US-09-906-158-64/c
; Sequence 64, Application US/09906158
; Publication No. US20030078217A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3 EXPRES
; FILE REFERENCE: RTS-0257
; CURRENT APPLICATION NUMBER: US/09/906,158
; CURRENT FILING DATE: 2001-07-14
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-906-158-64

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2681 TGGGTGAAATGGAGATT 2698
Db      19 TGGCTGAGATGGAGTTT 2

RESULT 3348
US-09-952-522B-50/c
; Sequence 50, Application US/09952522B
```

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RESULT 3340
US-09-232-785-75/c
; Sequence 75, Application US/09232785
; Publication No. US20030049612A1
; GENERAL INFORMATION:
; APPLICANT: International Paper Co.
; APPLICANT: Echt, Craig. S
; APPLICANT: Nelson, C. Dana
; TITLE OF INVENTION: MICROSATELLITE DNA MARKERS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 4481/1E18US1
; CURRENT APPLICATION NUMBER: US/09/232,785
; CURRENT FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: 09/232,884
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 397
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 75
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Pinus taeda L.
US-09-232-785-75

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2446 TTTTGGACATGGGATC 2463
Db      18 TTTCTGGGACAAGGGATC 1

RESULT 3341
US-09-784-674-560
; Sequence 560, Application US/09784674
; Publication No. US20030054346A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Karen W.
; Wolber, Paul K.
; Delenstarr, Glenda C.
; Webb, Peter G.
; Kincaid, Robert H.
; TITLE OF INVENTION: Methods for evaluating oligonucleotide
; probe sequences
; NUMBER OF SEQUENCES: 1165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
; Company M/S 20BO
; STREET: 3000 Hanover Street
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,674
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: No. US20030054346A1 available
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/021,701
; FILING DATE: 10-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Wendy A.
; REGISTRATION NUMBER: 36,697
; REFERENCE/DOCKET NUMBER: 10971464-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-236-2386
; TELEFAX: 650-852-8063
```

```
; INFORMATION FOR SEQ ID NO: 560:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 20 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 560:
US-09-784-674-560

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2176 TTTTCTTTTAACTTGTG 2193
Db      1 TTTTCTTTTAAACCTG 18

RESULT 3342
US-09-949-427-222
; Sequence 222, Application US/09949427
; Publication No. US20030054418A1
; GENERAL INFORMATION:
; APPLICANT: Bodnar, Jackie S.
; APPLICANT: Castellani, Lawrence W.
; APPLICANT: Chatterjee, Aurobindo
; APPLICANT: de Jong, Pieter
; APPLICANT: Lulis, Aldons J.
; APPLICANT: Ohmen, Jeff
; APPLICANT: Ross, David
; APPLICANT: Tafuri, Sherrie
; APPLICANT: Wu, Chenyan
; TITLE OF INVENTION: Gene and Sequence Variation Associated with Cancer
; FILE REFERENCE: 02810.0014.NPUS02
; CURRENT APPLICATION NUMBER: US/09/949,427
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/231,322
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 222
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-949-427-222

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2251 AAGCTTTATTGCATATT 2268
Db      1 AAGCCTCATTTGCATGTT 18

RESULT 3343
US-09-972-473-30/c
; Sequence 30, Application US/09972473
; Publication No. US20030068312A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NOVEL HUMAN DICKKOPF-RELATED PROTEIN AND NUCLEIC ACID
; TITLE OF INVENTION: MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-108CP2
; CURRENT APPLICATION NUMBER: US/09/972,473
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 09/263,022
; PRIOR FILING DATE: 1999-03-05
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;
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-824-322B-375

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2442 GACTTTTTCGACATGG 2459
      ||||| ||||| ||||| ||
Db 18 GACTTCCTTGAGACACGG 1

RESULT 3336
US-09-470-526-4
; Sequence 4, Application US/09470526
; Publication No. US20030041342A1
; GENERAL INFORMATION:
; APPLICANT: Yuejin Sun
; APPLICANT: Dilkes, Brian R.
; APPLICANT: Larkins, Brian A.
; APPLICANT: Lowe, Keith S.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Dante, Ricardo
; TITLE OF INVENTION: Cell Cycle Nucleic Acids, Polypeptides,
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 1015
; CURRENT APPLICATION NUMBER: US/09/470,526
; CURRENT FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: 60/109,414
; EARLIER FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(20)
US-09-470-526-4

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 269 GCCGGGCAGCACCTCTAC 286
      || ||||| ||||| |||||
Db 2 GCGCGGCAGCACTTCTAC 19

RESULT 3337
US-09-470-526-7
; Sequence 7, Application US/09470526
; Publication No. US20030041342A1
; GENERAL INFORMATION:
; APPLICANT: Yuejin Sun
; APPLICANT: Dilkes, Brian R.
; APPLICANT: Larkins, Brian A.
; APPLICANT: Lowe, Keith S.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Dante, Ricardo
; TITLE OF INVENTION: Cell Cycle Nucleic Acids, Polypeptides,
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 1015
; CURRENT APPLICATION NUMBER: US/09/470,526
; CURRENT FILING DATE: 1999-12-22
; EARLIER APPLICATION NUMBER: 60/109,414
; EARLIER FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 20

```

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;
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(20)
US-09-470-526-7

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 269 GCCGGGCAGCACCTCTAC 286
      || ||||| ||||| |||||
Db 2 GCGCGGCAGCACTTCTAC 19

RESULT 3338
US-09-880-313A-207
; Sequence 207, Application US/09880313A
; Publication No. US20030044791A1
; GENERAL INFORMATION:
; APPLICANT: Flemington, Erik K
; TITLE OF INVENTION: Adaptors and Methods of Use
; FILE REFERENCE: 9397/1000
; CURRENT APPLICATION NUMBER: US/09/880,313A
; CURRENT FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 207
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-880-313A-207

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 551 TCCGGGCTGCAGGGCGGC 568
      ||||| ||||| ||||| ||
Db 3 TCCGGGCTGCAGGGGGCC 20

RESULT 3339
US-09-828-344-61/c
; Sequence 61, Application US/09828344
; Publication No. US20030044979A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPID SCRAMBLASE I EXPRESSION
; FILE REFERENCE: RTS-0147
; CURRENT APPLICATION NUMBER: US/09/828,344
; CURRENT FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 61
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-828-344-61

Query Match          0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1200 TGGCAGCTAGGAAGACA 1217
      ||||| ||||| ||||| ||
Db 20 TGGCAGCCAGGAACAAA 3

```

;  
; PRIOR FILING DATE: 2000-10-06  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-972-714-11

Query Match 888 AAGTGACAGTGGCTGAAG 905  
Best Local Similarity 83.3%; Score 13.2; DB 1; Length 20;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 888 AAGTGACAGTGGCTGAAG 905  
Db 3 AAGTGACACTGGCAGCAG 20

RESULT 3332

US-09-969-373-3646  
; Sequence 3646, Application US/09969373  
; Patent No. US20020133852A1

GENERAL INFORMATION:

; APPLICANT: Effertz, Roger J.  
; APPLICANT: Hauge, Brian M.  
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
; FILE REFERENCE: 38-10(52679)A  
; CURRENT APPLICATION NUMBER: US/09/969,373  
; CURRENT FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US 09/754,853  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 09/760,427  
; PRIOR FILING DATE: 2001-01-13  
; PRIOR APPLICATION NUMBER: US 09/855,768  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 4593  
; SEQ ID NO 3646  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-969-373-3646

Query Match 2697 TTGGAATTGAACCTCTG 2714  
Best Local Similarity 83.3%; Score 13.2; DB 1; Length 20;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2697 TTGGAATTGAACCTCTG 2714  
Db 3 TTGGATTCAACTCTTTG 20

RESULT 3333

US-09-824-322B-54  
; Sequence 54, Application US/09824322B  
; Publication No. US20030022848A1

GENERAL INFORMATION:

; APPLICANT: Baker, Brenda  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Butler, Madeline M.  
; APPLICANT: Shanahan, William R.  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-ALPHA  
; FILE REFERENCE: ISPH-0501  
; CURRENT APPLICATION NUMBER: US/09/824,322B  
; CURRENT FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: US 09/313,932  
; PRIOR FILING DATE: 1999-05-18  
; PRIOR APPLICATION NUMBER: US 09/166,186  
; PRIOR FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 503  
; SEQ ID NO 54  
; LENGTH: 20  
; TYPE: DNA

;  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-824-322B-54

Query Match 2157 TTTTCTCCTTTT 2174  
Best Local Similarity 83.3%; Score 13.2; DB 1; Length 20;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2157 TTTTCTCCTTTT 2174  
Db 3 TCTTCTCCATGTTT 20

RESULT 3334

US-09-824-322B-358/c  
; Sequence 358, Application US/09824322B  
; Publication No. US20030022848A1

GENERAL INFORMATION:

; APPLICANT: Baker, Brenda  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Butler, Madeline M.  
; APPLICANT: Shanahan, William R.  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-ALPHA  
; FILE REFERENCE: ISPH-0501  
; CURRENT APPLICATION NUMBER: US/09/824,322B  
; CURRENT FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: US 09/313,932  
; PRIOR FILING DATE: 1999-05-18  
; PRIOR APPLICATION NUMBER: US 09/166,186  
; PRIOR FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 503  
; SEQ ID NO 358  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-09-824-322B-358

Query Match 2099 TCAAACGGGGCCTCTG 2116  
Best Local Similarity 83.3%; Score 13.2; DB 1; Length 20;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2099 TCAAACGGGGCCTCTG 2116  
Db 20 TCAAACGGGGCCTCCAG 3

RESULT 3335

US-09-824-322B-375/c  
; Sequence 375, Application US/09824322B  
; Publication No. US20030022848A1

GENERAL INFORMATION:

; APPLICANT: Baker, Brenda  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Butler, Madeline M.  
; APPLICANT: Shanahan, William R.  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-ALPHA  
; FILE REFERENCE: ISPH-0501  
; CURRENT APPLICATION NUMBER: US/09/824,322B  
; CURRENT FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: US 09/313,932  
; PRIOR FILING DATE: 1999-05-18  
; PRIOR APPLICATION NUMBER: US 09/166,186  
; PRIOR FILING DATE: 1998-10-05  
; NUMBER OF SEQ ID NOS: 503  
; SEQ ID NO 375  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

```
; APPLICANT: Muller-Schilling, Martina
; APPLICANT: Oren, Moshe
; TITLE OF INVENTION: p53 Binding Areas
; FILE REFERENCE: 4121-122
; CURRENT APPLICATION NUMBER: US/09/834,291
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/DE99/03343
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: DE 198 47 779.1
; PRIOR FILING DATE: 1998-10-16
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-834-291-14

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1759 TATTCAATTAAGCTTTT 1776
Db      3 TGTTCCTTAAGCTTTT 20

RESULT 3328
US-09-733-294A-42/c
; Sequence 42, Application US/09733294A
; Patent No. US20020045588A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: William Gaarde
; APPLICANT: Susan M. Freier
; APPLICANT: Edward V. Wancewicz
; TITLE OF INVENTION: ANTISENSE MODULATION OF TERT EXPRESSION
; FILE REFERENCE: ISPH-0527
; CURRENT APPLICATION NUMBER: US/09/733,294A
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/572,423
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 108
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-733-294A-42

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      626 CACGCCCTGGATGCCGCG 643
Db      18 CACCCCGCGATGCCGCG 1

RESULT 3329
US-09-854-883-102
; Sequence 102, Application US/09854883
; Patent No. US20020055479A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
; FILE REFERENCE: ISPH-0576
```

```
; CURRENT APPLICATION NUMBER: US/09/854,883
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 102
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-854-883-102

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1133 GCCGAATTCCTAGTAAA 1150
Db      2 GTCGAATATCCTGGTAAA 19

RESULT 3330
US-09-854-883-224/c
; Sequence 224, Application US/09854883
; Patent No. US20020055479A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/09/854,883
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 224
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-854-883-224

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1287 GGACCAGCAGGCTCGCCC 1304
Db      19 GGGCAAGCAGGCCCGCCC 2

RESULT 3331
US-09-972-714-11
; Sequence 11, Application US/09972714
; Patent No. US20020106738A1
; GENERAL INFORMATION:
; APPLICANT: Fousias, George
; APPLICANT: Diamandis, Eleftherios
; TITLE OF INVENTION: NOVEL SIGLEC GENE
; FILE REFERENCE: 11757.56USU1
; CURRENT APPLICATION NUMBER: US/09/972,714
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US 60/239,007
```

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/471,968  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HYZ-040CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 526-6000  
TELEFAX: (617) 526-5000  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-887-505-21

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GGCTGGGGGATCCTGGA 130  
Db 3 GGGAGGGGGGTCTCTGGA 20

RESULT 3324  
US-08-944-410-10/c  
Sequence 10, Application US/08944410  
Publication No. US20030050453A1  
GENERAL INFORMATION:  
APPLICANT: Sorge, Joseph A.  
TITLE OF INVENTION: COLLECTIONS OF UNIQUELY TAGGED MOLECULES  
FILE REFERENCE: 04121.0018-00000  
CURRENT APPLICATION NUMBER: US/08/944,410  
CURRENT FILING DATE: 1997-10-06  
NUMBER OF SEQ ID NOS: 113  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 10  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Synthetic primer  
US-08-944-410-10

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 574 GAGCGCCCGCAGGGATGC 591  
Db 19 GAACGCACGCGAATGC 2

RESULT 3325  
US-09-216-393-320  
Sequence 320, Application US/09216393  
Patent No. US20010014447A1  
GENERAL INFORMATION:  
APPLICANT: Milhausen, Michael James  
TITLE OF INVENTION: TOKOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND  
TITLE OF INVENTION: USES THEREOF  
FILE REFERENCE: TX-1-C2  
CURRENT APPLICATION NUMBER: US/09/216,393  
CURRENT FILING DATE: 1998-12-18  
EARLIER APPLICATION NUMBER: 08/994,825  
EARLIER FILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 364  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 320  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Primer  
US-09-216-393-320

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1485 AAACCCCTGGAGAAATGG 1502  
Db 2 AAACCTCTGGGAAACGG 19

RESULT 3326  
US-09-790-264-26  
Sequence 26, Application US/09790264  
Patent No. US20020028508A1  
GENERAL INFORMATION:  
APPLICANT: Holtzman, Douglas A.  
APPLICANT: Goodearl, Andrew D.J.  
APPLICANT: McCarthy, Sean A.  
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
TITLE OF INVENTION: PROGNASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
TITLE OF INVENTION: USES  
FILE REFERENCE: 07334-322001  
CURRENT APPLICATION NUMBER: US/09/790,264  
CURRENT FILING DATE: 2001-02-21  
PRIOR APPLICATION NUMBER: US 09/065,661  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: US 09/298,531  
PRIOR FILING DATE: 1999-04-23  
PRIOR APPLICATION NUMBER: US 09/065,363  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: US 09/337,930  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: US 09/102,705  
PRIOR FILING DATE: 1998-06-22  
PRIOR APPLICATION NUMBER: US 09/363,630  
PRIOR FILING DATE: 1999-07-29  
PRIOR APPLICATION NUMBER: US 09/124,538  
PRIOR FILING DATE: 1998-07-29  
NUMBER OF SEQ ID NOS: 68  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 26  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: oligonucleotide for PCR  
US-09-790-264-26

Query Match 0.5%; Score 13.2; DB 1; Length 20;  
Best Local Similarity 83.3%; Pred. No. 3.5e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1596 AACCCCTCCTGGCCTGGG 1613  
Db 1 AGCCCTCATGGCCTGTG 18

RESULT 3327  
US-09-834-291-14  
Sequence 14, Application US/09834291  
Patent No. US20020042064A1  
GENERAL INFORMATION:  
APPLICANT: Krammer, Peter



```

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02022
US-09-823-634A-15

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1514 AAATAAAATTGGAACGAA 1531
Db 2 AAAAAAAATTGGAAGAAA 19

RESULT 3320
US-09-823-647B-15
; Sequence 15, Application US/09823647B
; Patent No. US20020142309A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/09/823,647B
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02022
US-09-823-647B-15

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1514 AAATAAAATTGGAACGAA 1531
Db 2 AAAAAAAATTGGAAGAAA 19

RESULT 3321
US-10-367-470-15
; Sequence 15, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02022
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US-10-367-470-15

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1514 AAATAAAATTGGAACGAA 1531
Db 2 AAAAAAAATTGGAAGAAA 19

RESULT 3322
US-08-983-605-16/c
; Sequence 16, Application US/08983605A
; Publication No. US20020066118A1
; GENERAL INFORMATION:
; APPLICANT: Roder, Marion
; TITLE OF INVENTION: Microsatellite Markers for Plants of the Species
; TITLE OF INVENTION: Triticum Aestivum and Tribe Triticeae and the Use of
; TITLE OF INVENTION: Said Markers
; FILE REFERENCE: 2936.10400
; CURRENT APPLICATION NUMBER: US/08/983,605A
; CURRENT FILING DATE: 1998-05-01
; EARLIER APPLICATION NUMBER: DE 195 25 284.5
; EARLIER FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Triticum aestivum
; US-08-983-605-16

Query Match      0.5%; Score 13.2; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 389 CCCTACTCGCATCTGGGG 406
Db 20 CCCTTCTCCCATCTAGGG 3

RESULT 3323
US-08-887-505-21
; Sequence 21, Application US/08887505
; Publication No. US20020081577A1
; GENERAL INFORMATION:
; APPLICANT: Kilkuskie, Robert E.
; APPLICANT: Frank, Bruce L.
; APPLICANT: Goodchild, John
; APPLICANT: Wolfe, Jia L.
; APPLICANT: Roberts, Peter C.
; APPLICANT: Hamlin, Jr., Henry A.
; APPLICANT: Roberts, No. US20020081577A1 A.
; APPLICANT: Walther, Debra M.
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR
; TITLE OF INVENTION: HEPATITIS C VIRUS
; NUMBER OF SEQUENCES: 172
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr LLP
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,505
; FILING DATE:
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Db      2 ACUGGAAGCCCUUCCUGG 19
      ||:|| | ||| :||:|
RESULT 3315
US-10-206-705-147/c
; Sequence 147, Application US/10206705
; Publication No. US20040019001A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceutical, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Protein Tyrosine Phosphat
; FILE REFERENCE: 900/035 (MBHB02-738)
; CURRENT FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 147
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense r
US-10-206-705-147
Query Match      0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      2645 GCTGAACCCCTAAGGTGAG 2662
      ||||| ||| ||||| |
Db      19 GCTGATCCCAAAGGTGG 2
      ||||| ||| ||||| |
RESULT 3316
US-10-206-705-263/c
; Sequence 263, Application US/10206705
; Publication No. US20040019001A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceutical, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Protein Tyrosine Phosphat
; FILE REFERENCE: 900/035 (MBHB02-738)
; CURRENT FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 263
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-206-705-263
Query Match      0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1590 ACTGGAAGCCCTTCCTGG 1607
      ||||| | ||| |||||
Db      18 ACTGGAAGCCCTTCCTGG 1
      ||||| | ||| |||||
RESULT 3317
US-10-206-705-332
; Sequence 332, Application US/10206705
; Publication No. US20040019001A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceutical, Inc.
; APPLICANT: McSwiggen, James
```

```
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Protein Tyrosine Phosphate
; TITLE OF INVENTION: (PTP-1B) Gene Expression using Short Interfering RNA
; FILE REFERENCE: 900/035 (MBHB02-738)
; CURRENT APPLICATION NUMBER: US/10/206,705
; CURRENT FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 332
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-206-705-332
Query Match      0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 3.3e+03;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY      2645 GCTGAACCCCTAAGGTGAG 2662
      ||:|| ||| ||||| |
Db      1 GCUGAUCCCAAAGGUGG 18
      ||:|| ||| ||||| |
RESULT 3318
US-10-257-294-12/c
; Sequence 12, Application US/10257294
; Publication No. US20040023231A1
; GENERAL INFORMATION:
; APPLICANT: Abu-Khabar, Khalid
; APPLICANT: Williams, Bryan
; APPLICANT: Frevel, Mathias
; APPLICANT: Silverman, Robert
; TITLE OF INVENTION: System for Identifying and Analyzing Expression of ARE-Containing
; FILE REFERENCE: 26473/04185
; CURRENT APPLICATION NUMBER: US/10/257,294
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US01/11993
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/198,870
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-257-294-12
Query Match      0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      2255 TTTATTGTCATATTATT 2272
      ||||| | ||||| |
Db      18 TTTATTATTATTATTATT 1
      ||||| | ||||| |
RESULT 3319
US-09-823-634A-15
; Sequence 15, Application US/09823634A
; Patent No. US20020142308A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANALYZING NUCLEOTIDE SEQUENCE
; FILE REFERENCE: 47541-20006.00
; CURRENT APPLICATION NUMBER: US/09/823,634A
; CURRENT FILING DATE: 2002-02-28
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
```

```
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: downstream amplification primer 99-950 for SEQ 2237, in complement
US-10-349-143-10102

Query Match      0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2377 TTGAGTGTACAGATTTA 2394
      | | | | | | | | | | | | | | |
Db      1 TGGAGTGTTCAGATTTA 18

RESULT 3311
US-10-349-143-10254/c
; Sequence 10254, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10254
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: downstream amplification primer 99-10735 for SEQ 2389, in complement
US-10-349-143-10254
```

```
Query Match      0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2735 AATTGTTGTGTGTATGAT 2752
      | | | | | | | | | | | | | | |
Db      18 AATTGTTGTGTGTAGAT 1

RESULT 3312
US-10-444-925-320
; Sequence 320, Application US/10444925
; Publication No. US20040009946A1
; GENERAL INFORMATION:
; APPLICANT: Lewis, Stephen Patrick
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Wilson, Linda K.
; TITLE OF INVENTION: MODULATION OF PTP1B SIGNAL TRANSDUCTION
; TITLE OF INVENTION: BY RNA INTERFERENCE
; FILE REFERENCE: 200125.441
; CURRENT APPLICATION NUMBER: US/10/444,925
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 320
; LENGTH: 19
; TYPE: RNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-925-320

Query Match      0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 3.3e+03;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1274 CGGACACCCCATGGGACC 1291
      | | | | | | | | | | | | | | |
Db      2 CGGACAACCCCAUAGUACC 19

RESULT 3313
US-10-444-925-321
; Sequence 321, Application US/10444925
; Publication No. US20040009946A1
; GENERAL INFORMATION:
; APPLICANT: Lewis, Stephen Patrick
; APPLICANT: Klinghoffer, Richard
; APPLICANT: Wilson, Linda K.
; TITLE OF INVENTION: MODULATION OF PTP1B SIGNAL TRANSDUCTION
; TITLE OF INVENTION: BY RNA INTERFERENCE
; FILE REFERENCE: 200125.441
; CURRENT APPLICATION NUMBER: US/10/444,925
; CURRENT FILING DATE: 2003-05-23
; NUMBER OF SEQ ID NOS: 599
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 321
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Small interfering RNA
US-10-444-925-321

Query Match      0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 77.8%; Pred. No. 3.3e+03;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1274 CGGACACCCCATGGGACC 1291
      | | | | | | | | | | | | | | |
Db      1 CGGACAACCCCAUAGUACC 18

RESULT 3314
US-10-206-705-78
; Sequence 78, Application US/10206705
; Publication No. US20040019001A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceutical, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Protein Tyrosine Phosphat
; TITLE OF INVENTION: (PTP-1B) Gene Expression using Short Interfering RNA
; FILE REFERENCE: 900/035 (MBHB02-738)
; CURRENT APPLICATION NUMBER: US/10/206,705
; CURRENT FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 78
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense r
US-10-206-705-78

Query Match      0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 3.3e+03;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1590 ACTGGGAACCCCTCTCTGG 1607
```

```
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE OF INVENTION: Using the Same
; FILE REFERENCE: 21402-211
; CURRENT APPLICATION NUMBER: US/10/015,115
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: 60/248,153
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/249,598
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/264,240
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/266,127
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/269,562
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/304,348
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/309,261
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,283
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 170
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
; OTHER INFORMATION: Sequence
US-10-015-115-170

Query Match          0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      269 GCCGGGCAGCACCTCTAC 286
Db      1 GTCGGGCAGGACCTTTAC 18

RESULT 3308
US-10-349-143-4542
; Sequence 4542, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4542
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-15728 for SEQ 608,
US-10-349-143-4542

Query Match          0.5%; Score 13.2; DB 1; Length 19;
```

```
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1967 ATATTACCTTGAAAAAA 1984
Db      1 ATATTACCTGGAGAGAA 18

RESULT 3309
US-10-349-143-6906
; Sequence 6906, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6906
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-21312 for SEQ 2972,
US-10-349-143-6906

Query Match          0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2661 AGTGTGCAGTACAGTGTG 2678
Db      1 AGAGTGCAGTACATGGTG 18

RESULT 3310
US-10-349-143-10102
; Sequence 10102, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 10102
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
```



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; OTHER INFORMATION: potential microsequencing oligo for 5-140-120.mis2
US-10-126-704-130

Query Match      0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2178 TTTTCTTTTAACTTGAA 2195
      ||||| ||||| |||||
Db 19 TTTTCTTTTAACTTAGAA 2

RESULT 3304
US-10-251-117-844
; Sequence 844, Application US/10251117
; Publication No. US20030170891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor R
; FILE REFERENCE: 900/042 (MBHB02-468-A)
; CURRENT APPLICATION NUMBER: US/10/251,117
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/916,466
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/296,249
; NUMBER OF SEQ ID NOS: 1213
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 844
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense h
US-10-251-117-844

Query Match      0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 38.9%; Pred. No. 3.3e+03;
Matches 7; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1786 CCCATCTTTCCTTCTCT 1803
      ||||| :||| :|
Db 2 CCCAUUUUUCCUAUCU 19

RESULT 3305
US-10-251-117-1151/c
; Sequence 1151, Application US/10251117
; Publication No. US20030170891A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Epidermal Growth Factor R
; FILE REFERENCE: 900/042 (MBHB02-468-A)
; CURRENT APPLICATION NUMBER: US/10/251,117
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/393,924
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 10/163,552
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/916,466
; PRIOR FILING DATE: 2001-07-25
```

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; PRIOR APPLICATION NUMBER: US 60/296,249
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 1213
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1151
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-251-117-1151

Query Match      0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1786 CCCATCTTTCCTTCTCT 1803
      ||||| ||||| |||||
Db 18 CCCATTTTTCCTAATCT 1

RESULT 3306
US-10-400-382-296/c
; Sequence 296, Application US/10400382
; Publication No. US20030190659A1
; GENERAL INFORMATION:
; APPLICANT: LaCasse, Eric
; APPLICANT: McManus, Daniel
; APPLICANT: Durkin, Jonathan P.
; TITLE OF INVENTION: Antisense IAP Nucleobase Oligomers and
; FILE REFERENCE: 07891/025004
; CURRENT APPLICATION NUMBER: US/10/400,382
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/367,853
; PRIOR FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 296
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: based on Homo sapiens.
; OTHER INFORMATION: DNA/RNA hybrid.
US-10-400-382-296

Query Match      0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1318 GAACATACAGAACTGCTT 1335
      ||||| ||||| |||||
Db 19 GAACACATAGAACAGCTT 2

RESULT 3307
US-10-015-115-170
; Sequence 170, Application US/10015115
; Publication No. US20030207800A1
; GENERAL INFORMATION:
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Guo, Xiaojia
; APPLICANT: Kekuda, Ramesha
; APPLICANT: Gangolli, Esha A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier, Raymond J
; APPLICANT: Li, Li
; APPLICANT: Padigaru, Muralidhara
```

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; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 347
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 95
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target sequence/siNA sense r
US-10-224-005-95

Query Match          0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 3.3e+03;
Matches 12; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 112 GGGCTGGGGGATCCTGG 129
      |||||:||||| | :|||:|
Db 1 GGGCUGGGCAGGUCCUGG 18

RESULT 3300
US-10-224-005-256/c
; Sequence 256, Application US/10224005
; Publication No. US20030143732A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Fosnaugh, Kathy
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Adenosine A1 Receptor (AD
; TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
; FILE REFERENCE: 900/041 (MBHB01-1110-A)
; CURRENT APPLICATION NUMBER: US/10/224,005
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 347
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 256
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-224-005-256

Query Match          0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 112 GGGCTGGGGGATCCTGG 129
      |||||:||||| | |||||
Db 19 GGGCTGGGCAGGTCCTGG 2

RESULT 3301
US-10-391-413-19
; Sequence 19, Application US/10391413
; Publication No. US20030167482A1
; GENERAL INFORMATION:
; APPLICANT: KIMURA, Toru et al.
; TITLE OF INVENTION: NOVEL SEMAPHORIN Z AND GENE ENCODING THE SAME
; FILE REFERENCE: 0020-5120P
; CURRENT APPLICATION NUMBER: US/10/391,413
; CURRENT FILING DATE: 2003-03-19
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Adapter DNA used to ligate the various parts of the rsZexII
; OTHER INFORMATION: plasmid
US-10-391-413-19

Query Match          0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1724 GACCTATTATCAGAAGGT 1741
      |||||:||||| | |||
Db 2 GAACTATTATCAGGACGT 19

RESULT 3302
US-10-126-704-105
; Sequence 105, Application US/10126704
; Publication No. US20030170647A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
; TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
; FILE REFERENCE: 44.US5.DIV
; CURRENT APPLICATION NUMBER: US/10/126,704
; CURRENT FILING DATE: 2002-04-20
; PRIOR APPLICATION NUMBER: US 60/091,315
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/111,909
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patent.pm
; SEQ ID NO 105
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: potential microsequencing oligo for 5-129-144.misl
US-10-126-704-105

Query Match          0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2775 TGTTAGAAATTGAAAAAAA 2792
      |||||:||||| | |||||
Db 2 TCTTATAAATTAATAAAAAAA 19

RESULT 3303
US-10-126-704-130/c
; Sequence 130, Application US/10126704
; Publication No. US20030170647A1
; GENERAL INFORMATION:
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
; TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
; FILE REFERENCE: 44.US5.DIV
; CURRENT APPLICATION NUMBER: US/10/126,704
; CURRENT FILING DATE: 2002-04-20
; PRIOR APPLICATION NUMBER: US 60/091,315
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/111,909
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patent.pm
; SEQ ID NO 130
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
```

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; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: 07/961,813
; PRIOR FILING DATE: 1992-10-16
; PRIOR APPLICATION NUMBER: 08/359,945
; PRIOR FILING DATE: 1994-12-20
; PRIOR APPLICATION NUMBER: 08/221,655
; PRIOR FILING DATE: 1994-04-01
; PRIOR APPLICATION NUMBER: 07/967,622
; PRIOR FILING DATE: 1992-10-28
; PRIOR APPLICATION NUMBER: 08/376,062
; PRIOR FILING DATE: 1995-01-20
; PRIOR APPLICATION NUMBER: 08/010,829
; PRIOR FILING DATE: 1993-01-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EGF anti-sense
; OTHER INFORMATION: strand
US-10-199-830-4

Query Match          0.5%;   Score 13.2;   DB 1;   Length 19;
Best Local Similarity 83.3%;   Pred. No. 3.3e+03;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      1409 TACATCAAGAAGCCCTG 1426
      |||||
Db       19  TAAATAAAGATGCCCTG 2

RESULT 3296
US-10-005-956-65/c
; Sequence 65, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 65
; LENGTH: 19
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-65

Query Match          0.5%;   Score 13.2;   DB 1;   Length 19;
Best Local Similarity 83.3%;   Pred. No. 3.3e+03;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      47  GCGCGCGCGGGGGCGGC 64
      |||||
Db       19  GGGCGCGCGGGGGGAGC 2

RESULT 3297
US-10-005-956-129/c
; Sequence 129, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
```

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; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 129
; LENGTH: 19
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-005-956-129

Query Match          0.5%;   Score 13.2;   DB 1;   Length 19;
Best Local Similarity 83.3%;   Pred. No. 3.3e+03;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      47  GCGCGCGCGGGGGCGGC 64
      |||||
Db       18  GGGCGCGCGGGGGGCGC 1

RESULT 3298
US-10-239-316-26
; Sequence 26, Application US/10239316
; Publication No. US20030125253A1
; GENERAL INFORMATION:
; APPLICANT: TANIYAMA, Yoshio
; APPLICANT: KITA, Shunbun
; APPLICANT: SATOMI, Tomoko Komiyama
; TITLE OF INVENTION: No. US20030125253A1e1 Protein, Process for Producing The Same An
; FILE REFERENCE: 2703US0P
; CURRENT APPLICATION NUMBER: US/10/239,316
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: PCT/JP01/02279
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: JP2000-088595
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 59
; SEQ ID NO 26
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-239-316-26

Query Match          0.5%;   Score 13.2;   DB 1;   Length 19;
Best Local Similarity 83.3%;   Pred. No. 3.3e+03;
Matches 15;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

QY      451 CACAGGCAGCCAGCAGCA 468
      |||
Db       2  CACGGCCAGCCAGCAACA 19

RESULT 3299
US-10-224-005-95
; Sequence 95, Application US/10224005
; Publication No. US20030143732A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Fosnaugh, Kathy
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Adenosine A1 Receptor (Ad
; TITLE OF INVENTION: Gene Expression Using Short Interfering RNA
; FILE REFERENCE: 900/041 (MBHB01-1110-A)
; CURRENT APPLICATION NUMBER: US/10/224,005
```

GENERAL INFORMATION:  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)  
; TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.  
; FILE REFERENCE: GENSET.031A  
; CURRENT APPLICATION NUMBER: US/10/071,179  
; CURRENT FILING DATE: 2002-02-07  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/345,882  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/091,315  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/111,909  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: Patent.pm  
; SEQ ID NO 105  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: 1..19  
; OTHER INFORMATION: potential microsequencing oligo for 5-129-144.mis1  
US-10-071-179-105

Query Match 0.5%; Score 13.2; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2775 TGTTAGAATTGAAAAAA 2792  
| ||||| ||||| |||||  
Db 2 TCTTATAATTAAAAAA 19

RESULT 3293  
US-10-071-179-130/c  
; Sequence 130, Application US/10071179  
; Publication No. US2003010882A1  
; GENERAL INFORMATION:  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)  
; TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.  
; FILE REFERENCE: GENSET.031A  
; CURRENT APPLICATION NUMBER: US/10/071,179  
; CURRENT FILING DATE: 2002-02-07  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/345,882  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-30  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/091,315  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/111,909  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-10  
; NUMBER OF SEQ ID NOS: 140  
; SOFTWARE: Patent.pm  
; SEQ ID NO 130  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: 1..19  
; OTHER INFORMATION: potential microsequencing oligo for 5-140-120.mis2  
US-10-071-179-130

Query Match 0.5%; Score 13.2; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2178 TTTTCTTAACTTGA 2195  
| ||||| ||||| |||||  
Db 19 TTTTCTTAACTTGA 2

RESULT 3294

US-10-199-830-3  
; Sequence 3, Application US/10199830  
; Publication No. US20030109008A1  
; GENERAL INFORMATION:  
; APPLICANT: Weiss, Samuel  
; APPLICANT: Reynolds, Brent  
; APPLICANT: Hammang, Joseph P  
; APPLICANT: Baetge, E. E  
; TITLE OF INVENTION: Methods of Making cDNA Libraries  
; FILE REFERENCE: 17810-705 DIV12CON2  
; CURRENT APPLICATION NUMBER: US/10/199,830  
; CURRENT FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: 08/486,313  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/270,412  
; PRIOR FILING DATE: 1994-07-05  
; PRIOR APPLICATION NUMBER: 07/726,812  
; PRIOR FILING DATE: 1991-07-08  
; PRIOR APPLICATION NUMBER: 08/385,404  
; PRIOR FILING DATE: 1995-02-07  
; PRIOR APPLICATION NUMBER: 07/961,813  
; PRIOR FILING DATE: 1992-10-16  
; PRIOR APPLICATION NUMBER: 08/359,945  
; PRIOR FILING DATE: 1994-12-20  
; PRIOR APPLICATION NUMBER: 08/376,062  
; PRIOR FILING DATE: 1995-01-20  
; PRIOR APPLICATION NUMBER: 08/010,829  
; PRIOR FILING DATE: 1993-01-29  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: EGF sense  
; OTHER INFORMATION: strand  
US-10-199-830-3

Query Match 0.5%; Score 13.2; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1409 TACATCAAGAGCCCTG 1426  
| ||||| ||||| |||||  
Db 1 TAAATAAAGATGCCCTG 18

RESULT 3295  
US-10-199-830-4/c  
; Sequence 4, Application US/10199830  
; Publication No. US20030109008A1  
; GENERAL INFORMATION:  
; APPLICANT: Weiss, Samuel  
; APPLICANT: Reynolds, Brent  
; APPLICANT: Hammang, Joseph P  
; APPLICANT: Baetge, E. E  
; TITLE OF INVENTION: Methods of Making cDNA Libraries  
; FILE REFERENCE: 17810-705 DIV12CON2  
; CURRENT APPLICATION NUMBER: US/10/199,830  
; CURRENT FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: 08/486,313  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/270,412  
; PRIOR FILING DATE: 1994-07-05  
; PRIOR APPLICATION NUMBER: 07/726,812  
; PRIOR FILING DATE: 1991-07-08  
; PRIOR APPLICATION NUMBER: 08/385,404



; GENERAL INFORMATION:
; APPLICANT: LEGRAIN, Pierre
; APPLICANT: BENAROUS, Richard
; APPLICANT: BLOT, Guillaume
; APPLICANT: LASSOT, Irina
; TITLE OF INVENTION: PROTEINS THAT INTERACT WITH BETA TRCP
; FILE REFERENCE: B4717A
; CURRENT APPLICATION NUMBER: US/10/023,530
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/256,276
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: RasSFldsRNA185
; LOCATION: (1)..(19)
; OTHER INFORMATION: Sense strand sequence
; OTHER INFORMATION: Antisense strand SEQ ID NO.21
; FEATURE:
; NAME/KEY: RasSFldsRNA185
; LOCATION: (1)..(19)
; OTHER INFORMATION: Sense strand sequence (dtdt in 3')
US-10-023-530-20

Query Match 0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 834 TCTTCTGCTCAGTCCCTG 851
Db 19 TCTTCTGCTCAATCTCAG 2

RESULT 3289
US-10-079-429-77
; Sequence 77, Application US/10079429
; Publication No. US20030027177A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Human DNA Mismatch Repair Proteins
; FILE REFERENCE: PFI06P3D1
; CURRENT APPLICATION NUMBER: US/10/079,429
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: PCT/US95/01035
; PRIOR FILING DATE: 1995-01-25
; PRIOR APPLICATION NUMBER: 08/468,024
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/465,769
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/294,312
; PRIOR FILING DATE: 1994-08-23
; PRIOR APPLICATION NUMBER: 08/210,143
; PRIOR FILING DATE: 1994-03-16
; PRIOR APPLICATION NUMBER: 08/187,757
; PRIOR FILING DATE: 1994-01-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 77
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer useful for amplifying codons 439 to 472 of hMLH3
US-10-079-429-77

Query Match 0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 484 CCAGAGCCAGGAGGAGC 501
Db 2 CCAGAACCAAGAAGGAGC 19

RESULT 3290
US-10-220-310-5
; Sequence 5, Application US/10220310
; Publication No. US20030073660A1
; GENERAL INFORMATION:
; APPLICANT: Universit degli Studi di Ferrara
; APPLICANT: Associazione veneta per la lotta alla Talassemia
; APPLICANT: Associazione per la lotta alla Talassemia di Ferrara
; APPLICANT: Chiesi Farmaceutici S.p.A.
; TITLE OF INVENTION: Synthetic oligonucleotides as inducers of erythroid differentiation
; FILE REFERENCE: Erythroid differentiation
; CURRENT APPLICATION NUMBER: US/10/220,310
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: TO2000A000234
; PRIOR FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-220-310-5

Query Match 0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2166 TTTTCTTTCTTTCTTTT 2183
Db 2 TTTCTTTCTTTCTTTT 19

RESULT 3291
US-10-220-310-5/c
; Sequence 5, Application US/10220310
; Publication No. US20030073660A1
; GENERAL INFORMATION:
; APPLICANT: Universit degli Studi di Ferrara
; APPLICANT: Associazione veneta per la lotta alla Talassemia
; APPLICANT: Associazione per la lotta alla Talassemia di Ferrara
; APPLICANT: Chiesi Farmaceutici S.p.A.
; TITLE OF INVENTION: Synthetic oligonucleotides as inducers of erythroid differentiation
; FILE REFERENCE: Erythroid differentiation
; CURRENT APPLICATION NUMBER: US/10/220,310
; CURRENT FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: TO2000A000234
; PRIOR FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-220-310-5

Query Match 0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2786 AAAAAAATAAAAAA 2803
Db 19 AAAAAAGAAAGAAAGAA 2

RESULT 3292
US-10-071-179-105
; Sequence 105, Application US/10071179
; Publication No. US20030108882A1

US-10-398-519-32  
; Sequence 32, Application US/10398519  
; Publication No. US20040072258A1  
; GENERAL INFORMATION:  
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH &  
; APPLICANT: INDUSTRIAL DEVELOPMENT LTD.  
; TITLE OF INVENTION: ISOPRENOID-DEPENDENT RAS ANCHORAGE (IDRA) PROTEINS  
; FILE REFERENCE: THYREOS 3.4-007  
; CURRENT APPLICATION NUMBER: US/10/398,519  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: 60/237,858  
; PRIOR FILING DATE: 2000-10-04  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: antisense oligonucleotide  
US-10-398-519-32  
  
Query Match 0.5%; Score 13.2; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 999 TCGGGGAGAGTTGGACA 1016  
Db 1 TGTGGGGGACGTTGGACA 18  
  
RESULT 3286  
US-10-092-900A-381  
; Sequence 381, Application US/10092900A  
; Publication No. US20040043382A1  
; GENERAL INFORMATION:  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Taupier Jr., Raymond J.  
; APPLICANT: Pena, Carol E.A.  
; APPLICANT: Li, Li  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Gusev, Vladimir Y.  
; APPLICANT: Ji, Weizhen  
; APPLICANT: Gorman, Linda  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Gangolli, Esha A.  
; APPLICANT: Vernet, Corine A.M.  
; APPLICANT: Guo, Xiaojia Sasha  
; APPLICANT: Tchernev, Velizar T.  
; APPLICANT: Fernandes, Elma R.  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Liu, Yi  
; APPLICANT: Anderson, David W.  
; APPLICANT: Spaderna, Steven K.  
; APPLICANT: Catterton, Elina  
; APPLICANT: Leite, Mario W.  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Alsobrook, John P.  
; APPLICANT: Lepley, Denise M.  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Burgess, Catherine E.  
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-290C  
; CURRENT APPLICATION NUMBER: US/10/092,900A  
; CURRENT FILING DATE: 2002-03-07  
; PRIOR APPLICATION NUMBER: USSN 60/274,322  
; PRIOR FILING DATE: 2001-03-08

; PRIOR APPLICATION NUMBER: USSN 60/283,675  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: USSN 60/338,092  
; PRIOR FILING DATE: 2001-12-03  
; PRIOR APPLICATION NUMBER: USSN 60/274,281  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: USSN 60/274,191  
; PRIOR FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: USSN 60/325,681  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: USSN 60/304,354  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: USSN 60/279,995  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: USSN 60/294,899  
; PRIOR FILING DATE: 2001-05-31  
; PRIOR APPLICATION NUMBER: USSN 60/287,424  
; PRIOR FILING DATE: 2001-04-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 768  
; SEQ ID NO 381  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Forward Primer  
US-10-092-900A-381  
  
Query Match 0.5%; Score 13.2; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 269 GCCGGGCAGCACCTCTAC 286  
Db 1 GTCGGGCAGGACCTTTAC 18  
  
RESULT 3287  
US-10-415-657-18  
; Sequence 18, Application US/10415657  
; Publication No. US20040048277A1  
; GENERAL INFORMATION:  
; APPLICANT: Cenix Bioscience GmbH  
; TITLE OF INVENTION: Eukaryotic cell division genes and their use in diagnosis and treat  
; TITLE OF INVENTION: of proliferative diseases  
; FILE REFERENCE: CE61773US  
; CURRENT APPLICATION NUMBER: US/10/415,657  
; CURRENT FILING DATE: 2003-09-08  
; PRIOR APPLICATION NUMBER: US 60/246,750  
; PRIOR FILING DATE: 2000-11-09  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide for PCR amplification (example 3)  
US-10-415-657-18  
  
Query Match 0.5%; Score 13.2; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1492 GGAGAAAATGGAGAAACA 1509  
Db 2 GAAGAAATGGGAAACA 19  
  
RESULT 3288  
US-10-023-530-20/c  
; Sequence 20, Application US/10023530  
; Publication No. US20030007956A1

```

; PRIOR APPLICATION NUMBER: 08/338,730
; PRIOR FILING DATE: 1994-11-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:chemically
; OTHER INFORMATION: synthesized
US-09-925-911-3

Query Match      0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1409 TACATCAAAGAAGCCCTG 1426
Db 1 TAAATAAAAGATGCCCTG 18

RESULT 3282
US-09-925-911-4/c
; Sequence 4, Application US/09925911
; Publication No. US20030049837A1
; GENERAL INFORMATION:
; APPLICANT: Weiss et al.
; TITLE OF INVENTION: In Vitro and In Vivo Proliferation and Use of
; TITLE OF INVENTION: Multipotent Neural Stem Cells and Their Progeny
; FILE REFERENCE: 17810-705 (CTI-N5 DIV11CON)
; CURRENT APPLICATION NUMBER: US/09/925,911
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 08/484,203
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 08/270,412
; PRIOR FILING DATE: 1994-07-05
; PRIOR APPLICATION NUMBER: 07/726,812
; PRIOR FILING DATE: 1991-07-08
; PRIOR APPLICATION NUMBER: 08/385,404
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: 07/961,813
; PRIOR FILING DATE: 1992-10-16
; PRIOR APPLICATION NUMBER: 08/359,945
; PRIOR FILING DATE: 1994-12-20
; PRIOR APPLICATION NUMBER: 08/221,655
; PRIOR FILING DATE: 1994-04-01
; PRIOR APPLICATION NUMBER: 07/967,622
; PRIOR FILING DATE: 1992-10-28
; PRIOR APPLICATION NUMBER: 08/376,062
; PRIOR FILING DATE: 1995-01-20
; PRIOR APPLICATION NUMBER: 08/010,829
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: 08/149,508
; PRIOR FILING DATE: 1993-11-09
; PRIOR APPLICATION NUMBER: 08/311,099
; PRIOR FILING DATE: 1994-09-23
; PRIOR APPLICATION NUMBER: 08/338,730
; PRIOR FILING DATE: 1994-11-14
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:chemically
; OTHER INFORMATION: synthesized
US-09-925-911-4

Query Match      0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1409 TACATCAAAGAAGCCCTG 1426
Db 1 TAAATAAAAGATGCCCTG 18

RESULT 3283
US-09-902-176A-47/c
; Sequence 47, Application US/09902176A
; Publication No. US20030099943A1
; GENERAL INFORMATION:
; APPLICANT: Schreiber, Stefan
; APPLICANT: Hampe, Jochen
; APPLICANT: Mascheretti, Silvia
; TITLE OF INVENTION: Diagnostic Use of Polymorphisms in the Gene Coding for
; TITLE OF INVENTION: the TNF Receptor II and Method for Detecting
; TITLE OF INVENTION: No. US20030099943A1-Responders to Anti-TNF-Therapy
; FILE REFERENCE: 25481-P001US
; CURRENT APPLICATION NUMBER: US/09/902,176A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: EP 00114786.7
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-09-902-176A-47

Query Match      0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2566 CTCTGTTCTTGGCTTGA 2583
Db 19 CTCTGCTCTTGGCCTGCA 2

RESULT 3284
US-10-343-114-43
; Sequence 43, Application US/10343114
; Publication No. US20040072998A1
; GENERAL INFORMATION:
; APPLICANT: Wissenbach, Ulrich
; TITLE OF INVENTION: Trp8, Trp9 and Trp10, Novel Markers for Cancer
; FILE REFERENCE: 012627-034
; CURRENT APPLICATION NUMBER: US/10/343,114
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: PCT/EP01/08309
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
US-10-343-114-43

Query Match      0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 359 CAGCAGCTGGCCTACTCC 376
Db 2 CAGCTGCTGGTCTATTCC 19

RESULT 3285
```

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/263,959  
; FILING DATE: 05-MAR-1999  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mcmasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 920010.426C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 754:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-09-263-959-754

Query Match 0.5%; Score 13.2; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2256 TTATTTGCATATTATT 2273  
Db 19 TTATTTATTATTATT 2

RESULT 3279  
US-09-785-548-16/c  
; Sequence 16, Application US/09785548  
; Patent No. US20020155577A1  
; GENERAL INFORMATION:  
; APPLICANT: AVENTIS PHARMACEUTICALS, INC.  
; TITLE OF INVENTION: COMPOSITIONS THAT CAN BE USED FOR REGULATING THE ACTIVITY OF PARK  
; FILE REFERENCE: ST00005  
; CURRENT APPLICATION NUMBER: US/09/785,548  
; CURRENT FILING DATE: 2001-02-20  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Description of the artificial sequence:oligonucleotide  
US-09-785-548-16

Query Match 0.5%; Score 13.2; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1315 GACGAACATACAGAACTG 1332  
Db 19 GATGAACAGGCAGAACTG 2

RESULT 3280  
US-09-853-526-565  
; Sequence 565, Application US/09853526  
; Patent No. US20020165345A1

; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Ilya, Chumakov  
; APPLICANT: Bougueleret, Lydie  
; TITLE OF INVENTION: PROSTATE CANCER GENE  
; FILE REFERENCE: GENSET.18CPICP  
; CURRENT APPLICATION NUMBER: US/09/853,526  
; CURRENT FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 09/338,907  
; PRIOR FILING DATE: 1999-06-23  
; PRIOR APPLICATION NUMBER: 08/996,306  
; PRIOR FILING DATE: 1997-12-22  
; PRIOR APPLICATION NUMBER: 60/099,658  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 09/218,207  
; PRIOR FILING DATE: 1998-12-22  
; NUMBER OF SEQ ID NOS: 578  
; SOFTWARE: Patent.pm  
; SEQ ID NO 565  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1..19  
; OTHER INFORMATION: potential microsequencing oligo for 99-148-366.mis2  
US-09-853-526-565

Query Match 0.5%; Score 13.2; DB 1; Length 19;  
Best Local Similarity 83.3%; Pred. No. 3.3e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 560 GAGCGGGCGCGGTGAGC 577  
Db 1 GAGCGGCAGCCGTGAGC 18

RESULT 3281  
US-09-925-911-3  
; Sequence 3, Application US/09925911  
; Publication No. US20030049837A1  
; GENERAL INFORMATION:  
; APPLICANT: Weiss et al.  
; TITLE OF INVENTION: In Vitro and In Vivo Proliferation and Use of  
; FILE REFERENCE: 17810-705 (CTI-N5 DIV11CON)  
; CURRENT APPLICATION NUMBER: US/09/925,911  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 08/484,203  
; PRIOR FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: 08/270,412  
; PRIOR FILING DATE: 1994-07-05  
; PRIOR APPLICATION NUMBER: 07/726,812  
; PRIOR FILING DATE: 1991-07-08  
; PRIOR APPLICATION NUMBER: 08/385,404  
; PRIOR FILING DATE: 1995-02-07  
; PRIOR APPLICATION NUMBER: 07/961,813  
; PRIOR FILING DATE: 1992-10-16  
; PRIOR APPLICATION NUMBER: 08/359,945  
; PRIOR FILING DATE: 1994-12-20  
; PRIOR APPLICATION NUMBER: 08/221,655  
; PRIOR FILING DATE: 1994-04-01  
; PRIOR APPLICATION NUMBER: 07/967,622  
; PRIOR FILING DATE: 1992-10-28  
; PRIOR APPLICATION NUMBER: 08/376,062  
; PRIOR FILING DATE: 1995-01-20  
; PRIOR APPLICATION NUMBER: 08/010,829  
; PRIOR FILING DATE: 1993-01-29  
; PRIOR APPLICATION NUMBER: 08/149,508  
; PRIOR FILING DATE: 1993-11-09  
; PRIOR APPLICATION NUMBER: 08/311,099  
; PRIOR FILING DATE: 1994-09-23



```
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-7792 for SEQ 1988,
US-10-349-143-5922

Query Match      0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 343 CTTTCCCTCCCTCCCTACCA 360
Db 18 CTTTATCCCTCCCTTCCA 1

RESULT 3275
US-10-349-143-7191
; Sequence 7191, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7191
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-2765 for SEQ 3257,
US-10-349-143-7191

Query Match      0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 773 AACCTCTGAACCTCCCC 790
Db 1 AACACTCTCAACCTCCTC 18

RESULT 3276
US-10-416-041-19
; Sequence 19, Application US/10416041
; Publication No. US20040093635A1
; GENERAL INFORMATION:
; APPLICANT: Van Enckevort, Lenora Johanna Gertruda
; APPLICANT: Jacobsen, Evert
; APPLICANT: Stiekema, Willem Johannes
; APPLICANT: Pereira, Andy
; TITLE OF INVENTION: DNA SEQUENCES ENCODING PROTEINS CONFERRING PHYTOPHTHORA
; TITLE OF INVENTION: INFESTANS RESISTANCE ON PLANTS
; FILE REFERENCE: U 014591-5
; CURRENT APPLICATION NUMBER: US/10/416,041
; CURRENT FILING DATE: 2003-10-24
; PRIOR APPLICATION NUMBER: EP 00203911.3
; PRIOR FILING DATE: 2000-11-09
```

```
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-416-041-19

Query Match      0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1913 AACAAATACCTTTTTC 1930
Db 1 AACAAATGCCTTCTCTC 18

RESULT 3277
US-09-901-484A-565
; Sequence 565, Application US/09901484A
; Patent No. US20020119460A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Prostate Cancer Gene
; FILE REFERENCE: GEN-T111XC3D2
; CURRENT APPLICATION NUMBER: US/09/901,484A
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 08/996,306
; PRIOR FILING DATE: 1997-12-22
; PRIOR APPLICATION NUMBER: US 60/099,658
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: US 09/218,207
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 09/338,907
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: US 09/853,526
; PRIOR FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 578
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 565
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(19)
; OTHER INFORMATION: potential microsequencing oligo for 99-148-366.mis2
US-09-901-484A-565

Query Match      0.5%; Score 13.2; DB 1; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 560 GAGCGGGCGCGGTGAGC 577
Db 1 GAGCGGGCAGCCGTGAGC 18

RESULT 3278
US-09-263-959-754/c
; Sequence 754, Application US/09263959
; Patent No. US20020150891A1
; GENERAL INFORMATION:
; APPLICANT: Hood, Leroy E.
; APPLICANT: Rowen, Lee
; APPLICANT: Koop, Ben F.
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
; NUMBER OF SEQUENCES: 1279
```

RESULT 3271  
US-10-388-263-192/c  
; Sequence 192, Application US/10388263  
; Publication No. US20030228597A1  
; GENERAL INFORMATION:  
; APPLICANT: Cowser, Lex M.  
; APPLICANT: Baker, Brenda F.  
; APPLICANT: McNeil, John  
; APPLICANT: Freier, Susan M.  
; APPLICANT: Sasnor, Henri M.  
; APPLICANT: Brooks, Douglas G.  
; APPLICANT: Ohashi, Cara  
; APPLICANT: Wyatt, Jacqueline R.  
; APPLICANT: Borchers, Alexander  
; APPLICANT: Vickers, Timothy A.  
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR  
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND  
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION  
; FILE REFERENCE: ISIS-4503  
; CURRENT APPLICATION NUMBER: US/10/388,263  
; CURRENT FILING DATE: 2003-03-12  
; NUMBER OF SEQ ID NOS: 947  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 192  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-388-263-192

Query Match 0.5%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 3.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1150 ACCAGTGGCAGCAATATTT 1167  
| | | | | | | | | | | | | | | | | |  
Db 18 ACCAGTGGAGAACAAATT 1

RESULT 3272  
US-10-388-263-867  
; Sequence 867, Application US/10388263  
; Publication No. US20030228597A1  
; GENERAL INFORMATION:  
; APPLICANT: Cowser, Lex M.  
; APPLICANT: Baker, Brenda F.  
; APPLICANT: McNeil, John  
; APPLICANT: Freier, Susan M.  
; APPLICANT: Sasnor, Henri M.  
; APPLICANT: Brooks, Douglas G.  
; APPLICANT: Ohashi, Cara  
; APPLICANT: Wyatt, Jacqueline R.  
; APPLICANT: Borchers, Alexander  
; APPLICANT: Vickers, Timothy A.  
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR  
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND  
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION  
; FILE REFERENCE: ISIS-4503  
; CURRENT APPLICATION NUMBER: US/10/388,263  
; CURRENT FILING DATE: 2003-03-12  
; NUMBER OF SEQ ID NOS: 947  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 867  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-388-263-867

Query Match 0.5%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 3.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1777 TTTTGAACCCCATTCCTT 1794  
| | | | | | | | | | | | | | | | | |  
Db 1 TGTTCAGGCCCATTCCTT 18

RESULT 3273  
US-10-336-213B-47  
; Sequence 47, Application US/10336213B  
; Publication No. US20040002153A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Lex M. Cowser  
; APPLICANT: Robert McKay  
; APPLICANT: Tim Vickers  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTEN EXPRESSION  
; FILE REFERENCE: ISIS0004-100  
; CURRENT APPLICATION NUMBER: US/10/336,213B  
; CURRENT FILING DATE: 2003-01-03  
; PRIOR APPLICATION NUMBER: US 60/411,780  
; PRIOR FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: US 09/878,582  
; PRIOR FILING DATE: 2001-06-11  
; PRIOR APPLICATION NUMBER: US 09/577,902  
; PRIOR FILING DATE: 2000-05-24  
; PRIOR APPLICATION NUMBER: PCT/US99/29594  
; PRIOR FILING DATE: 1999-12-14  
; PRIOR APPLICATION NUMBER: US 09/358,381  
; PRIOR FILING DATE: 1999-07-21  
; NUMBER OF SEQ ID NOS: 88  
; SEQ ID NO 47  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-10-336-213B-47

Query Match 0.5%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 3.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1777 TTTTGAACCCCATTCCTT 1794  
| | | | | | | | | | | | | | | | | |  
Db 1 TGTTCAGGCCCATTCCTT 18

RESULT 3274  
US-10-349-143-5922/c  
; Sequence 5922, Application US/10349143  
; Publication No. US20040005584A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET.020CP1  
; CURRENT APPLICATION NUMBER: US/10/349,143  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US/09/422,978  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 5922  
; LENGTH: 18



```
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus
US-10-043-875-875

Query Match      0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      679 TCACCAGATGGACGAGGT 696
Db      1 TCAATACATGGACGAGGT 18

RESULT 3263
US-10-067-125-180
; Sequence 180, Application US/10067125
; Publication No. US20030055015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda F.
; APPLICANT: Cowser, Lex M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Xu, Xiaoxing S.
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRAF EXPRESSION
; FILE REFERENCE: ISPH-0321
; CURRENT APPLICATION NUMBER: US/10/067,125
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/167,109
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 180
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antisense sequence
US-10-067-125-180

Query Match      0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1565 GCAAAATCTCTCTCCAC 1582
Db      1 GCAAAACTCCGTCCTCTAC 18

RESULT 3264
US-10-209-608-48
; Sequence 48, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOI
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 199953USOXDIV
; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/725,265
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentln version 3.1
```

```
; SEQ ID NO 48
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-48

Query Match      0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1771 TTTT TTTT TTTT GAACCC 1788
Db      1 TTTT TTTT TTTT TCCCCC 18

RESULT 3265
US-10-197-290-39/c
; Sequence 39, Application US/10197290
; Publication No. US20030083300A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-2
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTSP-0421
; CURRENT APPLICATION NUMBER: US/10/197,290
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 09/857,299
; PRIOR FILING DATE: 2001-20-04
; PRIOR APPLICATION NUMBER: PCT/US99/22083
; PRIOR FILING DATE: 1999-09-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-197-290-39

Query Match      0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1150 ACCAGTGGCAGAAATATT 1167
Db      18 ACCAGTGGAAAGAACAATT 1

RESULT 3266
US-10-357-488-36/c
; Sequence 36, Application US/10357488
; Publication No. US20030194730A1
; GENERAL INFORMATION:
; APPLICANT: Centre For DNA Fingerprinting and Diagnostics
; TITLE OF INVENTION: No. US20030194730A1el FISSR-PCR primers and markers and a method c
; TITLE OF INVENTION: primers and markers for identifying genetic constitution and bree
; TITLE OF INVENTION: varieties.
; FILE REFERENCE: 782-indian
; CURRENT APPLICATION NUMBER: US/10/357,488
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 260/MAS/2002
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 69  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 28  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-10-462-261-28

Query Match 0.5%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 3.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 253 CCCCCACCTCTCCTCCGC 270  
| | | | | | | | | | | | | | | |  
Db 1 CGCCACACCTCCCTCCTC 18

RESULT 3259  
US-10-683-386-48  
; Sequence 48, Application US/10683386  
; Publication No. US20040063137A1  
; GENERAL INFORMATION:  
; APPLICANT: KURANE, RYUICHIRO  
; APPLICANT: KANAGAWA, TAKAHIRO  
; APPLICANT: KAMAGATA, YOICHI  
; APPLICANT: YAMADA, KAZUTAKA  
; APPLICANT: YOKOMAKU, TOYOKAZU  
; APPLICANT: KOYAMA, OSAMU  
; APPLICANT: FURUSHO, KENTA  
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MOL  
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT  
; TITLE OF INVENTION: THE METHOD  
; FILE REFERENCE: 0163-0758-0X  
; CURRENT APPLICATION NUMBER: US/10/683,386  
; CURRENT FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US/09/556,127  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: JP 1999-111601  
; PRIOR FILING DATE: 1999-04-20  
; NUMBER OF SEQ ID NOS: 70  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 48  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: SYNTHETIC DNA  
US-10-683-386-48

Query Match 0.5%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 3.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1771 TTTT TTTT TTTTGAACCC 1788  
| | | | | | | | | | | | | | | |  
Db 1 TTTT TTTT TTTTCCCCC 18

RESULT 3260  
US-10-252-155-90/c  
; Sequence 90, Application US/10252155  
; Publication No. US20040068096A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS IN ORGANIC ANION TRANSPORT  
; TITLE OF INVENTION: MULTI-DRUG RESISTANT PROTEINS  
; FILE REFERENCE: D0152 NP  
; CURRENT APPLICATION NUMBER: US/10/252,155  
; CURRENT FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: US 60/324,172

; PRIOR FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: US 60/333,700  
; PRIOR FILING DATE: 2001-11-27  
; NUMBER OF SEQ ID NOS: 783  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 90  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-252-155-90

Query Match 0.5%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 3.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 658 CCTGGGCTCCACGACAT 675  
| | | | | | | | | | | | | | | |  
Db 18 CATGGGCTCCACGACCT 1

RESULT 3261  
US-10-028-056-17  
; Sequence 17, Application US/10028056  
; Publication No. US20020152483A1  
; GENERAL INFORMATION:  
; APPLICANT: REUE, KAREN  
; APPLICANT: PTERFY, MIKLOS  
; TITLE OF INVENTION: A NOVEL GENE ASSOCIATED WITH REGULATION OF ADIPOSITY AND INSULIN  
; FILE REFERENCE: 407T-898010US  
; CURRENT APPLICATION NUMBER: US/10/028,056  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: US 60/257,772  
; PRIOR FILING DATE: 2000-12-22  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 17  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: PCR primer  
US-10-028-056-17

Query Match 0.5%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 3.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 113 GGCTGGGGGATCCTGGA 130  
| | | | | | | | | | | | | | | |  
Db 1 GGTGTGGGGACCTGGA 18

RESULT 3262  
US-10-043-875-875  
; Sequence 875, Application US/10043875  
; Publication No. US20030054339A1  
; GENERAL INFORMATION:  
; APPLICANT: De Smet, Koenraad  
; APPLICANT: Stuyver, Lieven  
; TITLE OF INVENTION: Method for Detection of Drug-Induced Mutations in the HIV Reverse  
; TITLE OF INVENTION: Transcriptase Gene  
; FILE REFERENCE: 11362-0033-NPUS01 (INNS:033)  
; CURRENT APPLICATION NUMBER: US/10/043,875  
; CURRENT FILING DATE: 2002-04-03  
; PRIOR APPLICATION NUMBER: 60/286,102  
; PRIOR FILING DATE: 2001-04-24  
; PRIOR APPLICATION NUMBER: EP 01870085.6  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: EP 01870005.4  
; NUMBER OF SEQ ID NOS: 884  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 875

```
RESULT 3255
US-09-961-077-1159/c
; Sequence 1159, Application US/09961077
; Publication No. US20030014775A1
; GENERAL INFORMATION:
; APPLICANT: Zwick, Michael G.
; Edington, Brent E.
; McSwiggen, James A.
; Merlo, Patricia Ann Owens
; Guo, Lining
; Skokut, Thomas A.
; Young, Scott A.
; Folkerts, Otto
; Merlo, Donald J.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
; MODULATION OF GENE EXPRESSION
; IN PLANTS
; NUMBER OF SEQUENCES: 1263
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/961,077
; FILING DATE: 21-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/679,645
; FILING DATE: July 12, 1996
; APPLICATION NUMBER: 60/001,135
; FILING DATE: July 13, 1995
; APPLICATION NUMBER: 08/300,726
; FILING DATE: September 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 219/247
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 1159:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1159:
US-09-961-077-1159
```

```
Query Match 0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY 42 GGCCCGCGCGCGGGG 59
Db 18 GGCGCGGAGCGGGG 1
```

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RESULT 3256
US-09-950-935-9/c
; Sequence 9, Application US/09950935
; Publication No. US20030032022A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Hill, Joseph A.
; APPLICANT: Wang, Zhigang C.
; TITLE OF INVENTION: Variants of IL-1 Beta Gene CD46 Gene for Diagnosing Unexplained Re
; TITLE OF INVENTION: Pregnancy Loss
; FILE REFERENCE: B0801/7227 (ERP)
; CURRENT APPLICATION NUMBER: US/09/950,935
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/231,785
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 18
; TYPE: DNA
; ORGANISM: homo sapiens
; MODULATION: US-09-950-935-9
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```
Query Match 0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 1751 TGGCTCTTTATTCAATAA 1768
Db 18 TGGCCCTGTCTTCAATAA 1
```

```
RESULT 3257
US-10-462-261-19
; Sequence 19, Application US/10462261
; Publication No. US20040029248A1
; GENERAL INFORMATION:
; APPLICANT: Garrett M. Brodeur
; APPLICANT: Peter S. White
; TITLE OF INVENTION: CHD5 ENCODING NUCLEIC ACIDS,
; TITLE OF INVENTION: POLYPEPTIDES, ANTIBODIES AND METHODS OF USE THEREOF
; FILE REFERENCE: CHOP0162
; CURRENT APPLICATION NUMBER: US/10/462,261
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/388,848
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-462-261-19
```

```
Query Match 0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 253 CCCCCACCTCTCTCCGC 270
Db 1 CGCCACCTCCCTCCTC 18
```

```
RESULT 3258
US-10-462-261-28
; Sequence 28, Application US/10462261
; Publication No. US20040029248A1
; GENERAL INFORMATION:
; APPLICANT: Garrett M. Brodeur
; APPLICANT: Peter S. White
; TITLE OF INVENTION: CHD5 ENCODING NUCLEIC ACIDS,
; TITLE OF INVENTION: POLYPEPTIDES, ANTIBODIES AND METHODS OF USE THEREOF
; FILE REFERENCE: CHOP0162
; CURRENT APPLICATION NUMBER: US/10/462,261
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/388,848
```

APPLICANT: Hauge, Brian M.  
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping  
; FILE REFERENCE: 38-10(52679)A  
; CURRENT APPLICATION NUMBER: US/09/969,373  
; CURRENT FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: US 09/754,853  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: US 09/760,427  
; PRIOR FILING DATE: 2001-01-13  
; PRIOR APPLICATION NUMBER: US 09/855,768  
; PRIOR FILING DATE: 2001-05-15  
; NUMBER OF SEQ ID NOS: 4593  
; SEQ ID NO 2933  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-09-969-373-2933

Query Match 0.5%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 3.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2317 TTGTTGCTGCTGTGCACC 2334  
Db 18 TTGTTGCTGCTGTGCCC 1

RESULT 3253

US-09-263-959-759/c  
; Sequence 759, Application US/09263959  
; Patent No. US20020150891A1  
; GENERAL INFORMATION:  
; APPLICANT: Hood, Leroy E.  
; APPLICANT: Rowen, Lee  
; APPLICANT: Koop, Ben F.  
; TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI  
; NUMBER OF SEQUENCES: 1279  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed and Berry LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/263,959  
; FILING DATE: 05-MAR-1999  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMasters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 920010.426C2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 759:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-263-959-759

Query Match 0.5%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 3.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2255 TTTATTGTCATATTATT 2272

Db 18 TTTATTATTATTATTATT 1

RESULT 3254

US-09-961-077-607/c  
; Sequence 607, Application US/09961077  
; Publication No. US20030014775A1  
; GENERAL INFORMATION:  
; APPLICANT: Zwick, Michael G.  
; Edington, Brent E.  
; McSwiggen, James A.  
; Merlo, Patricia Ann Owens  
; Guo, Lining  
; Skokut, Thomas A.  
; Young, Scott A.  
; Folkerts, Otto  
; Merlo, Donald J.  
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR  
; MODULATION OF GENE EXPRESSION  
; IN PLANTS  
; NUMBER OF SEQUENCES: 1263  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/961,077  
; FILING DATE: 21-Sep-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/679,645  
; FILING DATE: July 12, 1996  
; APPLICATION NUMBER: 60/001,135  
; FILING DATE: July 13, 1995  
; APPLICATION NUMBER: 08/300,726  
; FILING DATE: September 2, 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 219/247  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 607:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 18 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 607:  
US-09-961-077-607

Query Match 0.5%; Score 13.2; DB 1; Length 18;  
Best Local Similarity 83.3%; Pred. No. 3.1e+03;  
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 152 GGGACGCGGACGCCATG 169

Db 18 GGGATGGCGGCGCCCATG 1

; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DATA
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 19953US0XDIV
; CURRENT APPLICATION NUMBER: US/10/209,608
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/725,265
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: US 09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-209-608-44

Query Match 0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1771 TTTTGTGACCCCATTCCTT 1788
| | | | | | | | | | | | | | | |
Db 18 TTTTGTGACCCCATTCCTT 1

RESULT 3249
US-10-057-783A-46
; Sequence 46, Application US/10057783A
; Publication No. US20040091955A1
; GENERAL INFORMATION:
; APPLICANT: Forster, Anthony C.
; TITLE OF INVENTION: Process and compositions for peptide, protein and
; TITLE OF INVENTION: peptidomimetic synthesis
; FILE REFERENCE: 1
; CURRENT APPLICATION NUMBER: US/10/057,783A
; CURRENT FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FROM SYNTHETIC
; OTHER INFORMATION: DNA
US-10-057-783A-46

Query Match 0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2172 TTTTGTGACCCCATTCCTT 2189
| | | | | | | | | | | | | | | |
Db 1 TTTTGTGACCCCATTCCTT 18

RESULT 3250
US-09-878-582-47
; Sequence 47, Application US/09878582
; Patent No. US20020058638A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTEN EXPRESSION
; FILE REFERENCE: ISPH-0463
; CURRENT APPLICATION NUMBER: US/09/878,582
; CURRENT FILING DATE: 2001-06-11

; PRIOR APPLICATION NUMBER: 09/577,902
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/358,381
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: PCT/US99/29594,
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 51
; SEQ ID NO 47
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-878-582-47

Query Match 0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1777 TTTTGTGACCCCATTCCTT 1794
| | | | | | | | | | | | | | | |
Db 1 TTTTGTGACCCCATTCCTT 18

RESULT 3251
US-09-891-517-44/c
; Sequence 44, Application US/09891517
; Patent No. US20020106653A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: TORIMURA, MASAKI
; APPLICANT: KURATA, SHINYA
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; TITLE OF INVENTION: NOVEL NUCLEIC ACID PROBES, METHOD FOR DETERMINING CONCENTRATIONS (
; TITLE OF INVENTION: NUCLEIC ACID BY USING THE PROBES, AND METHOD FOR ANALYZING DATA (
; TITLE OF INVENTION: METHOD
; FILE REFERENCE: 210352US-1994-163-0-X
; CURRENT APPLICATION NUMBER: US/09/891,517
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: JP2000-193133
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: JP2000-236115
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP2000-292483
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA
US-09-891-517-44

Query Match 0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1771 TTTTGTGACCCCATTCCTT 1788
| | | | | | | | | | | | | | | |
Db 18 TTTTGTGACCCCATTCCTT 1

RESULT 3252
US-09-969-373-2933/c
; Sequence 2933, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.



```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-880-727-7
Query Match 0.5%; Score 13.2; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.3e+03;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAA 2798
Db 2 VAAAAAAAAAAAAA 15

RESULT 3246
US-09-880-727-7/c
; Sequence 7, Application US/09880727
; Publication No. US20030064364A1
; GENERAL INFORMATION:
; APPLICANT: Lockhart, David J.
; Chee, Mark
; Gunderson, Kevin
; Chaoqiang, Lai
; Wodicka, Lisa
; Cronin, Maureen T.
; Lee, Danny
; Tran, Huu M.
; Matsuzaki, Hajime
; McGall, Glenn H.
; TITLE OF INVENTION: NUCLEIC ACID ANALYSIS TECHNIQUES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Joe Liebeschuetz
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,727
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,649
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/035,170
; FILING DATE: 09-JAN-1997
; APPLICATION NUMBER: PCT/US97/01603
; FILING DATE: 22-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-019410US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-880-727-7
Query Match 0.5%; Score 13.2; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.3e+03;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTT 2179
Db 15 TTTTTTTTTTTTB 2

RESULT 3247
US-10-683-386-44/c
; Sequence 44, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MO
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/10/683,386
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US/09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-44
Query Match 0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1771 TTTTTTTTTTGAACCCC 1788
Db 18 TTTTTTTTTTTTCCCCC 1

RESULT 3248
US-10-209-608-44/c
; Sequence 44, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MO
```

```

; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: YES
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-880-727-7
Query Match 0.5%; Score 13.2; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 2.3e+03;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2166 TTTTTTTTTTTT 2179
Db 15 TTTTTTTTTTTTB 2

RESULT 3247
US-10-683-386-44/c
; Sequence 44, Application US/10683386
; Publication No. US20040063137A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MO
; TITLE OF INVENTION: NUCLEIC ACID PROBES FOR THE METHOD, AND METHOD FOR ANALYZING DAT
; TITLE OF INVENTION: THE METHOD
; FILE REFERENCE: 0163-0758-0X
; CURRENT APPLICATION NUMBER: US/10/683,386
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US/09/556,127
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: JP 1999-111601
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 18
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC DNA
US-10-683-386-44
Query Match 0.5%; Score 13.2; DB 1; Length 18;
Best Local Similarity 83.3%; Pred. No. 3.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1771 TTTTTTTTTTGAACCCC 1788
Db 18 TTTTTTTTTTTTCCCCC 1

RESULT 3248
US-10-209-608-44/c
; Sequence 44, Application US/10209608
; Publication No. US20030082592A1
; GENERAL INFORMATION:
; APPLICANT: KURANE, RYUICHIRO
; APPLICANT: KANAGAWA, TAKAHIRO
; APPLICANT: KAMAGATA, YOICHI
; APPLICANT: YAMADA, KAZUTAKA
; APPLICANT: YOKOMAKU, TOYOKAZU
; APPLICANT: KOYAMA, OSAMU
; APPLICANT: FURUSHO, KENTA
; TITLE OF INVENTION: METHOD FOR DETERMINING A CONCENTRATION OF TARGET NUCLEIC ACID MO
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; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecmica Sequence Listing Engine
; SEQ ID NO 1296
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-675-685-1296

Query Match      0.5%; Score 13.4; DB 1; Length 25;
Best Local Similarity 73.9%; Pred. No. 3.7e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAA 2801
      ||||| | ||||| |||||
Db 2 AGAAGGGGGA 24

RESULT 3243
US-10-291-808-65
; Sequence 65, Application US/10291808
; Publication No. US20030224382A1
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/10/291,808
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US/09/300,958
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-291-808-65

Query Match      0.5%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.1e+03;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAA 2798
      :||| ||||| |||||
Db 14 BAAAAA 1

RESULT 3245
US-09-880-727-7
; Sequence 7, Application US/09880727
; Publication No. US20030064364A1
; GENERAL INFORMATION:
; APPLICANT: Lockhart, David J.
; APPLICANT: Chee, Mark
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chaoqiang, Lai
; APPLICANT: Wodicka, Lisa
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Lee, Danny
; APPLICANT: Tran, Huu M.
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: McGall, Glenn H.
; TITLE OF INVENTION: NUCLEIC ACID ANALYSIS TECHNIQUES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Joe Liebeschuetz
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,727
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,649
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/035,170
; FILING DATE: 09-JAN-1997
; APPLICATION NUMBER: PCT/US97/01603
; FILING DATE: 22-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-019410US
```

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; CURRENT APPLICATION NUMBER: US/10/291,808
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US/09/300,958
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-291-808-65

Query Match      0.5%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 2.1e+03;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2785 GAAAAA 2798
      :||| ||||| |||||
Db 14 BAAAAA 1

RESULT 3245
US-09-880-727-7
; Sequence 7, Application US/09880727
; Publication No. US20030064364A1
; GENERAL INFORMATION:
; APPLICANT: Lockhart, David J.
; APPLICANT: Chee, Mark
; APPLICANT: Gunderson, Kevin
; APPLICANT: Chaoqiang, Lai
; APPLICANT: Wodicka, Lisa
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Lee, Danny
; APPLICANT: Tran, Huu M.
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: McGall, Glenn H.
; TITLE OF INVENTION: NUCLEIC ACID ANALYSIS TECHNIQUES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Joe Liebeschuetz
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/880,727
; FILING DATE: 13-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,649
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/035,170
; FILING DATE: 09-JAN-1997
; APPLICATION NUMBER: PCT/US97/01603
; FILING DATE: 22-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-019410US
```

; Sequence 2602, Application US/10688706  
; Publication No. US20040102412A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corp.  
; APPLICANT: Broschat, Kay  
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION  
; FILE REFERENCE: 01393/1  
; CURRENT APPLICATION NUMBER: US/10/688,706  
; CURRENT FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: 60/419,268  
; PRIOR FILING DATE: 2002-10-17  
; NUMBER OF SEQ ID NOS: 3071  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2602  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: human GFAT antisense  
US-10-688-706-2602

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1925 TTTTTCAGTGTTAAG 1939  
|||||  
Db 5 TTTTTCAGTTTAAAG 19

RESULT 3239  
US-09-782-837-34  
; Sequence 34, Application US/09782837  
; Patent No. US20020127714A1  
; GENERAL INFORMATION:  
; APPLICANT: HOUSMAN, DAVID E.  
; APPLICANT: LEDLEY, FRED D.  
; APPLICANT: STANTON, VINCENT P., JR.  
; TITLE OF INVENTION: INHIBITORS OF ALTERNATIVE ALLELES OF GENES ENCODING  
; TITLE OF INVENTION: PRODUCTS THAT MEDIATE CELL RESPONSE TO ENVIRONMENTAL  
; FILE REFERENCE: 233/055  
; CURRENT APPLICATION NUMBER: US/09/782,837  
; CURRENT FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: 09/045,054  
; PRIOR FILING DATE: 1998-03-19  
; NUMBER OF SEQ ID NOS: 44  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 34  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Glutamate-ammonia ligase (glutamine synthase)  
; OTHER INFORMATION: The letter "r" stands for a or g.  
US-09-782-837-34

Query Match 0.5%; Score 13.4; DB 1; Length 21;  
Best Local Similarity 82.4%; Pred. No. 3.4e+03;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2802  
|||  
Db 5 AACATAAAAAAAAAAA 21

RESULT 3240  
US-10-374-686-4/c  
; Sequence 4, Application US/10374686  
; Publication No. US20040002089A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubertret, Benoit  
; APPLICANT: Calame, Michel

; APPLICANT: Libchaber, Albert  
; TITLE OF INVENTION: Methods Employing Fluorescent Quenching  
; TITLE OF INVENTION: by Metal Surfaces  
; FILE REFERENCE: 600-1-260PCTUS  
; CURRENT APPLICATION NUMBER: US/10/374,686  
; CURRENT FILING DATE: 2003-02-26  
; PRIOR APPLICATION NUMBER: PCT/US01/41941  
; PRIOR FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: 60/228728  
; PRIOR FILING DATE: 2000-08-29  
; PRIOR APPLICATION NUMBER: 60/280350  
; PRIOR FILING DATE: 2001-03-30  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
US-10-374-686-4

Query Match 0.5%; Score 13.4; DB 1; Length 21;  
Best Local Similarity 93.3%; Pred. No. 3.4e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTGTGTTTTTTT 2180  
|||||  
Db 16 TTTTGTGTTTTTTT 2

RESULT 3241  
US-09-827-998-1296  
; Sequence 1296, Application US/09827998  
; Patent No. US20020102252A1  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E  
; FILE REFERENCE: MDMORF-8  
; CURRENT APPLICATION NUMBER: US/09/827,998  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 1881  
; SOFTWARE: Aeomica Sequence Listing Engine  
; SEQ ID NO 1296  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-827-998-1296

Query Match 0.5%; Score 13.4; DB 1; Length 25;  
Best Local Similarity 73.9%; Pred. No. 3.7e+03;  
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2779 AGAATTGAAAAAAAAAAAAA 2801  
|||||  
Db 2 AGAAGGGGGGAAAAAAAAAGAA 24

RESULT 3242  
US-10-675-685-1296  
; Sequence 1296, Application US/10675685  
; Publication No. US20040063134A1  
; GENERAL INFORMATION:  
; APPLICANT: Gu, Yizhong  
; APPLICANT: Shannon, Mark  
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E  
; FILE REFERENCE: PB0114  
; CURRENT APPLICATION NUMBER: US/10/675,685

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; FILE REFERENCE: HTS-0055
; CURRENT APPLICATION NUMBER: US/10/303,541
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 28
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-541-28

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2712 CTGCTGTAAATGTT 2726
Db      6 CTGCTGTAAATGTT 20

RESULT 3234
US-10-303-541-64/c
; Sequence 64, Application US/10303541
; Publication No. US20040102399A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF HYPOTHETICAL PROTEIN 669 EXPRESSION
; FILE REFERENCE: HTS-0055
; CURRENT APPLICATION NUMBER: US/10/303,541
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 78
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-303-541-64

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2712 CTGCTGTAAATGTT 2726
Db      6 CTGCTGTAAATGTT 20

RESULT 3235
US-10-688-706-144
; Sequence 144, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 144
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-144

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2712 CTGCTGTAAATGTT 2726
Db      15 CTGCTGTAAATGTT 1

RESULT 3236
US-10-688-706-227
; Sequence 227, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 227
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-227

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2503 ATAACACATCATAAG 2517
Db      6 ATCACACATCATAAG 20

RESULT 3237
US-10-688-706-2305
; Sequence 2305, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2305
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-2305

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1925 TTTTTCAGTGTAAAG 1939
Db      6 TTTTTCAGTGTAAAG 20

RESULT 3238
US-10-688-706-2602
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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2504 TAAACACATCATAAG 2518
Db      1 TCACACATCATAAG 15

RESULT 3236
US-10-688-706-227
; Sequence 227, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 227
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-227

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2503 ATAACACATCATAAG 2517
Db      6 ATCACACATCATAAG 20

RESULT 3237
US-10-688-706-2305
; Sequence 2305, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2305
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-2305

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1925 TTTTTCAGTGTAAAG 1939
Db      6 TTTTTCAGTGTAAAG 20

RESULT 3238
US-10-688-706-2602
```



; SEQ ID NO 469  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-012-231A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
| | | | | | | | | | | | | | | | | |  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3229  
US-10-298-994-50  
; Sequence 50, Application US/10298994  
; Publication No. US20040097446A1  
; GENERAL INFORMATION:  
; APPLICANT: William Gaarde  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: MODULATION OF CHECKPOINT KINASE 1 EXPRESSION  
; FILE REFERENCE: HTS-0006  
; CURRENT APPLICATION NUMBER: US/10/298,994  
; CURRENT FILING DATE: 2002-11-16  
; NUMBER OF SEQ ID NOS: 228  
; SEQ ID NO 50  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-298-994-50

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1654 ACTGGTTCTGCATCA 1668  
| | | | | | | | | | | | | | | | | |  
Db 4 ACTGGTTCTGCATGA 18

RESULT 3230  
US-10-298-994-91  
; Sequence 91, Application US/10298994  
; Publication No. US20040097446A1  
; GENERAL INFORMATION:  
; APPLICANT: William Gaarde  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: MODULATION OF CHECKPOINT KINASE 1 EXPRESSION  
; FILE REFERENCE: HTS-0006  
; CURRENT APPLICATION NUMBER: US/10/298,994  
; CURRENT FILING DATE: 2002-11-16  
; NUMBER OF SEQ ID NOS: 228  
; SEQ ID NO 91  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-298-994-91

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1654 ACTGGTTCTGCATCA 1668  
| | | | | | | | | | | | | | | | | |  
Db 2 ACTGGTTCTGCATGA 16

RESULT 3231  
US-10-298-994-165/c  
; Sequence 165, Application US/10298994  
; Publication No. US20040097446A1  
; GENERAL INFORMATION:  
; APPLICANT: William Gaarde  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: MODULATION OF CHECKPOINT KINASE 1 EXPRESSION  
; FILE REFERENCE: HTS-0006  
; CURRENT APPLICATION NUMBER: US/10/298,994  
; CURRENT FILING DATE: 2002-11-16  
; NUMBER OF SEQ ID NOS: 228  
; SEQ ID NO 165  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: H. sapiens  
; FEATURE:  
US-10-298-994-165

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1654 ACTGGTTCTGCATCA 1668  
| | | | | | | | | | | | | | | | | |  
Db 17 ACTGGTTCTGCATGA 3

RESULT 3232  
US-10-298-994-198/c  
; Sequence 198, Application US/10298994  
; Publication No. US20040097446A1  
; GENERAL INFORMATION:  
; APPLICANT: William Gaarde  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: MODULATION OF CHECKPOINT KINASE 1 EXPRESSION  
; FILE REFERENCE: HTS-0006  
; CURRENT APPLICATION NUMBER: US/10/298,994  
; CURRENT FILING DATE: 2002-11-16  
; NUMBER OF SEQ ID NOS: 228  
; SEQ ID NO 198  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-298-994-198

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1654 ACTGGTTCTGCATCA 1668  
| | | | | | | | | | | | | | | | | |  
Db 19 ACTGGTTCTGCATGA 5

RESULT 3233  
US-10-303-541-28  
; Sequence 28, Application US/10303541  
; Publication No. US20040102399A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: MODULATION OF HYPOTHETICAL PROTEIN 669 EXPRESSION

```
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2626 TTGTCTCGTTCTCG 2640
Db 1 TTGGCTCGTTCTCG 15

RESULT 3224
US-10-289-762-5708/c
; Sequence 5708, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5708
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-5708

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 275 CAGCACCTCTACAGC 289
Db 15 CAGCAGCTCTACAGC 1

RESULT 3225
US-10-289-762-6474/c
; Sequence 6474, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 6474
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-6474

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 744 TTCGAAAGGTCCCA 758
Db 20 TTCGAAAGATCCCA 6

RESULT 3226
US-10-188-777-36/c
; Sequence 36, Application US/10188777
; Publication No. US20040006220A1
; GENERAL INFORMATION:
; APPLICANT: Sanjay Bhanot
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF INSULIN-LIKE GROWTH FACTOR 2 EXPRESSION
; FILE REFERENCE: RTS-0358
; CURRENT APPLICATION NUMBER: US/10/188,777
```

```
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-188-777-36

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 232 CAGCAATGGGAATCC 246
Db 17 CACCAATGGGAATCC 3

RESULT 3227
US-10-188-777-98
; Sequence 98, Application US/10188777
; Publication No. US20040006220A1
; GENERAL INFORMATION:
; APPLICANT: Sanjay Bhanot
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF INSULIN-LIKE GROWTH FACTOR 2 EXPRESSION
; FILE REFERENCE: RTS-0358
; CURRENT APPLICATION NUMBER: US/10/188,777
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 140
; SEQ ID NO 98
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-188-777-98

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 232 CAGCAATGGGAATCC 246
Db 4 CACCAATGGGAATCC 18

RESULT 3228
US-10-012-231A-469/c
; Sequence 469, Application US/10012231A
; Publication No. US20040014130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C23
; CURRENT APPLICATION NUMBER: US/10/012,231A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
```

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; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-2377

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2361 TTTAAGAAACAGTGC 2375
      |||||
Db 6 TTTAAGAAACGGTGC 20

RESULT 3219
US-10-289-762-2867/c
; Sequence 2867, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2867
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-2867

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2626 TTTGTCTCGTTCCTG 2640
      |||||
Db 15 TTTGGCTCGTTCCTG 1

RESULT 3220
US-10-289-762-3480
; Sequence 3480, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3480
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-3480

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1548 AGGGAAGGAACAGGA 1562
      |||||
Db 6 AGGGAAGGAACAGAA 20

RESULT 3221
US-10-289-762-3520
; Sequence 3520, Application US/10289762
; Publication No. US20040006218A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3520
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-3520

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 794 CAGAAGGAGCTGGTG 808
      |||||
Db 5 CAGAAGGACCTGGTG 19

RESULT 3222
US-10-289-762-4153/c
; Sequence 4153, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4153
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-4153

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1706 AGCTATCTCCTAACT 1720
      |||||
Db 18 AGCTATCTCCTTACT 4

RESULT 3223
US-10-289-762-5364
; Sequence 5364, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5364
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-5364

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1548 AGGGAAGGAACAGGA 1562
      |||||
Db 6 AGGGAAGGAACAGAA 20

RESULT 3221
US-10-289-762-3520
; Sequence 3520, Application US/10289762
; Publication No. US20040006218A1
```

```
RESULT 3214
US-10-165-216-11/c
; Sequence 11, Application US/10165216
; Publication No. US20030228675A1
; GENERAL INFORMATION:
; APPLICANT: Otterness, Diane M.
; APPLICANT: Abraham, Robert T.
; TITLE OF INVENTION: ATM Related Kinase ATX, Nucleic Acids
; TITLE OF INVENTION: Encoding Same and Methods of Use
; FILE REFERENCE: P-LJ 5222
; CURRENT APPLICATION NUMBER: US/10/165,216
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-165-216-11

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      487 GAGCCAGGAGGGAGC 501
      ||| ||||| ||||| |||
Db      20 GAGACAGGAGGGAGC 6

RESULT 3215
US-10-174-020-67/c
; Sequence 67, Application US/10174020
; Publication No. US20030232770A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HYPOTHETICAL TUMOR ENDOTHELIAL MARKER EXP
; FILE REFERENCE: RTS-0369
; CURRENT APPLICATION NUMBER: US/10/174,020
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 149
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-174-020-67

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2133 AGAACGAGCCTGC 2147
      ||||| ||||| ||||| |||
Db      17 AGAACGAGCCTGC 3

RESULT 3216
US-10-174-020-134
; Sequence 134, Application US/10174020
; Publication No. US20030232770A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HYPOTHETICAL TUMOR ENDOTHELIAL MARKER EXP
; FILE REFERENCE: RTS-0369
; CURRENT APPLICATION NUMBER: US/10/174,020
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 149
; SEQ ID NO 134
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-174-020-134

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2133 AGAACGAGCCTGC 2147
      ||||| ||||| ||||| |||
Db      4 AGAACGAGCCTGC 18

RESULT 3217
US-10-011-795A-469/c
; Sequence 469, Application US/10011795A
; Publication No. US20040005626A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C25
; CURRENT APPLICATION NUMBER: US/10/011,795A
; CURRENT FILING DATE: 2001-12-07
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-011-795A-469

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      203 GAGGACTGCGAGGAT 217
      ||||| ||||| ||||| |||
Db      19 GAGGACGCGAGGAT 5

RESULT 3218
US-10-289-762-2377
; Sequence 2377, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2377
; LENGTH: 20
```



; PRIOR APPLICATION NUMBER: 60/101472  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101474  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101475  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101476  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101477  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101479  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101738  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101741  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101743  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101915  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101916  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/102207  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102240  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102307  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102330  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102331  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102484  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102487  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102570  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102571  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102684  
; PRIOR FILING DATE: 1998-10-01  
; PRIOR APPLICATION NUMBER: 60/102687  
; PRIOR FILING DATE: 1998-10-01  
; PRIOR APPLICATION NUMBER: 60/102965  
; PRIOR FILING DATE: 1998-10-02  
; PRIOR APPLICATION NUMBER: 60/103258  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 60/103314  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103315  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103328  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103395  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103396  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103401  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103449  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 60/103633  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103678  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103679  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103711  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/104257  
; PRIOR FILING DATE: 1998-10-14  
; PRIOR APPLICATION NUMBER: 60/104987

; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105000  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105002  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105104  
; PRIOR FILING DATE: 1998-10-21  
; PRIOR APPLICATION NUMBER: 60/105169  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105266  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105693  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105694  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105807  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105881  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105882  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/106023  
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
||| ||| ||| ||| ||| ||| |||  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3213

US-10-388-263-506/c  
; Sequence 506, Application US/10388263  
; Publication No. US20030228597A1  
; GENERAL INFORMATION:  
; APPLICANT: Cowser, Lex M.  
; APPLICANT: Baker, Brenda F.  
; APPLICANT: McNeil, John  
; APPLICANT: Freier, Susan M.  
; APPLICANT: Sasmor, Henri M.  
; APPLICANT: Brooks, Douglas G.  
; APPLICANT: Ohashi, Cara  
; APPLICANT: Wyatt, Jacqueline R.  
; APPLICANT: Borchers, Alexander  
; APPLICANT: Vickers, Timothy A.  
; TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR  
; TITLE OF INVENTION: MODULATION BY OLIGONUCLEOTIDES AND  
; TITLE OF INVENTION: GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION  
; FILE REFERENCE: ISIS-4503  
; CURRENT APPLICATION NUMBER: US/10/388,263  
; CURRENT FILING DATE: 2003-03-12  
; NUMBER OF SEQ ID NOS: 947  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 506  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-388-263-506

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 835 CTTCTGCTCAGTCCC 849  
||| ||| ||| ||| ||| ||| |||  
Db 15 CTTCTGCTCAGGCCC 1

```
RESULT 3211
US-10-360-510-210/c
; Sequence 210, Application US/10360510
; Publication No. US20030220282A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/10/360,510
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US/09/854,883
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 210
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-360-510-210

Query Match          0.5%;   Score 13.4;   DB 1;   Length 20;
Best Local Similarity 93.3%;   Pred. No. 3.3e+03;
Matches 14;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      479  GGCCGCCAGCCAG 493
          |||||
Db       18  GGCCGCCAGCCAG 4

RESULT 3212
US-10-006-746A-469/c
; Sequence 469, Application US/10006746A
; Publication No. US20030220471A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC5
; CURRENT APPLICATION NUMBER: US/10/006,746A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
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; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
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; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-394A-469

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGAGGAT 217
      ||||| ||||| |||||
Db      19 GAGGACGCGGAGGAT 5

RESULT 3208
US-10-015-390A-469/c
; Sequence 469, Application US/10015390A
; Publication No. US20030216562A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C53
; CURRENT APPLICATION NUMBER: US/10/015,390A
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-390A-469

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGAGGAT 217
      ||||| ||||| |||||
Db      19 GAGGACGCGGAGGAT 5

RESULT 3209
US-10-156-603-18/c
; Sequence 18, Application US/10156603
; Publication No. US20030220275A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Erich Koller
; TITLE OF INVENTION: ANTISENSE MODULATION OF KINESIN-LIKE 1 EXPRESSION
; FILE REFERENCE: HTS-0016
; CURRENT APPLICATION NUMBER: US/10/156,603
; CURRENT FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-156-603-18

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2187 AACTTTGAAAGTTAA 2201
      ||||| ||||| |||||
Db      17 AACTTTGCAAGTTAA 3

RESULT 3210
US-10-360-510-130
; Sequence 130, Application US/10360510
; Publication No. US20030220282A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/10/360,510
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US/09/854,883
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 130
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-360-510-130

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2003 CTTCTTCAGAGATCA 2017
      ||||| ||||| |||||
Db      6 CATCTTCAGAGATCA 20

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY      203 GAGGACTGCGAGGAT 217
      ||||| ||||| |||||
Db      19 GAGGACGCGGAGGAT 5

RESULT 3209
US-10-156-603-18/c
; Sequence 18, Application US/10156603
; Publication No. US20030220275A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Erich Koller
; TITLE OF INVENTION: ANTISENSE MODULATION OF KINESIN-LIKE 1 EXPRESSION
; FILE REFERENCE: HTS-0016
; CURRENT APPLICATION NUMBER: US/10/156,603
; CURRENT FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 18
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-156-603-18

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2187 AACTTTGAAAGTTAA 2201
      ||||| ||||| |||||
Db      17 AACTTTGCAAGTTAA 3

RESULT 3210
US-10-360-510-130
; Sequence 130, Application US/10360510
; Publication No. US20030220282A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/10/360,510
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US/09/854,883
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 130
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-360-510-130

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2003 CTTCTTCAGAGATCA 2017
      ||||| ||||| |||||
Db      6 CATCTTCAGAGATCA 20

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C49
; CURRENT APPLICATION NUMBER: US/10/015,519A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-519A-469

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGGAGGAT 217
        ||||| ||||| |||||
Db      19 GAGGACGGCGGAGGAT 5

RESULT 3205
US-10-005-344-214/c
; Sequence 214, Application US/10005344
; Publication No. US20030203862A1
; GENERAL INFORMATION:
; APPLICANT: Loren J. Miraglia
; APPLICANT: Pamela Nero
; APPLICANT: Mark J. Graham
; APPLICANT: Brett P. Monia
; APPLICANT: Erich Koller
; APPLICANT: Mingyi Chiang
; APPLICANT: Mano Manoharan
; TITLE OF INVENTION: Antisense Modulation of mdm2 expression.
; FILE REFERENCE: ISPH-0622
; CURRENT APPLICATION NUMBER: US/10/005,344
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 09/048,810
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: US 09/280,805
; PRIOR FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 379
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-005-344-214

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2520 TTTATTTCATATATAT 2534
        ||||| ||||| |||||

```

```

Db      15 TTTATTTCATATAT 1

RESULT 3206
US-10-013-915A-469/c
; Sequence 469, Application US/10013915A
; Publication No. US20030204053A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C37
; CURRENT APPLICATION NUMBER: US/10/013,915A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-915A-469

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGGAGGAT 217
        ||||| ||||| |||||
Db      19 GAGGACGGCGGAGGAT 5

RESULT 3207
US-10-015-394A-469/c
; Sequence 469, Application US/10015394A
; Publication No. US20030204054A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C41
; CURRENT APPLICATION NUMBER: US/10/015,394A
; CURRENT FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723

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US-10-012-753A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
| | | | | | | | | | | | | | | |  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3201

US-10-015-385A-469/c  
; Sequence 469, Application US/10015385A  
; Publication No. US20030195347A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830P1C51

; CURRENT APPLICATION NUMBER: US/10/015,385A

; CURRENT FILING DATE: 2002-07-25

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 469

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic oligonucleotide probe

US-10-015-385A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
| | | | | | | | | | | | | | | |  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3202

US-10-007-236A-469/c  
; Sequence 469, Application US/10007236A  
; Publication No. US2003019893A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C12  
; CURRENT APPLICATION NUMBER: US/10/007,236A  
; CURRENT FILING DATE: 2002-06-25

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 469

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic oligonucleotide probe

US-10-007-236A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
| | | | | | | | | | | | | | | |  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3203

US-10-015-389A-469/c  
; Sequence 469, Application US/10015389A  
; Publication No. US20030199675A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830P1C48

; CURRENT APPLICATION NUMBER: US/10/015,389A

; CURRENT FILING DATE: 2002-06-25

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 469

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic oligonucleotide probe

US-10-015-389A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
| | | | | | | | | | | | | | | |  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3204

US-10-015-519A-469/c  
; Sequence 469, Application US/10015519A  
; Publication No. US20030203401A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 13.4; DB 1; Length 20;

Best Local Similarity 93.3%; Pred. No. 3.3e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217
||||| |||||
Db 19 GAGGACGGCGAGGAT 5

RESULT 3198

US-10-015-388A-469/c
; Sequence 469, Application US/10015388A
; Publication No. US20030191299A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C44
; CURRENT APPLICATION NUMBER: US/10/015,388A
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-388A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;

Best Local Similarity 93.3%; Pred. No. 3.3e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217
||||| |||||
Db 19 GAGGACGGCGAGGAT 5

RESULT 3199
US-10-302-262-16/c
; Sequence 16, Application US/10302262
; Publication No. US20030191300A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, QingQing
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0528
; CURRENT APPLICATION NUMBER: US/10/302,262
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/734,846
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/277,020
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 09/167,921
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/323,743
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-302-262-16

Query Match 0.5%; Score 13.4; DB 1; Length 20;

Best Local Similarity 93.3%; Pred. No. 3.3e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2104 CGGGGGCCTTCTGGT 2118
||||| |||||
Db 20 CGGGGTCCTTCTGGT 6

RESULT 3200

US-10-012-753A-469/c
; Sequence 469, Application US/10012753A
; Publication No. US20030195334A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C17
; CURRENT APPLICATION NUMBER: US/10/012,753A
; CURRENT FILING DATE: 2001-12-07
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe



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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C50
; CURRENT APPLICATION NUMBER: US/10/015,480A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-480A-469

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGGAGGAT 217
      ||||| ||||| |||||
Db       19 GAGGACGGCGGAGGAT 5

RESULT 3195
US-10-015-715A-469/c
; Sequence 469, Application US/10015715A
; Publication No. US20030190668A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C56
; CURRENT APPLICATION NUMBER: US/10/015,715A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-715A-469

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGGAGGAT 217
      ||||| ||||| |||||
Db       19 GAGGACGGCGGAGGAT 5

RESULT 3196
US-10-012-237A-469/c
; Sequence 469, Application US/10012237A
; Publication No. US20030191281A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
```

```
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C21
; CURRENT APPLICATION NUMBER: US/10/012,237A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-237A-469

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGGAGGAT 217
      ||||| ||||| |||||
Db       19 GAGGACGGCGGAGGAT 5

RESULT 3197
US-10-013-906A-469/c
; Sequence 469, Application US/10013906A
; Publication No. US20030191282A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C36
; CURRENT APPLICATION NUMBER: US/10/013,906A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-906A-469/c
```



```

; CURRENT APPLICATION NUMBER: US/10/013,912A
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-912A-469

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGAGGAT 217
      ||||| ||||| |||||
Db      19 GAGGACGGCGAGGAT 5

RESULT 3192
US-10-015-653A-469/c
; Sequence 469, Application US/10015653A
; Publication No. US20030187195A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C43
; CURRENT APPLICATION NUMBER: US/10/015,653A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe

```

```

US-10-015-653A-469

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGAGGAT 217
      ||||| ||||| |||||
Db      19 GAGGACGGCGAGGAT 5

RESULT 3193
US-10-012-101B-469/c
; Sequence 469, Application US/10012101B
; Publication No. US20030187239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C6
; CURRENT APPLICATION NUMBER: US/10/012,101B
; CURRENT FILING DATE: 2001-12-06
; Prior application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-101B-469

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGAGGAT 217
      ||||| ||||| |||||
Db      19 GAGGACGGCGAGGAT 5

RESULT 3194
US-10-015-480A-469/c
; Sequence 469, Application US/10015480A
; Publication No. US20030190667A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

```

; PRIOR APPLICATION NUMBER: 60/100848  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/100849  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/100919  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100930  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/101014  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101068  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101071  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101279  
; PRIOR FILING DATE: 1998-09-22  
; PRIOR APPLICATION NUMBER: 60/101471  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101472  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101474  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101475  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101476  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101477  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101479  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101738  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101741  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101743  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101915  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101916  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/102207  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102240  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102307  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102330  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102331  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102484  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102487  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102570  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102571  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102684  
; PRIOR FILING DATE: 1998-10-01  
; PRIOR APPLICATION NUMBER: 60/102687  
; PRIOR FILING DATE: 1998-10-01  
; PRIOR APPLICATION NUMBER: 60/102965  
; PRIOR FILING DATE: 1998-10-02  
; PRIOR APPLICATION NUMBER: 60/103258  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 60/103314  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103315  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103328  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103395

; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103396  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103401  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103449  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 60/103633  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103678  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103679  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103711  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/104257  
; PRIOR FILING DATE: 1998-10-14  
; PRIOR APPLICATION NUMBER: 60/104987  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105000  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105002  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105104  
; PRIOR FILING DATE: 1998-10-21  
; PRIOR APPLICATION NUMBER: 60/105169  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105266  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105693  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105694  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105807  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105881  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105882  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/106023  
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
||| ||| ||| ||| |||  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3191  
US-10-013-912A-469/c  
; Sequence 469, Application US/10013912A  
; Publication No. US20030187194A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C32

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-754A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217
||||| |||||||
Db 19 GAGGACGCGAGGAT 5

RESULT 3189
US-10-013-910A-469/c
; Sequence 469, Application US/10013910A
; Publication No. US20030187192A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C33
; CURRENT APPLICATION NUMBER: US/10/013,910A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-910A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217
||||| |||||||
Db 19 GAGGACGCGAGGAT 5

RESULT 3190
US-10-013-911A-469/c
; Sequence 469, Application US/10013911A
; Publication No. US20030187193A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C39
; CURRENT APPLICATION NUMBER: US/10/013,911A
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17

US-10-093-311-27  
; Sequence 27, Application US/10093311  
; Publication No. US20030186439A1  
; GENERAL INFORMATION:  
; APPLICANT: Nakauchi, Hiromitsu  
; APPLICANT: Suzuki, Atsushi  
; APPLICANT: Taniguchi, Hideki  
; APPLICANT: Fukao, Katashi  
; TITLE OF INVENTION: Self-Renewing Pluripotent Hepatic Stem  
; TITLE OF INVENTION: Cells  
; FILE REFERENCE: 59150-8016  
; CURRENT APPLICATION NUMBER: US/10/093,311  
; CURRENT FILING DATE: 2002-03-06  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: primer  
US-10-093-311-27

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2427 TGGTGCACCTTCTTAC 2441  
Db 5 TGGTGCACCTTCTTAC 19

RESULT 3186  
US-10-012-137A-469/c  
; Sequence 469, Application US/10012137A  
; Publication No. US20030187189A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C29  
; CURRENT APPLICATION NUMBER: US/10/012,137A  
; CURRENT FILING DATE: 2002-06-25  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 469  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-012-137A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 203 GAGGACTGCGAGGAT 217  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3187  
US-10-012-752A-469/c  
; Sequence 469, Application US/10012752A  
; Publication No. US20030187190A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C24  
; CURRENT APPLICATION NUMBER: US/10/012,752A  
; CURRENT FILING DATE: 2002-06-25  
; Prior application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 469  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-012-752A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 203 GAGGACTGCGAGGAT 217  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3188  
US-10-012-754A-469/c  
; Sequence 469, Application US/10012754A  
; Publication No. US20030187191A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C18  
; CURRENT APPLICATION NUMBER: US/10/012,754A  
; CURRENT FILING DATE: 2002-06-25  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 469  
; LENGTH: 20



GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C35  
; CURRENT APPLICATION NUMBER: US/10/013,909A  
; CURRENT FILING DATE: 2002-06-25  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 469  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-013-909A-469  
  
Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 203 GAGGACTGCGGAGGAT 217  
Db 19 GAGGACGGCGGAGGAT 5  
  
RESULT 3183  
US-10-015-671A-469/c  
; Sequence 469, Application US/10015671A  
; Publication No. US20030186319A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C47  
; CURRENT APPLICATION NUMBER: US/10/015,671A  
; CURRENT FILING DATE: 2001-12-11  
; Prior application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 469  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-015-671A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 203 GAGGACTGCGGAGGAT 217  
Db 19 GAGGACGGCGGAGGAT 5  
  
RESULT 3184  
US-10-015-610A-469/c  
; Sequence 469, Application US/10015610A  
; Publication No. US20030186361A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C52  
; CURRENT APPLICATION NUMBER: US/10/015,610A  
; CURRENT FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098803  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098821  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098843  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/099536  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099596  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099598  
; PRIOR FILING DATE: 1998-09-09  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 469  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-015-610A-469  
  
Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 203 GAGGACTGCGGAGGAT 217  
Db 19 GAGGACGGCGGAGGAT 5  
  
RESULT 3185

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; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGGAGGAT 217
Db      19 GAGGACGGCGGAGGAT 5

RESULT 3180
US-10-012-064A-469/c
; Sequence 469, Application US/10012064A
; Publication No. US20030180836A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Guirney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C19
; CURRENT APPLICATION NUMBER: US/10/012,064A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-064A-469

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGGAGGAT 217
Db      19 GAGGACGGCGGAGGAT 5

RESULT 3180
US-10-013-909A-469/c
; Sequence 469, Application US/10013909A
; Publication No. US20030186318A1
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Db      19 GAGGACGGCGGAGGAT 5

RESULT 3181
US-10-331-907-164/c
; Sequence 164, Application US/10331907
; Publication No. US20030181660A1
; GENERAL INFORMATION:
; APPLICANT: Todd, John A
; APPLICANT: Hess, John W
; APPLICANT: Caskey, Charles T
; APPLICANT: Cox, Roger D
; APPLICANT: Gerhold, David
; APPLICANT: Hammond, Holly
; APPLICANT: Hey, Patricia
; APPLICANT: Kawaguchi, Yoshihiko
; APPLICANT: Merriman, Tony R
; APPLICANT: Metzker, Michael L
; TITLE OF INVENTION: No. US20030181660A1 LDL-Receptor
; NUMBER OF SEQUENCES: 455
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon and Vanderhye
; STREET: 1100 No. US20030181660A1th Glebe Road, Eighth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: US
; ZIP: VA 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/331,907
; FILING DATE: 31-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,923A
; FILING DATE: 14-Feb-2001
; APPLICATION NUMBER: PCT/GB98/01102
; FILING DATE: 15-APR-1998
; APPLICATION NUMBER: US 60/043,553
; FILING DATE: 15-APR-1997
; APPLICATION NUMBER: US 60/048,740
; FILING DATE: 05-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: B.J.Sadoff
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 620-81
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4091
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 164:
US-10-331-907-164

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      914 CGACTGTCCCCACCT 928
Db      20 CAACTGTCCCCACCT 6

RESULT 3182
US-10-013-909A-469/c
; Sequence 469, Application US/10013909A
; Publication No. US20030186318A1
```

[illegible]

```
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C66
; CURRENT APPLICATION NUMBER: US/10/017,306A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-017-306A-469

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGAGGAT 217
      ||||| ||||| |||||
Db       19 GAGGACGGCGAGGAT 5

RESULT 3178
US-10-211-884-164/c
; Sequence 164, Application US/10211884
; Publication No. US20030175900A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Pitti, Robert M.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stone, Donna M.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
; FILE REFERENCE: P2931R1C1
; CURRENT APPLICATION NUMBER: US/10/211,884
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/014699
; PRIOR FILING DATE: 1996-04-01
; PRIOR APPLICATION NUMBER: 60/026943
; PRIOR FILING DATE: 1996-09-23
; PRIOR APPLICATION NUMBER: 60/059121
; PRIOR FILING DATE: 1997-07-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/062037
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/066511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
;
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; PRIOR FILING DATE: 1997-11-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 258
; SEQ ID NO 164
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Probe.
US-10-211-884-164

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGAGGAT 217
      ||||| ||||| |||||
Db       19 GAGGACGGCGAGGAT 5

RESULT 3179
US-10-017-867A-469/c
; Sequence 469, Application US/10017867A
; Publication No. US20030180792A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C60
; CURRENT APPLICATION NUMBER: US/10/017,867A
; CURRENT FILING DATE: 2001-12-13
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
;
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;  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-017-253A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3172

US-10-015-392A-469/c  
; Sequence 469, Application US/10015392A  
; Publication No. US20030166901A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C58  
; CURRENT APPLICATION NUMBER: US/10/015,392A  
; CURRENT FILING DATE: 2001-12-12  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098803  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098821  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098843  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/099536  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099596  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099598  
; PRIOR FILING DATE: 1998-09-09  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 477

;  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-015-392A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3173

US-10-210-951-164/c  
; Sequence 164, Application US/10210951  
; Publication No. US20030170228A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Marsters, Scot A.  
; APPLICANT: Pan, James  
; APPLICANT: Pitti, Robert M.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stone, Donna M.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR  
; FILE REFERENCE: P2931R1C1  
; CURRENT APPLICATION NUMBER: US/10/210,951  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: 60/014699  
; PRIOR FILING DATE: 1996-04-01  
; PRIOR APPLICATION NUMBER: 60/026943  
; PRIOR FILING DATE: 1996-09-23  
; PRIOR APPLICATION NUMBER: 60/059121  
; PRIOR FILING DATE: 1997-07-17  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/062037  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: 60/063755  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063045  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/066511  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/066772  
; PRIOR FILING DATE: 1997-11-24  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 258

;  
; LENGTH: 20  
; TYPE: DNA

;  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide Probe.

US-10-210-951-164

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3174

US-10-092-208-12  
; Sequence 12, Application US/10092208  
; Publication No. US20030170637A1  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Hyunsoo

; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101477  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101479  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101738  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101741  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101743  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101915  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101916  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/102207  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102240  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102307  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102330  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102331  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102484  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102487  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102570  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102571  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102684  
; PRIOR FILING DATE: 1998-10-01  
; PRIOR APPLICATION NUMBER: 60/102687  
; PRIOR FILING DATE: 1998-10-01  
; PRIOR APPLICATION NUMBER: 60/102965  
; PRIOR FILING DATE: 1998-10-02  
; PRIOR APPLICATION NUMBER: 60/103258  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 60/103314  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103315  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103328  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103395  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103396  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103401  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103449  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 60/103633  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103678  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103679  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103711  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/104257  
; PRIOR FILING DATE: 1998-10-14  
; PRIOR APPLICATION NUMBER: 60/104987  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105000  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105002  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105104  
; PRIOR FILING DATE: 1998-10-21

; PRIOR APPLICATION NUMBER: 60/105169  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105266  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105693  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105694  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105807  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105881  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105882  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/106023  
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred.No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
||||| |||||  
Db 19 GAGGACGGCAGGAT 5

RESULT 3171

US-10-017-253A-469/c  
; Sequence 469, Application US/10017253A  
; Publication No. US20030166055A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C62  
; CURRENT APPLICATION NUMBER: US/10/017,253A  
; CURRENT FILING DATE: 2001-12-13  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098803  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098821  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098843  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/099536  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099596  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099598  
; PRIOR FILING DATE: 1998-09-09  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 469

```

; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C7
; CURRENT APPLICATION NUMBER: US/10/006,130A
; CURRENT FILING DATE: 2002-03-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-130A-469

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217
Db 19 GAGGACGGCGAGGAT 5
||||| |||||||

RESULT 3170
US-10-006-172A-469/c
; Sequence 469, Application US/10006172A
; Publication No. US20030153000A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C11
; CURRENT APPLICATION NUMBER: US/10/006,172A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
```



Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
||||| |||||

Db 19 GAGGACGGCGAGGAT 5

RESULT 3166  
US-10-006-041A-469/c  
; Sequence 469, Application US/10006041A  
; Publication No. US20030130490A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan l.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C8  
; CURRENT APPLICATION NUMBER: US/10/006,041A  
; CURRENT FILING DATE: 2001-12-06  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 469  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-006-041A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
||||| |||||

Db 19 GAGGACGGCGAGGAT 5

RESULT 3167  
US-10-015-822A-469/c  
; Sequence 469, Application US/10015822A  
; Publication No. US20030130491A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan l.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C38  
; CURRENT APPLICATION NUMBER: US/10/015,822A

; CURRENT FILING DATE: 2002-06-10  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 469  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-015-822A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
||||| |||||

Db 19 GAGGACGGCGAGGAT 5

RESULT 3168  
US-10-015-387A-469/c  
; Sequence 469, Application US/10015387A  
; Publication No. US20030135034A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan l.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C54  
; CURRENT APPLICATION NUMBER: US/10/015,387A  
; CURRENT FILING DATE: 2001-12-12  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 469  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-015-387A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
||||| |||||

Db 19 GAGGACGGCGAGGAT 5

RESULT 3169  
US-10-006-130A-469/c  
; Sequence 469, Application US/10006130A  
; Publication No. US20030148375A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan l.  
; APPLICANT: Ferrara, Napoleone

```

; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C59
; CURRENT APPLICATION NUMBER: US/10/015,391A
; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-391A-469

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217
Db 19 GAGGACGGCGAGGAT 5
||||| |||||||

RESULT 3163
US-10-000-213-81/c
; Sequence 81, Application US/10000213
; Publication No. US20030125271A1
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Mark P. Roach
; APPLICANT: Kenneth Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF VITAMIN D NUCLEAR RECEPTOR EXPRESSION
; FILE REFERENCE: RTS-0327
; CURRENT APPLICATION NUMBER: US/10/000,213
; CURRENT FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 94
; SEQ ID NO 81
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-000-213-81

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2143 CCTGCTGATTGATTT 2157
Db 20 CCTGCTGAATGATTT 6
||||| |||||||

RESULT 3164
US-10-017-407A-469/c
; Sequence 469, Application US/10017407A
; Publication No. US20030125535A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
```

```

; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C61
; CURRENT APPLICATION NUMBER: US/10/017,407A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-017-407A-469

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217
Db 19 GAGGACGGCGAGGAT 5
||||| |||||||

RESULT 3165
US-10-011-833A-469/c
; Sequence 469, Application US/10011833A
; Publication No. US20030129650A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C22
; CURRENT APPLICATION NUMBER: US/10/011,833A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-011-833A-469

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
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; PRIOR APPLICATION NUMBER: 60/104987
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105000
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105002
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 60/105104
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217
Db 19 GAGGACGGCGAGGAT 5

RESULT 3160
US-10-006-063A-469/c
; Sequence 469, Application US/10006063A
; Publication No. US20030114652A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C3
; CURRENT APPLICATION NUMBER: US/10/006,063A
; CURRENT FILING DATE: 2002-03-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-063A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217

Db 19 GAGGACGGCGAGGAT 5

RESULT 3161
US-10-020-063A-469/c
; Sequence 469, Application US/10020063A
; Publication No. US20030119097A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C65
; CURRENT APPLICATION NUMBER: US/10/020,063A
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-020-063A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217
Db 19 GAGGACGGCGAGGAT 5

RESULT 3162
US-10-015-391A-469/c
; Sequence 469, Application US/10015391A
; Publication No. US20030120053A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.





US-10-002-491-84  
; Sequence 84, Application US/10002491  
; Publication No. US20030109467A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF FXR EXPRESSION  
; FILE REFERENCE: RTS-0239  
; CURRENT APPLICATION NUMBER: US/10/002,491  
; CURRENT FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 88  
; SEQ ID NO 84  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-002-491-84

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1897 CCTAGATCAACAGAT 1911  
||||| |||||||  
Db 1 CCTAGTTCACAGAT 15

RESULT 3157  
US-10-011-692A-469/c  
; Sequence 469, Application US/10011692A  
; Publication No. US20030109672A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830P1C30  
; CURRENT APPLICATION NUMBER: US/10/011,692A  
; CURRENT FILING DATE: 2001-12-07  
; Prior application removed - See file Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 469  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-011-692A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
||||| |||||||  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3158  
US-10-006-768A-469/c

; Sequence 469, Application US/10006768A  
; Publication No. US20030113793A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830P1C10  
; CURRENT APPLICATION NUMBER: US/10/006,768A  
; CURRENT FILING DATE: 2002-03-05  
; NUMBER OF SEQ ID NOS: 477  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 469  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-006-768A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
||||| |||||||  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3159  
US-10-017-610A-469/c  
; Sequence 469, Application US/10017610A  
; Publication No. US20030113795A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830P1C64  
; CURRENT APPLICATION NUMBER: US/10/017,610A  
; CURRENT FILING DATE: 2001-12-13  
; Prior Application Number: 60/098716  
; Prior Filing Date: 1998-09-01  
; Prior Application Number: 60/098723  
; Prior Filing Date: 1998-09-01  
; Prior Application Number: 60/098749  
; Prior Filing Date: 1998-09-01  
; Prior Application Number: 60/098750  
; Prior Filing Date: 1998-09-01

```
;
; GENERAL INFORMATION:
; APPLICANT: Froehler, Brian
; APPLICANT: Wagner, Rick
; APPLICANT: Mateucci, Mark
; APPLICANT: Jones, Robert J.
; APPLICANT: Gutierrez, Arnold J.
; APPLICANT: Pudlo, Jeff
; TITLE OF INVENTION: Enhanced Triple-Helix And Double-Helix Formation With Oligomers
; TITLE OF INVENTION: Containing Modified Pyrimidines
; FILE REFERENCE: GLIS0143
; CURRENT APPLICATION NUMBER: US/10/024,818
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 08/599,738
; PRIOR FILING DATE: 1996-02-12
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
US-10-024-818-14
Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 77.8%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2166 TTTTNTTTTNTTTTNTTTT 2183
Db       2 TTTTNTTNATTTTNTTT 19

RESULT 3154
US-10-024-818-14/c
; Sequence 14, Application US/10024818
; Publication No. US20030096980A1
; GENERAL INFORMATION:
; APPLICANT: Froehler, Brian
; APPLICANT: Wagner, Rick
; APPLICANT: Mateucci, Mark
; APPLICANT: Jones, Robert J.
; APPLICANT: Gutierrez, Arnold J.
; APPLICANT: Pudlo, Jeff
; TITLE OF INVENTION: Enhanced Triple-Helix And Double-Helix Formation With Oligomers
; TITLE OF INVENTION: Containing Modified Pyrimidines
; FILE REFERENCE: GLIS0143
; CURRENT APPLICATION NUMBER: US/10/024,818
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 08/599,738
; PRIOR FILING DATE: 1996-02-12
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
;
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (20)..(20)
; OTHER INFORMATION: This position is C'= 5-methyl-2'-deoxycytidine
US-10-024-818-14
Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 77.8%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2786 AAAAAAAAAAAAAAAAAA 2803
Db       19 AAAAAAAAAATNAAAAAA 2

RESULT 3155
US-10-015-386A-469/c
; Sequence 469, Application US/10015386A
; Publication No. US20030099625A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C55
; CURRENT APPLICATION NUMBER: US/10/015,386A
; CURRENT FILING DATE: 2001-12-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-386A-469
Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGGAGGAT 217
Db       19 GAGGACGGCGGAGGAT 5

RESULT 3156
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; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101477  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101479  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101738  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101741  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101743  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101915  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101916  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/102207  
; PRIOR FILING DATE: 1998-09-29  
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; PRIOR FILING DATE: 1998-09-29  
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; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102330  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102331  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102484  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102487  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102570  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102571  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102684  
; PRIOR FILING DATE: 1998-10-01  
; PRIOR APPLICATION NUMBER: 60/102687  
; PRIOR FILING DATE: 1998-10-01  
; PRIOR APPLICATION NUMBER: 60/102965  
; PRIOR FILING DATE: 1998-10-02  
; PRIOR APPLICATION NUMBER: 60/103258  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 60/103314  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103315  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103328  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103395  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103396  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103401  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103449  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 60/103633  
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; PRIOR APPLICATION NUMBER: 60/104257  
; PRIOR FILING DATE: 1998-10-14  
; PRIOR APPLICATION NUMBER: 60/104987  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105000  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105002  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105104  
; PRIOR FILING DATE: 1998-10-21

; PRIOR APPLICATION NUMBER: 60/105169  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105266  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105693  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105694  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105807  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105881  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105882  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/106023  
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred.No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
||||| |||||  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3152

US-10-012-755A-469/c  
; Sequence 469, Application US/10012755A  
; Publication No. US20030096955A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C28  
; CURRENT APPLICATION NUMBER: US/10/012,755A  
; CURRENT FILING DATE: 2002-06-10  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 469  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-012-755A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred.No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
||||| |||||  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3153

US-10-024-818-14  
; Sequence 14, Application US/10024818  
; Publication No. US20030096980A1

```
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C31
; CURRENT APPLICATION NUMBER: US/10/013,430A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-430A-469

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGAGGAT 217
Db       19 GAGGACGCGAGGAT 5
      ||||| ||||| |||||
      ||||| ||||| |||||

RESULT 3151
US-10-011-671A-469/c
; Sequence 469, Application US/10011671A
; Publication No. US20030096954A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C27
; CURRENT APPLICATION NUMBER: US/10/011,671A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
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; PRIOR FILING DATE: 1998-09-18
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; PRIOR FILING DATE: 1998-09-23
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; PRIOR APPLICATION NUMBER: 60/102571  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102684  
; PRIOR FILING DATE: 1998-10-01  
; PRIOR APPLICATION NUMBER: 60/102687

; PRIOR FILING DATE: 1998-10-01  
; PRIOR APPLICATION NUMBER: 60/102965  
; PRIOR FILING DATE: 1998-10-02  
; PRIOR APPLICATION NUMBER: 60/103258  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 60/103314  
; PRIOR FILING DATE: 1998-10-07  
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; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105266  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105693  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105694  
; PRIOR FILING DATE: 1998-10-26  
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; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105881  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105882  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/106023  
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
Db 19 GAGGACGGCGAGGAT 5  
|||||

RESULT 3150  
US-10-013-430A-469/c  
; Sequence 469, Application US/10013430A  
; Publication No. US20030092883A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone

; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: 60/105169
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105266
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: 60/105693
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105694
; PRIOR FILING DATE: 1998-10-26
; PRIOR APPLICATION NUMBER: 60/105807
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105881
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/105882
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: 60/106023
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217
||||| |||||||
Db 19 GAGGACGGCGAGGAT 5

RESULT 3148

US-10-013-913A-469/c
; Sequence 469, Application US/10013913A
; Publication No. US20030083462A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C40
; CURRENT APPLICATION NUMBER: US/10/013,913A
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-013-913A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217
||||| |||||||
Db 19 GAGGACGGCGAGGAT 5

RESULT 3149

US-10-007-194A-469/c
; Sequence 469, Application US/10007194A

; Publication No. US20030092061A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan l.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C6
; CURRENT APPLICATION NUMBER: US/10/007,194A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16



; PRIOR FILING DATE: 1998-10-01  
; PRIOR APPLICATION NUMBER: 60/102965  
; PRIOR FILING DATE: 1998-10-02  
; PRIOR APPLICATION NUMBER: 60/103258  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 60/103314  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103315  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103328  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103395  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103396  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103401  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103449  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 60/103633  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103678  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103679  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103711  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/104257  
; PRIOR FILING DATE: 1998-10-14  
; PRIOR APPLICATION NUMBER: 60/104987  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105000  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105002  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105104  
; PRIOR FILING DATE: 1998-10-21  
; PRIOR APPLICATION NUMBER: 60/105169  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105266  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105693  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105694  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105807  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105881  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105882  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/106023  
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
||||| |||||||  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3146  
US-10-006-117A-469/c  
; Sequence 469, Application US/10006117A  
; Publication No. US20030082627A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan l.  
; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830PIC13  
; CURRENT APPLICATION NUMBER: US/10/006,117A  
; CURRENT FILING DATE: 2002-03-19  
; Prior Application removed - See File Wrapper or Palm  
; PRIOR FILING DATE: 2001-07-09  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 469  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-006-117A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
||||| |||||||  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3147  
US-10-017-527A-469/c  
; Sequence 469, Application US/10017527A  
; Publication No. US20030082628A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan l.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830PIC63  
; CURRENT APPLICATION NUMBER: US/10/017,527A  
; CURRENT FILING DATE: 2001-12-13  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098803  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098821  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098843  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/099536



Publication No. US20030082626A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2830P1C15  
; CURRENT APPLICATION NUMBER: US/10/006,116A  
; CURRENT FILING DATE: 2001-12-16  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098803  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098821  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098843  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/099536  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099596  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099598  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099602  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099642  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099741  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099754  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099763  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099792  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099808  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099812  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099815  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099816  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/100385  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100388  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100390  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100584  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100627  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100661  
; PRIOR FILING DATE: 1998-09-16

; PRIOR APPLICATION NUMBER: 60/100662  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100664  
; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100683  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100684  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100710  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100711  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100848  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/100849  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/100919  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100930  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/101014  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101068  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101071  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101279  
; PRIOR FILING DATE: 1998-09-22  
; PRIOR APPLICATION NUMBER: 60/101471  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101472  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101474  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101475  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101476  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101477  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101479  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101738  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101741  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101743  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101915  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101916  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/102207  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102240  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102307  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102330  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102331  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102484  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102487  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102570  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102571  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102684  
; PRIOR FILING DATE: 1998-10-01  
; PRIOR APPLICATION NUMBER: 60/102687

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-006-818A-469

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGAGGAT 217
Db      19  GAGGACGGCGAGGAT 5

RESULT 3142
US-10-015-393A-469/c
; Sequence 469, Application US/10015393A
; Publication No. US20030069179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C46
; CURRENT APPLICATION NUMBER: US/10/015,393A
; CURRENT FILING DATE: 2002-06-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-393A-469

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGAGGAT 217
Db      19  GAGGACGGCGAGGAT 5

RESULT 3143
US-10-015-869A-469/c
; Sequence 469, Application US/10015869A
; Publication No. US20030073130A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C20
; CURRENT APPLICATION NUMBER: US/10/012,121A
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-121A-469

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGAGGAT 217
Db      19  GAGGACGGCGAGGAT 5

RESULT 3145
US-10-006-116A-469/c
; Sequence 469, Application US/10006116A
```

```
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C45
; CURRENT APPLICATION NUMBER: US/10/015,869A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-015-869A-469

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGAGGAT 217
Db      19  GAGGACGGCGAGGAT 5

RESULT 3144
US-10-012-121A-469/c
; Sequence 469, Application US/10012121A
; Publication No. US20030073810A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C20
; CURRENT APPLICATION NUMBER: US/10/012,121A
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 469
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-012-121A-469

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      203 GAGGACTGCGAGGAT 217
Db      19  GAGGACGGCGAGGAT 5

RESULT 3145
US-10-006-116A-469/c
; Sequence 469, Application US/10006116A
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APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2830P1C68  
CURRENT APPLICATION NUMBER: US/10/226,254A  
CURRENT FILING DATE: 2002-08-21  
PRIOR APPLICATION NUMBER: 60/098716  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098723  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098749  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098750  
PRIOR FILING DATE: 1998-09-01  
PRIOR APPLICATION NUMBER: 60/098803  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098821  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/098843  
PRIOR FILING DATE: 1998-09-02  
PRIOR APPLICATION NUMBER: 60/099536  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099596  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 469  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-226-254A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
||||| |||||||  
Db 19 GAGGACGCGAGGAT 5

RESULT 3139  
US-10-144-140-62  
Sequence 62, Application US/10144140  
Publication No. US20030211606A1  
GENERAL INFORMATION:  
APPLICANT: Kenneth W. Dobie  
APPLICANT: Susan M. Freier  
TITLE OF INVENTION: ANTISENSE MODULATION OF DYRK4 EXPRESSION  
FILE REFERENCE: RTS-0362  
CURRENT APPLICATION NUMBER: US/10/144,140  
CURRENT FILING DATE: 2002-05-10  
NUMBER OF SEQ ID NOS: 87  
SEQ ID NO 62  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-10-144-140-62

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 924 CACCTGAATGCTTAA 938  
||||| |||||||  
Db 1 CACCTGAATGCTGAA 15

RESULT 3140  
US-10-006-856A-469/c  
Sequence 469, Application US/10006856A  
Publication No. US20030044841A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2830P1C14  
CURRENT APPLICATION NUMBER: US/10/006,856A  
CURRENT FILING DATE: 2002-05-10  
NUMBER OF SEQ ID NOS: 477  
Prior Application removed - See File Wrapper or Palm  
SEQ ID NO 469  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-006-856A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
||||| |||||||  
Db 19 GAGGACGCGAGGAT 5

RESULT 3141  
US-10-006-818A-469/c  
Sequence 469, Application US/10006818A  
Publication No. US20030054406A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2830P1C4  
CURRENT APPLICATION NUMBER: US/10/006,818A  
CURRENT FILING DATE: 2001-12-06  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 469  
LENGTH: 20  
TYPE: DNA

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C34  
; CURRENT APPLICATION NUMBER: US/10/013,907A  
; CURRENT FILING DATE: 2001-12-10  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 469  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-013-907A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGGAGGAT 217  
||||| |||||||  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3136  
US-10-015-499A-469/c  
; Sequence 469, Application US/10015499A  
; Publication No. US20030065142A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C42  
; CURRENT APPLICATION NUMBER: US/10/015,499A  
; CURRENT FILING DATE: 2001-12-11  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477

; SEQ ID NO 469  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-015-499A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGGAGGAT 217  
||||| |||||||  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3137  
US-10-211-858-164/c  
; Sequence 164, Application US/10211858  
; Publication No. US20030211096A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Marsters, Scot A.  
; APPLICANT: Pan, James  
; APPLICANT: Pitti, Robert M.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stone, Donna M.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR  
; FILE REFERENCE: P2931R1C1  
; CURRENT APPLICATION NUMBER: US/10/211,858  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: 60/014699  
; PRIOR FILING DATE: 1996-04-01  
; PRIOR APPLICATION NUMBER: 60/026943  
; PRIOR FILING DATE: 1996-09-23  
; PRIOR APPLICATION NUMBER: 60/059121  
; PRIOR FILING DATE: 1997-07-17  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/062037  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: 60/063755  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063045  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/066511  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/066772  
; PRIOR FILING DATE: 1997-11-24  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 258

; SEQ ID NO 164  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Oligonucleotide Probe.  
US-10-211-858-164

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGGAGGAT 217  
||||| |||||||  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3138  
US-10-226-254A-469/c  
; Sequence 469, Application US/10226254A  
; Publication No. US20030224478A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100711  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100848  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/100849  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/100919  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/100930  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/101014  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101068  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101071  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/101279  
; PRIOR FILING DATE: 1998-09-22  
; PRIOR APPLICATION NUMBER: 60/101471  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101472  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101474  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101475  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101476  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101477  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101479  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101738  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101741  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101743  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101915  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101916  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/102207  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102240  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102307  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102330  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102331  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102484  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102487  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102570  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102571  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102684  
; PRIOR FILING DATE: 1998-10-01  
; PRIOR APPLICATION NUMBER: 60/102687  
; PRIOR FILING DATE: 1998-10-01  
; PRIOR APPLICATION NUMBER: 60/102965  
; PRIOR FILING DATE: 1998-10-02  
; PRIOR APPLICATION NUMBER: 60/103258  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 60/103314  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103315  
; PRIOR FILING DATE: 1998-10-07

; PRIOR APPLICATION NUMBER: 60/103328  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103395  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103396  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103401  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103449  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 60/103633  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103678  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103679  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103711  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/104257  
; PRIOR FILING DATE: 1998-10-14  
; PRIOR APPLICATION NUMBER: 60/104987  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105000  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105002  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105104  
; PRIOR FILING DATE: 1998-10-21  
; PRIOR APPLICATION NUMBER: 60/105169  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105266  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105693  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105694  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105807  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105881  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/105882  
; PRIOR FILING DATE: 1998-10-27  
; PRIOR APPLICATION NUMBER: 60/106023  
; PRIOR FILING DATE: 1998-10-28

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGGAGGAT 217  
||| ||| ||| ||| ||| |||  
Db 19 GAGGACGGCGGAGGAT 5

RESULT 3135  
US-10-013-907A-469/c  
; Sequence 469, Application US/10013907A  
; Publication No. US20030064925A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan I.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.

; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-619-220-78

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2441 CGACTTTTGTGAGAC 2455
Db 1 CGGCTTTTGTGAGAC 15

RESULT 3133
US-09-949-428-228
; Sequence 228, Application US/09949428
; Publication No. US20030064372A1
; GENERAL INFORMATION:
; APPLICANT: Bodnar, Jackie S.
; APPLICANT: Castellani, Lawrence W.
; APPLICANT: Chatterjee, Aurobindo
; APPLICANT: de Jong, Pieter
; APPLICANT: Lusis, Aldons J.
; APPLICANT: Ohmen, Jeff
; APPLICANT: Ross, David
; APPLICANT: Tafuri, Sherrie
; APPLICANT: Wu, Chenyan
; TITLE OF INVENTION: Gene and Sequence Variation Associated with Lipid Disorder
; FILE REFERENCE: 02810.0014.NPUS01
; CURRENT APPLICATION NUMBER: US/09/949,428
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/231,322
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 228
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-949-428-228

Query Match 0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2427 TGGTGCACTTCTTAC 2441
Db 1 TGGTGCACTTCTTCC 15

RESULT 3134
US-10-006-485A-469/c
; Sequence 469, Application US/10006485A
; Publication No. US20030064062A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C9
; CURRENT APPLICATION NUMBER: US/10/006,485A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710

NUMBER OF SEQUENCES: 250  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/510,378  
FILING DATE: 22-Feb-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/544,381  
FILING DATE: <Unknown>  
APPLICATION NUMBER: US 08/510,521  
FILING DATE: 02-AUG-1995  
APPLICATION NUMBER: PCT/US94/12305  
FILING DATE: 26-OCT-1994  
APPLICATION NUMBER: US 08/284,064  
FILING DATE: 02-AUG-1994  
APPLICATION NUMBER: US 08/143,312  
FILING DATE: 26-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebeschuetz, Joe  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 018547-004130US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-576-0200  
TELEFAX: 415-576-0300  
INFORMATION FOR SEQ ID NO: 224:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (probe)  
SEQUENCE DESCRIPTION: SEQ ID NO: 224:  
US-09-510-378-224

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2205 TTCAAATGGGAGACT 2219  
Db 18 TTAAATGGGAGACT 4

RESULT 3130  
US-09-838-028-12/c  
Sequence 12, Application US/09838028  
Publication No. US20030175857A1  
GENERAL INFORMATION:  
APPLICANT: Lind, Peter  
APPLICANT: Berthold, Malin  
TITLE OF INVENTION: No. US20030175857A1el G Protein-Coupled Receptor  
FILE REFERENCE: 00125US2  
CURRENT APPLICATION NUMBER: US/09/838,028  
CURRENT FILING DATE: 2001-04-19  
PRIOR APPLICATION NUMBER: 60/198,600  
PRIOR FILING DATE: 2000-04-19  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 12  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence

FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Primer  
US-09-838-028-12

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2674 GTGTGTGGGTGAA 2688  
Db 15 GGGTGTGGGTGAA 1

RESULT 3131  
US-10-015-395A-469/c  
Sequence 469, Application US/10015395A  
Publication No. US20040073015A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2830PIC57  
CURRENT APPLICATION NUMBER: US/10/015,395A  
CURRENT FILING DATE: 2001-12-12  
Prior application removed - See file Wrapper or Palm  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 469  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic oligonucleotide probe  
US-10-015-395A-469

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3132  
US-10-619-220-78  
Sequence 78, Application US/10619220  
Publication No. US20040033979A1  
GENERAL INFORMATION:  
APPLICANT: Dean, Nicholas M.  
APPLICANT: Marcusson, Eric G.  
APPLICANT: Wyatt, Jacqueline  
APPLICANT: Zhang, Hong  
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
FILE REFERENCE: ISPH-545  
CURRENT APPLICATION NUMBER: US/10/619,220  
CURRENT FILING DATE: 2003-07-14  
PRIOR APPLICATION NUMBER: 09/802,669  
PRIOR FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: US 09/665,615

; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102331  
; PRIOR FILING DATE: 1998-09-29  
; PRIOR APPLICATION NUMBER: 60/102484  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102487  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102570  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102571  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 60/102684  
; PRIOR FILING DATE: 1998-10-01  
; PRIOR APPLICATION NUMBER: 60/102687  
; PRIOR FILING DATE: 1998-10-01  
; PRIOR APPLICATION NUMBER: 60/102965  
; PRIOR FILING DATE: 1998-10-02  
; PRIOR APPLICATION NUMBER: 60/103258  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 60/103314  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103315  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103328  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103395  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103396  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103401  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 60/103449  
; PRIOR FILING DATE: 1998-10-06  
; PRIOR APPLICATION NUMBER: 60/103633  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103678  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103679  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/103711  
; PRIOR FILING DATE: 1998-10-08  
; PRIOR APPLICATION NUMBER: 60/104257  
; PRIOR FILING DATE: 1998-10-14  
; PRIOR APPLICATION NUMBER: 60/104987  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105000  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105002  
; PRIOR FILING DATE: 1998-10-20  
; PRIOR APPLICATION NUMBER: 60/105104  
; PRIOR FILING DATE: 1998-10-21  
; PRIOR APPLICATION NUMBER: 60/105169  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105266  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105693  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105694  
; PRIOR FILING DATE: 1998-10-26  
; PRIOR APPLICATION NUMBER: 60/105807

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 203 GAGGACTGCGAGGAT 217  
||||| |||||  
Db 19 GAGGACGGCGAGGAT 5

RESULT 3127  
US-09-906-158-57/c  
; Sequence 57, Application US/09906158

; Publication No. US20030078217A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3 EXPRESSION  
; FILE REFERENCE: RTS-0257  
; CURRENT APPLICATION NUMBER: US/09/906,158  
; CURRENT FILING DATE: 2001-07-14  
; NUMBER OF SEQ ID NOS: 168  
; SEQ ID NO 57  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-906-158-57

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 835 CTTCTGCTCAGTCCC 849  
||||| |||||  
Db 15 CTTCTGCTCAGGCC 1

RESULT 3128  
US-09-816-460C-20/c  
; Sequence 20, Application US/09816460C  
; Publication No. US20030087235A1  
; GENERAL INFORMATION:  
; APPLICANT: Dairkee, Shanaz H.  
; APPLICANT: Li, Zheng  
; TITLE OF INVENTION: PROGNOSTIC METHODS FOR BREAST CANCER  
; FILE REFERENCE: CPMC-010/00US  
; CURRENT APPLICATION NUMBER: US/09/816,460C  
; CURRENT FILING DATE: 2001-03-23  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 20  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic primer  
US-09-816-460C-20

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1543 AGAGTAGGGAAGGAA 1557  
||||| |||||  
Db 19 AGAGTGGGAAGGAA 5

RESULT 3129  
US-09-510-378-224/c  
; Sequence 224, Application US/09510378  
; Publication No. US20030165823A1  
; GENERAL INFORMATION:  
; APPLICANT: Cronin, Maureen T.  
; Miyada, Charles Garrett  
; Hubbell, Earl A.  
; Chee, Mark  
; Fodor, Stephen P.A.  
; Huang, Xiachua C.  
; Lipshutz, Robert J.  
; Lobban, Peter E.  
; Morris, Macdonald S.  
; Sheldon, Edward L.  
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes for  
; Detecting Cystic Fibrosis



```
Db          1 TGGTGCACCTCTCTCC 15
|||||
RESULT 3126
US-09-946-374-469/c
; Sequence 469, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946,374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/099536
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099792
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102240
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102307
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 60/102330
```

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; NUMBER OF SEQ ID NOS: 503
; SEQ ID NO 467
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-824-322B-467

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2098 TTCAACGGGGGCCT 2112
Db 16 TTCAAACTGGGGCCT 2

RESULT 3123
US-09-232-785-218/c
; Sequence 218, Application US/09232785
; Publication No. US20030049612A1
; GENERAL INFORMATION:
; APPLICANT: International Paper Co.
; APPLICANT: Nelson, C. Dana
; APPLICANT: Eght, Craig. S
; TITLE OF INVENTION: MICROSATELITE DNA MARKERS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 4481/1E18US1
; CURRENT APPLICATION NUMBER: US/09/232,785
; CURRENT FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: 09/232,884
; PRIOR FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 397
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 218
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Pinus taeda L.
US-09-232-785-218

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 228 GGAGCAGCAATGGGA 242
Db 20 GGAGCAACAATGGGA 6

RESULT 3124
US-09-784-674-553
; Sequence 553, Application US/09784674
; Publication No. US20030054346A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Karen W.
; APPLICANT: Wolber, Paul K.
; APPLICANT: Delenstarr, Glenda C.
; APPLICANT: Webb, Peter G.
; APPLICANT: Kincaid, Robert H.
; TITLE OF INVENTION: Methods for evaluating oligonucleotide
; probe sequences
; NUMBER OF SEQUENCES: 1165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
; COMPANY M/S 20BO
; STREET: 3000 Hanover Street
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,674
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: No. US20030054346A1 available
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/021,701
; FILING DATE: 10-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Wendy A.
; REGISTRATION NUMBER: 36,697
; REFERENCE/DOCKET NUMBER: 10971464-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-236-2386
; TELEFAX: 650-852-8063
; INFORMATION FOR SEQ ID NO: 553:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 553:
US-09-784-674-553

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2174 TTTT TTTT TTTT TTTT TTTT AA 2188
Db 6 TTTT TCTTTT TTTT AA 20

RESULT 3125
US-09-949-427-228
; Sequence 228, Application US/09949427
; Publication No. US20030054418A1
; GENERAL INFORMATION:
; APPLICANT: Bodnar, Jackie S.
; APPLICANT: Castellani, Lawrence W.
; APPLICANT: Chatterjee, Aurobindo
; APPLICANT: de Jong, Pieter
; APPLICANT: Lulis, Aldons J.
; APPLICANT: Ohmen, Jeff
; APPLICANT: Ross, David
; APPLICANT: Tafuri, Sherrie
; APPLICANT: Wu, Chenyan
; TITLE OF INVENTION: Gene and Sequence Variation Associated with Cancer
; FILE REFERENCE: 02810.0014.NPUS02
; CURRENT APPLICATION NUMBER: US/09/949,427
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/231,322
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 228
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-949-427-228

Query Match          0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2427 TGGTGCAC TTTCTTAC 2441
```

```

; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-I
; CURRENT APPLICATION NUMBER: US/09/898,234
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hybridization
; OTHER INFORMATION: probe
US-09-898-234-42

Query Match          0.5%;   Score 13.4;   DB 1;   Length 20;
Best Local Similarity 93.3%;   Pred. No. 3.3e+03;
Matches 14;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      1964 TAAATATTTACCTTG 1978
Db      15 TATATATTACCTTG 1

RESULT 3120
US-09-899-429A-52/c
; Sequence 52, Application US/09899429A
; Patent No. US20020169118A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98-385-J
; CURRENT APPLICATION NUMBER: US/09/899,429A
; CURRENT FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 09/792,356
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1955-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hybridization
; OTHER INFORMATION: probe

```

```

US-09-899-429A-52

Query Match          0.5%;   Score 13.4;   DB 1;   Length 20;
Best Local Similarity 93.3%;   Pred. No. 3.3e+03;
Matches 14;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      1964 TAAATATTTACCTTG 1978
Db      15 TATATATTACCTTG 1

RESULT 3121
US-09-792-356-42/c
; Sequence 42, Application US/09792356
; Publication No. US20020183485A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-G
; CURRENT APPLICATION NUMBER: US/09/792,356
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 08/477,639
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hybridization
; OTHER INFORMATION: probe
US-09-792-356-42

Query Match          0.5%;   Score 13.4;   DB 1;   Length 20;
Best Local Similarity 93.3%;   Pred. No. 3.3e+03;
Matches 14;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

QY      1964 TAAATATTTACCTTG 1978
Db      15 TATATATTACCTTG 1

RESULT 3122
US-09-824-322B-467/c
; Sequence 467, Application US/09824322B
; Publication No. US20030022848A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Brenda
; APPLICANT: Bennett, C. Frank
; APPLICANT: Butler, Madeline M.
; APPLICANT: Shanahan, William R.
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF TUMOR NECROSIS FACTOR-ALPHA
; TITLE OF INVENTION: ALPHA) EXPRESSION
; FILE REFERENCE: ISPH-0501
; CURRENT APPLICATION NUMBER: US/09/824,322B
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: US 09/313,932
; PRIOR FILING DATE: 1999-05-18
; PRIOR APPLICATION NUMBER: US 09/166,186
; PRIOR FILING DATE: 1998-10-05

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; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 09/290,640
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-802-669-78

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2441 CGACTTTTGTGAGAC 2455
Db      1 CGGCTTTTGTGAGAC 15

RESULT 3116
US-09-854-883-130
; Sequence 130, Application US/09854883
; Patent No. US20020055479A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/09/854,883
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 130
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-854-883-130

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2003 CTCTTCAGAGATCA 2017
Db      6 CATCTTCAGAGATCA 20

RESULT 3117
US-09-854-883-210/c
; Sequence 210, Application US/09854883
; Patent No. US20020055479A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/09/854,883
```

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; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 210
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-854-883-210

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      479 GGCCGCCAGAGCCAG 493
Db      18 GGCCGCCAGAGCGAG 4

RESULT 3118
US-09-899-422-42/c
; Sequence 42, Application US/09899422
; Patent No. US20020090676A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
; APPLICANT: Himmler, Adolph
; APPLICANT: Maurer-Fogy, Ingrid
; APPLICANT: Stratowa, Christian
; TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
; TITLE OF INVENTION: Them
; FILE REFERENCE: 98,385-H
; CURRENT APPLICATION NUMBER: US/09/899,422
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/525,998
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 08/383,676
; PRIOR FILING DATE: 1995-02-01
; PRIOR APPLICATION NUMBER: 08/153,287
; PRIOR FILING DATE: 1993-11-17
; PRIOR APPLICATION NUMBER: 07/821,750
; PRIOR FILING DATE: 1992-01-02
; PRIOR APPLICATION NUMBER: 07/511,430
; PRIOR FILING DATE: 1990-04-20
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hybridization
; OTHER INFORMATION: probe
US-09-899-422-42

Query Match      0.5%; Score 13.4; DB 1; Length 20;
Best Local Similarity 93.3%; Pred. No. 3.3e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1964 TAAATATTACCTTG 1978
Db      15 TATATATTACCTTG 1

RESULT 3119
US-09-898-234-42/c
; Sequence 42, Application US/09898234
; Patent No. US20020155112A1
; GENERAL INFORMATION:
; APPLICANT: Hauptmann, Rudolph
```



QY 1492 GGAGAAATGGAGAA 1506  
Db 15 GGAGAAATGGAGCA 1

RESULT 3112

US-09-734-846-16/c  
; Sequence 16, Application US/09734846  
; Patent No. US20010007025A1  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Nickoloff, Brian J.  
; APPLICANT: Zhang, QingQing  
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
; FILE REFERENCE: ISPH-0528  
; CURRENT APPLICATION NUMBER: US/09/734,846  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 09/277,020  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 09/167,921  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 09/323,743  
; PRIOR FILING DATE: 1999-06-02  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 16  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-734-846-16

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2104 CGGGGGCCTTCTGGT 2118  
Db 20 CGGGGTCCTTCTGGT 6

RESULT 3113

US-09-752-983-214/c  
; Sequence 214, Application US/09752983  
; Patent No. US20010016575A1  
; GENERAL INFORMATION:  
; APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.  
; APPLICANT: Graham, Brett P. Monia  
; TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 271  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Jane Massey Licata  
; STREET: 66 East Main Street  
; CITY: Marlton  
; STATE: NJ  
; COUNTRY: U.S.A.  
; ZIP: 08053  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
; COMPUTER: IBM PC  
; OPERATING SYSTEM: WINDOWS 95  
; SOFTWARE: WORDPERFECT 6.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/752,983  
; FILING DATE: 02-Jan-2001  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/280,805  
; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:  
; NAME: Licata, Jane Massey  
; REGISTRATION NUMBER: 32,257  
; REFERENCE/DOCKET NUMBER: ISPH-0346  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-810-1515  
; TELEFAX: 609-810-1454  
; INFORMATION FOR SEQ ID NO: 214:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 base pairs  
; TYPE: Nucleic Acid  
; STRANDEDNESS: Single  
; TOPOLOGY: Linear  
; ANTI-SENSE: Yes  
US-09-752-983-214

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2520 TTTATTTCATATATAT 2534  
Db 15 TTTATTTCATATAT 1

RESULT 3114

US-09-758-881-100/c  
; Sequence 100, Application US/09758881  
; Patent No. US20010029250A1  
; GENERAL INFORMATION:  
; APPLICANT: Karras, James G  
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3  
; TITLE OF INVENTION: Expression  
; FILE REFERENCE: ISPH-0532  
; CURRENT APPLICATION NUMBER: US/09/758,881  
; CURRENT FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: PCT/US00/09054  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 09/288,461  
; PRIOR FILING DATE: 1999-04-08  
; NUMBER OF SEQ ID NOS: 152  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 100  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-758-881-100

Query Match 0.5%; Score 13.4; DB 1; Length 20;  
Best Local Similarity 93.3%; Pred. No. 3.3e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2673 AGTGTGTGGGTGA 2687  
Db 16 AGTGAGTGTGGGTGA 2

RESULT 3115

US-09-802-669-78  
; Sequence 78, Application US/09802669  
; Patent No. US20020004490A1  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Marcusson, Eric G.  
; APPLICANT: Wyatt, Jacqueline  
; APPLICANT: Zhang, Hong  
; TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
; FILE REFERENCE: ISPH-545  
; CURRENT APPLICATION NUMBER: US/09/802,669  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: US 09/665,615

RESULT 3110  
US-10-400-382-87/c  
; Sequence 87, Application US/10400382  
; Publication No. US20030190659A1  
; GENERAL INFORMATION:  
; APPLICANT: LaCasse, Eric  
; APPLICANT: McManus, Daniel  
; APPLICANT: Durkin, Jonathan P.  
; TITLE OF INVENTION: Antisense IAP Nucleobase Oligomers and  
; TITLE OF INVENTION: Uses Thereof  
; FILE REFERENCE: 07891/025004  
; CURRENT APPLICATION NUMBER: US/10/400,382  
; CURRENT FILING DATE: 2003-03-27  
; PRIOR APPLICATION NUMBER: US 60/367,853  
; PRIOR FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 460  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 87  
; LENGTH: 19  
; TYPE: DNA

Query Match	0.5%	Score 13.4;	DB 1;	Length 20;
Best Local Similarity	93.3%;	Pred. NO. 3.3e+03;		
Matches 14;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-996-263-33

Query Match          0.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2164 CCTTTT TTTT TTTT 2178
Db 18 CGTTT TTTT TTTT 4

RESULT 3105
US-09-370-541-4
; Sequence 4, Application US/09370541
; Publication No. US2003008079A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Nucleosidic Compounds And Oligomeric
; TITLE OF INVENTION: Compounds Prepared Therefrom
; FILE REFERENCE: ISIS3993
; CURRENT APPLICATION NUMBER: US/09/370,541
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: 09/130,973
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 09/016,520
; EARLIER FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; EARLIER APPLICATION NUMBER: 09/344,260
; EARLIER FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: sequence
US-09-370-541-4

Query Match          0.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAA AAAAAA 2799
Db 2 GCAAAA AAAAAA 16

RESULT 3106
US-09-370-541-4/c
; Sequence 4, Application US/09370541
; Publication No. US2003008079A1
; GENERAL INFORMATION:
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Prakash, Thazha P
; APPLICANT: Kawasaki, Andrew M
; TITLE OF INVENTION: Aminoxy-Modified Nucleosidic Compounds And Oligomeric
; TITLE OF INVENTION: Compounds Prepared Therefrom
; FILE REFERENCE: ISIS3993
; CURRENT APPLICATION NUMBER: US/09/370,541
; CURRENT FILING DATE: 1999-08-09
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; EARLIER APPLICATION NUMBER: 09/130,973
; EARLIER FILING DATE: 1998-08-07
; EARLIER APPLICATION NUMBER: 09/016,520
; EARLIER FILING DATE: 1998-01-30
; EARLIER APPLICATION NUMBER: 60/037,143
; EARLIER FILING DATE: 1997-02-14
; EARLIER APPLICATION NUMBER: 09/344,260
; EARLIER FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: antisense
; OTHER INFORMATION: sequence
US-09-370-541-4

Query Match          0.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2164 CCTTTT TTTT TTTT 2178
Db 18 CGTTT TTTT TTTT 4

RESULT 3107
US-09-791-190A-16/c
; Sequence 16, Application US/09791190A
; Publication No. US20030104372A1
; GENERAL INFORMATION:
; APPLICANT: Pyrosequencing AB
; APPLICANT: Ahmadian, Afshin
; APPLICANT: Lundberg, Joakim
; APPLICANT: Nyren, Pal
; TITLE OF INVENTION: Allele Specific Primer Extension Assay
; FILE REFERENCE: Docket 14259
; CURRENT APPLICATION NUMBER: US/09/791,190A
; CURRENT FILING DATE: 2002-09-25
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()...()
; OTHER INFORMATION: Primer
US-09-791-190A-16

Query Match          0.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 431 CCCCTG CACCGCCG 445
Db 16 CCCCTG CACCGAGCAG 2

RESULT 3108
US-10-352-586-33
; Sequence 33, Application US/10352586
; Publication No. US20030187240A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Phillip Dan
; APPLICANT: Kawasaki, Andrew
; TITLE OF INVENTION: 2'-Modified Oligonucleotides
; FILE REFERENCE: ISIS5137
; CURRENT APPLICATION NUMBER: US/10/352,586
; CURRENT FILING DATE: 2003-01-28
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; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 2979
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-2979

Query Match 0.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2317 TTGTTGCTGCTTGTC 2331
||| |||||
Db 5 TTGTAGCTGCTTGTC 19

RESULT 3102
US-09-969-373-3523
; Sequence 3523, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 3523
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-3523

Query Match 0.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1189 ACAGAAATGAGATGGC 1203
||| |||||
Db 2 ACCAAATGAGATGGC 16

RESULT 3103
US-09-996-263-33
; Sequence 33, Application US/09996263
; Publication No. US20030004325A1
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; Andrew Kawasaki
; TITLE OF INVENTION: Sugar Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030004325A1ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/996,263
; FILING DATE: 28-NO. US20030004325A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/471,973
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-996-263-33

Query Match 0.5%; Score 13.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 3.1e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2785 GAAAAAAAAAAAAA 2799
| |||||
Db 2 GCAAAAAAAAAAAAAA 16

RESULT 3104
US-09-996-263-33/c
; Sequence 33, Application US/09996263
; Publication No. US20030004325A1
; GENERAL INFORMATION:
; APPLICANT: Phillip Dan Cook
; Andrew Kawasaki
; TITLE OF INVENTION: Sugar Modified Oligonucleotides
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030004325A1ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/996,263
; FILING DATE: 28-NO. US20030004325A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/471,973
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 33:

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk, 720 Kb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/996,263
; FILING DATE: 28-NO. US20030004325A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/471,973
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph Lucci
; REGISTRATION NUMBER: 33,307
; REFERENCE/DOCKET NUMBER: ISIS-2005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 33:



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; ORGANISM: Homo sapiens
US-10-138-674-1503

Query Match      0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      1340 CATTTCAGCCTGATT 1354
Db      1 CAUUCAGCCUGAAU 15

RESULT 3097
US-10-680-341-14/c
; Sequence 14, Application US/10680341
; Publication No. US20040091923A1
; GENERAL INFORMATION:
; APPLICANT: Reyes, Antonio A.
; APPLICANT: Wallace, Robert B.
; APPLICANT: Ugozzoli, Luis A.
; TITLE OF INVENTION: Linked Linear Amplification of Nucleic Acids
; FILE REFERENCE: 3239-0105P
; CURRENT APPLICATION NUMBER: US/10/680,341
; CURRENT FILING DATE: 2003-10-06
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule: URACIL
; OTHER INFORMATION: NUCLEOSIDE IS A RIBONUCLEOSIDE
US-10-680-341-14

Query Match      0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1936 TAAGGTAATGGTTGG 1950
Db      18 TAAGGGAATGGTTGG 4

RESULT 3098
US-10-680-341-16/c
; Sequence 16, Application US/10680341
; Publication No. US20040091923A1
; GENERAL INFORMATION:
; APPLICANT: Reyes, Antonio A.
; APPLICANT: Wallace, Robert B.
; APPLICANT: Ugozzoli, Luis A.
; TITLE OF INVENTION: Linked Linear Amplification of Nucleic Acids
; FILE REFERENCE: 3239-0105P
; CURRENT APPLICATION NUMBER: US/10/680,341
; CURRENT FILING DATE: 2003-10-06
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-680-341-16

Query Match      0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1936 TAAGGTAATGGTTGG 1950
Db      18 TAAGGGAATGGTTGG 4

; ORGANISM: Homo sapiens
US-10-138-674-1503/c
; Sequence 1414, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1414
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1414

Query Match      0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      474 GGCCCGGCCGCCAGA 488
Db      15 GACCCGGCGGCCAGA 1

RESULT 3100
US-10-287-949A-1503
; Sequence 1503, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1503
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1503

Query Match      0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      1340 CATTTCAGCCTGATT 1354
Db      1 CAUUCAGCCUGAAU 15

RESULT 3101
US-09-969-373-2979
; Sequence 2979, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: an artificially synthesized p
US-10-108-260A-4912

Query Match          0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1944 TGGTGGTGTGTTTGTG 1958
Db 3 TGGTGGATTTTGTG 17

RESULT 3093
US-10-349-143-4649/c
; Sequence 4649, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4649
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-16740 for SEQ 715,
US-10-349-143-4649

Query Match          0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1501 GGAGAAACACAGGAA 1515
Db 16 GGAGAAACAGAGGAA 2

RESULT 3094
US-10-349-143-7270
; Sequence 7270, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
```

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; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 7270
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-3373 for SEQ 3336,
US-10-349-143-7270

Query Match          0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1907 CAGATCAACAATACC 1921
Db 3 CAGCTCAACAATACC 17

RESULT 3095
US-10-138-674-1414/c
; Sequence 1414, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1414
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-10-138-674-1414

Query Match          0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 474 GGCCCGCGCCGCGAGA 488
Db 15 GACCCGCGCCGCGAGA 1

RESULT 3096
US-10-138-674-1503
; Sequence 1503, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1503
; LENGTH: 18
; TYPE: RNA
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; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: CAH oligo 7 for mutation site 2
US-10-152-297-77

Query Match      0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 108 TTGGGGGCTGGGGG 122
Db 17 TTGGGGGCTGAGGG 3

RESULT 3089
US-10-156-433-69/c
; Sequence 69, Application US/10156433
; Publication No. US20030144489A1
; GENERAL INFORMATION:
; APPLICANT: Burgin, Alex
; APPLICANT: Beigelman, Leonid
; APPLICANT: Bellon, Laurent
; APPLICANT: Zinnen, Shawn
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Method for Screening Nucleic Acid Catalysts
; FILE REFERENCE: MBHB00-943-E (500.007)
; CURRENT APPLICATION NUMBER: US/10/156,433
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: US 10/112,814
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 09/216,584
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: US 09/094,381
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: US 60/068,212
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: US 60/049,002
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Position X18 of library synthesis
US-10-156-433-69

Query Match      0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 676 GCCTCACCAGATGGA 690
Db 17 GCCTCATCAGATGGA 3

RESULT 3090
US-10-297-068-21/c
; Sequence 21, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: KAGIYA, Taeko
; APPLICANT: ICHIHARA, Tatsuo
; APPLICANT: Matsumura, Yoshiyuki
; APPLICANT: MORIYA, Shogo
; APPLICANT: NISHIDA, Michio
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
; FILE REFERENCE: 1314OP1174
; CURRENT APPLICATION NUMBER: US/10/297,068
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; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: JP 2000-164798
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 1298
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:capture
US-10-297-068-21

Query Match      0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1326 AGAACTGCTGTCTC 1340
Db 18 AGAACTGCTGTCTC 4

RESULT 3091
US-10-297-068-1061/c
; Sequence 1061, Application US/10297068
; Publication No. US20030228585A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: KAGIYA, Taeko
; APPLICANT: ICHIHARA, Tatsuo
; APPLICANT: Matsumura, Yoshiyuki
; APPLICANT: MORIYA, Shogo
; APPLICANT: NISHIDA, Michio
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES
; FILE REFERENCE: 1314OP1174
; CURRENT APPLICATION NUMBER: US/10/297,068
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: JP 2000-164798
; PRIOR FILING DATE: 2000-06-01
; NUMBER OF SEQ ID NOS: 1298
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1061
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:capture
US-10-297-068-1061

Query Match      0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 CCACGCACAGCCCT 633
Db 18 CCACGCACAGCCCT 4

RESULT 3092
US-10-108-260A-4912
; Sequence 4912, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4912
; LENGTH: 18
; TYPE: DNA
```

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-239-912-16

Query Match          0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2162 CTCCTTTTGTGTTTTT 2176
Db       15 CTCCTTTTGTGTTTTT 1

RESULT 3085
US-10-239-912-22/c
; Sequence 22, Application US/10239912
; Publication No. US20030212012A1
; GENERAL INFORMATION:
; APPLICANT: Henry, James L
; APPLICANT: Fundytus, Marian E
; APPLICANT: Vaudreuil, Terrasse
; TITLE OF INVENTION: Oligonucleotide For Metabotropic Glutamate Receptor
; TITLE OF INVENTION: Type 1 (MGLUR1)
; FILE REFERENCE: 457-107PCT
; CURRENT APPLICATION NUMBER: US/10/239,912
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: 60/144,004
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-239-912-22

Query Match          0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2162 CTCCTTTTGTGTTTTT 2176
Db       15 CTCCTTTTGTGTTTTT 1

RESULT 3086
US-10-239-912-33/c
; Sequence 33, Application US/10239912
; Publication No. US20030212012A1
; GENERAL INFORMATION:
; APPLICANT: Henry, James L
; APPLICANT: Fundytus, Marian E
; APPLICANT: Vaudreuil, Terrasse
; TITLE OF INVENTION: Oligonucleotide For Metabotropic Glutamate Receptor
; TITLE OF INVENTION: Type 1 (MGLUR1)
; FILE REFERENCE: 457-107PCT
; CURRENT APPLICATION NUMBER: US/10/239,912
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: 60/144,004
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-239-912-33

Query Match          0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2162 CTCCTTTTGTGTTTTT 2176
Db       15 CTCCTTTTGTGTTTTT 1

RESULT 3087
US-10-403-902A-78/c
; Sequence 78, Application US/10403902A
; Publication No. US20030224418A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bansal, Aruna
; APPLICANT: Kleytn, Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
; FILE REFERENCE: 24736-2048B
; CURRENT APPLICATION NUMBER: US/10/403,902A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/802,640
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-403-902A-78

Query Match          0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      647 CTGCCCGAGAACCTG 661
Db       15 CTGCCCGAGATCCTG 1

RESULT 3088
US-10-152-297-77/c
; Sequence 77, Application US/10152297
; Publication No. US20030077621A1
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Lieppe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J.
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
; FILE REFERENCE: PRO-104 6868/75529
; CURRENT APPLICATION NUMBER: US/10/152,297
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US/09/383,316
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/252,436
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 09/042,287
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 09/358,972
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
```



Best Local Similarity 82.4%; Pred. No. 2.9e+03;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1241 TGTAAGAATTACACAGA 1257  
| | | | | | | | | | | | | | | | | |  
Db 17 TGTAAGAAGACTCTAG 1

RESULT 3081  
US-10-027-632-52415/c  
; Sequence 52415, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 52415  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-52415

Query Match 0.5%; Score 13.4; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 2.9e+03;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1241 TGTAAGAATTACACAGA 1257  
| | | | | | | | | | | | | | | | | |  
Db 17 TGTAAGAAGACTCTAG 1

RESULT 3082  
US-09-804-014A-59/c  
; Sequence 59, Application US/09804014A  
; Publication No. US20030064489A1  
; GENERAL INFORMATION:  
; APPLICANT: Li, Li  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Vernet, Corine  
; APPLICANT: Fernandes, Elma  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Spaderna, Steven  
; APPLICANT: Majumder, Kumud  
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same  
; FILE REFERENCE: 15966-721 US  
; CURRENT APPLICATION NUMBER: US/09/804,014A  
; PRIOR FILING DATE: 2002-04-24  
; CURRENT APPLICATION NUMBER: 60/188,316  
; PRIOR FILING DATE: 2000-03-10  
; PRIOR APPLICATION NUMBER: 60/188,277  
; PRIOR FILING DATE: 2000-03-10  
; PRIOR APPLICATION NUMBER: 60/189,139  
; PRIOR FILING DATE: 2000-03-14  
; PRIOR APPLICATION NUMBER: 60/189,140

; PRIOR FILING DATE: 2000-03-14  
; PRIOR APPLICATION NUMBER: 60/190,401  
; PRIOR FILING DATE: 2000-03-17  
; PRIOR APPLICATION NUMBER: 60/190,231  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 59  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:  
; OTHER INFORMATION: Oligonucleotide primer  
US-09-804-014A-59

Query Match 0.5%; Score 13.4; DB 1; Length 18;  
Best Local Similarity 93.3%; Pred. No. 2.9e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1602 TCCTGGCCTGGGGA 1616  
| | | | | | | | | | | | | | | | | |  
Db 17 TCCTGGCCTGTGGA 3

RESULT 3083  
US-10-239-912-5/c  
; Sequence 5, Application US/10239912  
; Publication No. US20030212012A1  
; GENERAL INFORMATION:  
; APPLICANT: Henry, James L  
; APPLICANT: Fundytus, Marian E  
; APPLICANT: Vaudreuil, Terrasse  
; TITLE OF INVENTION: Oligonucleotide For Metabotropic Glutamate Receptor  
; TITLE OF INVENTION: Type 1 (MGLUR1)  
; FILE REFERENCE: 457-107PCT  
; CURRENT APPLICATION NUMBER: US/10/239,912  
; CURRENT FILING DATE: 2002-09-26  
; PRIOR APPLICATION NUMBER: 60/144,004  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-239-912-5

Query Match 0.5%; Score 13.4; DB 1; Length 18;  
Best Local Similarity 93.3%; Pred. No. 2.9e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2162 CTCCTTTTGTGTTT 2176  
| | | | | | | | | | | | | | | | | |  
Db 15 CTCCTTTTGTGTTT 1

RESULT 3084  
US-10-239-912-16/c  
; Sequence 16, Application US/10239912  
; Publication No. US20030212012A1  
; GENERAL INFORMATION:  
; APPLICANT: Henry, James L  
; APPLICANT: Fundytus, Marian E  
; APPLICANT: Vaudreuil, Terrasse  
; TITLE OF INVENTION: Oligonucleotide For Metabotropic Glutamate Receptor  
; TITLE OF INVENTION: Type 1 (MGLUR1)  
; FILE REFERENCE: 457-107PCT  
; CURRENT APPLICATION NUMBER: US/10/239,912  
; CURRENT FILING DATE: 2002-09-26  
; PRIOR APPLICATION NUMBER: 60/144,004  
; PRIOR FILING DATE: 1999-07-15  
; NUMBER OF SEQ ID NOS: 39

; GENERAL INFORMATION:  
; APPLICANT: COLOSI, Peter  
; TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE IN RECOMBINANT ADENO-ASSOCIATED VIRUS  
; TITLE OF INVENTION: VIRION PRODUCTION  
; FILE REFERENCE: 0800-0023  
; CURRENT APPLICATION NUMBER: US/09/839,583  
; PRIOR FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 60/200,453  
; PRIOR FILING DATE: 2000-04-28  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 5  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: oligo  
US-09-839-583-5

Query Match 0.5%; Score 13.4; DB 1; Length 18;  
Best Local Similarity 93.3%; Pred. No. 2.9e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2057 ACTAGTTAATAAGTG 2071  
|||||  
Db 18 ACTAGTTAATTAGTG 4

RESULT 3078  
US-10-027-632-52400/c  
; Sequence 52400, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 52400  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-52400

Query Match 0.5%; Score 13.4; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 2.9e+03;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1241 TGTAAGAAGAAATTCACAGA 1257  
|||||  
Db 17 TGTAAGAAGAACTCCTAGA 1

RESULT 3079  
US-10-027-632-52400/c  
; Sequence 52400, Application US/10027632

; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 52400  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-52400

Query Match 0.5%; Score 13.4; DB 1; Length 18;  
Best Local Similarity 82.4%; Pred. No. 2.9e+03;  
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1241 TGTAAGAAGAAATTCACAGA 1257  
|||||  
Db 17 TGTAAGAAGAACTCCTAGA 1

RESULT 3080  
US-10-027-632-52415/c  
; Sequence 52415, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 52415  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-52415

Query Match 0.5%; Score 13.4; DB 1; Length 18;

```

; APPLICANT: Hong, Zhi
; APPLICANT: Ferrari, Eric
; TITLE OF INVENTION: HCV REPLICASE COMPLEXES
; FILE REFERENCE: IN01165
; CURRENT APPLICATION NUMBER: US/09/828,034
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: U.S. 60/195,852
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic RNA
US-09-828-034-15

Query Match          0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2165 CTTTTTTTTTTTTTTT 2179
Db 15 CTGTTTTTTTTTTTTT 1

RESULT 3074
US-09-802-640-78/c
; Sequence 78, Application US/09802640
; Publication No. US20030036057A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bonsal Aruna
; APPLICANT: Kleyn Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
; FILE REFERENCE: 24736-2048
; CURRENT APPLICATION NUMBER: US/09/802,640
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-802-640-78

Query Match          0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 647 CTGCCCGAGACCTG 661
Db 15 CTGCCCGAGATCCTG 1

RESULT 3075
US-09-924-981-24/c
; Sequence 24, Application US/09924981
; Publication No. US20030049624A1
; GENERAL INFORMATION:
; APPLICANT: Andrews, Christine N.
; APPLICANT: Olson, Ryan J.
; APPLICANT: Shultz, John W.
; TITLE OF INVENTION: Pyrophosphorolysis and Incorporation of Nucleotide
; TITLE OF INVENTION: Method for Nucleic Acid Detection
; FILE REFERENCE: 6868/82379
; CURRENT APPLICATION NUMBER: US/09/924,981
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 09/358,972
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; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/788,847
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/406,064
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 09/252,436
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 09/042,287
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-924-981-24

Query Match          0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 108 TTGGGGGCTGGGGG 122
Db 17 TTGGGGGCTGGAGGG 3

RESULT 3076
US-09-788-847-27/c
; Sequence 27, Application US/09788847
; Publication No. US20030194699A1
; GENERAL INFORMATION:
; APPLICANT: Shultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Leippe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Wood, Keith V.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: MULTIPLEX METHOD FOR NUCLEIC ACID DETECTION
; FILE REFERENCE: PRO-107.0 (6868/75532)
; CURRENT APPLICATION NUMBER: US/09/788,847
; CURRENT FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 09/406,064
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 09/252,436
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 09/042,287
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-788-847-27

Query Match          0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 108 TTGGGGGCTGGGGG 122
Db 17 TTGGGGGCTGGAGGG 3

RESULT 3077
US-09-839-583-5/c
; Sequence 5, Application US/09839583
; Publication No. US20020052485A1
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; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 703
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-703

Query Match      0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      626 CACGCCCTGGATGCC 640
      |||||:|||||
Db      2 CAGGCCCUUGGAUGCC 16

RESULT 3070
US-10-712-672-1121/c
; Sequence 1121, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBH00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1121
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-1121

Query Match      0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      458 AGCCAGCAGCAGGCC 472
      |||||:|||||
Db      16 ATCCAGCAGCAGGCC 2

RESULT 3071
US-10-712-672-1841
; Sequence 1841, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBH00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
```

```
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1841
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-1841

Query Match      0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      288 GCCCCGCGCCACCCC 302
      |||||:|||||
Db      3 GCCCCGCGCCACCCC 17

RESULT 3072
US-09-790-417-220/c
; Sequence 220, Application US/09790417
; Patent No. US20010031470A1
; GENERAL INFORMATION:
; APPLICANT: Schultz, John W
; APPLICANT: Lewis, Martin K.
; APPLICANT: Lieppe, Donna
; APPLICANT: Mandrekar, Michelle
; APPLICANT: Kephart, Daniel
; APPLICANT: Rhodes, Richard B.
; APPLICANT: Andrews, Christine A.
; APPLICANT: Hartnett, James R.
; APPLICANT: Gu, Trent
; APPLICANT: Olson, Ryan J.
; APPLICANT: Wood, Keith W.
; APPLICANT: Welch, Roy
; TITLE OF INVENTION: Nucleic Acid Detection
; FILE REFERENCE: Pro-103 6868/75528
; CURRENT APPLICATION NUMBER: US/09/790,417
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/358,972
; PRIOR FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/042,287
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 220
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: CAH oligo 7 for mutation site 2
US-09-790-417-220

Query Match      0.5%; Score 13.4; DB 1; Length 18;
Best Local Similarity 93.3%; Pred. No. 2.9e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      108 TTGGGGCTGGGGG 122
      |||||:|||||
Db      17 TTGGGGCTGGAGGG 3

RESULT 3073
US-09-828-034-15/c
; Sequence 15, Application US/09828034
; Patent No. US20020064771A1
; GENERAL INFORMATION:
; APPLICANT: Zhong, Weidong
```



```
RESULT 3065
US-10-287-949A-1634
; Sequence 1634, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1634
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-1634
```

```
Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 60.0%; Pred. No. 2.7e+03;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2698 TGGAAATTGAACTCTC 2712
      :||||:||||:|
Db 3 UGGAUUGAACUAUC 17
```

```
RESULT 3066
US-10-287-949A-3296/C
; Sequence 3296, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3296
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Mus musculus
US-10-287-949A-3296
```

```
Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2488 GTGATGGGTAATCT 2502
      ||||| |||||
Db 15 GTGATGGAGTAATCT 1
```

```
RESULT 3067
US-10-287-949A-6327
; Sequence 6327, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
```

```
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions R
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6327
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-6327
```

```
Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 86.7%; Pred. No. 2.7e+03;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1503 AGAAACACAGGAAT 1517
      ||| ||||| |||||
Db 3 AGAGACACAGGAUU 17
```

```
RESULT 3068
US-10-712-672-702
; Sequence 702, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 702
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-702
```

```
Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 2.7e+03;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 626 CAGCCCTGGATGCC 640
      || ||||| |||||
Db 3 CAGGCCCUUGGAGGCC 17
```

```
RESULT 3069
US-10-712-672-703
; Sequence 703, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MBHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
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QY 1561 GACTGCAAAAATCCT 1575  
| | | | | | | | | | | | | | | |  
Db 16 GACTGCAAAAAGTCCT 2  
  
RESULT 3056  
US-10-138-674-579/c  
; Sequence 579, Application US/10138674  
; Publication No. US20040077565A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/138,674  
; CURRENT FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 579  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-138-674-579

Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1561 GACTGCAAAAATCCT 1575  
| | | | | | | | | | | | | | | |  
Db 15 GACTGCAAAAAGTCCT 1  
  
RESULT 3057  
US-10-138-674-734  
; Sequence 734, Application US/10138674  
; Publication No. US20040077565A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/138,674  
; CURRENT FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 734  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-138-674-734

Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 13.3%; Pred. No. 2.7e+03;  
Matches 2; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

QY 2176 TTTTNTTTTAACT 2190  
: : : : : : : : : : : : : : : :  
Db 1 UUUUUUUUUUGACU 15  
  
RESULT 3058  
US-10-138-674-1634  
; Sequence 1634, Application US/10138674

; Publication No. US20040077565A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/138,674  
; CURRENT FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1634  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-138-674-1634

Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 60.0%; Pred. No. 2.7e+03;  
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2698 TGGAAATTGAACTCTC 2712  
: | | | | : : | | | | : : |  
Db 3 UGGAUUGACUAUC 17

RESULT 3059  
US-10-138-674-3296/c  
; Sequence 3296, Application US/10138674  
; Publication No. US20040077565A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/138,674  
; CURRENT FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3296  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Mus musculus  
US-10-138-674-3296

Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2488 GTGATGGGGTAATCT 2502  
| | | | | | | | | | | | | | | |  
Db 15 GTGATGGAGTAATCT 1

RESULT 3060  
US-10-138-674-6327  
; Sequence 6327, Application US/10138674  
; Publication No. US20040077565A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re  
; FILE REFERENCE: MBHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/138,674  
; CURRENT FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6327  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-138-674-6327

; PRIOR FILING DATE: 2000-06-01  
; NUMBER OF SEQ ID NOS: 1298  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1167  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:capture  
US-10-297-068-1167

Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 CCACGCACACGCCCT 633  
Db 17 CCACGCACACGCCCT 3

RESULT 3052  
US-10-297-068-1168/c  
; Sequence 1168, Application US/10297068  
; Publication No. US20030228585A1  
; GENERAL INFORMATION:  
; APPLICANT: INOKO, Hidetoshi  
; APPLICANT: KAGIYA, Taeko  
; APPLICANT: ICHIHARA, Tatsuo  
; APPLICANT: Matsumura, Yoshiyuki  
; APPLICANT: MORIYA, Shogo  
; APPLICANT: NISHIDA, Michio  
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES  
; FILE REFERENCE: 1314OP1174  
; CURRENT APPLICATION NUMBER: US/10/297,068  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: JP 2000-164798  
; PRIOR FILING DATE: 2000-06-01  
; NUMBER OF SEQ ID NOS: 1298  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1168  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:capture  
US-10-297-068-1168

Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 CCACGCACACGCCCT 633  
Db 17 CCACGCACACGCCCT 3

RESULT 3053  
US-10-608-062-26  
; Sequence 26, Application US/10608062  
; Publication No. US20040014122A1  
; GENERAL INFORMATION:  
; APPLICANT: BREEN, ALEXANDER  
; APPLICANT: SINGLETON, FREDDIE  
; TITLE OF INVENTION: DETECTION OF SPORE FORMING BACTERIA  
; FILE REFERENCE: B1113P  
; CURRENT APPLICATION NUMBER: US/10/608,062  
; CURRENT FILING DATE: 2003-06-27  
; PRIOR APPLICATION NUMBER: US 09/356,677  
; PRIOR FILING DATE: 1999-07-20  
; PRIOR APPLICATION NUMBER: US 09/085,359  
; PRIOR FILING DATE: 1998-05-27  
; NUMBER OF SEQ ID NOS: 52  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 26  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: clostridium thermoaceticum  
US-10-608-062-26

Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 368 GCCTACTCCCGTCG 382  
Db 3 GACTACTCCCGTCG 17

RESULT 3054  
US-10-138-674-577/c  
; Sequence 577, Application US/10138674  
; Publication No. US20040077565A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/138,674  
; CURRENT FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 577  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-138-674-577

Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1561 GACTGCAAAATCCT 1575  
Db 17 GACTGCAAAAGTCCT 3

RESULT 3055  
US-10-138-674-578/c  
; Sequence 578, Application US/10138674  
; Publication No. US20040077565A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Pavco, Pam  
; APPLICANT: McSwiggen, Jim  
; APPLICANT: Stinchcomb, Dan  
; APPLICANT: Escobedo, Jaime  
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel  
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
; FILE REFERENCE: MBHB00-876-N (400/049)  
; CURRENT APPLICATION NUMBER: US/10/138,674  
; CURRENT FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 20822  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 578  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-138-674-578

Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Fosnaugh, Kathy  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDI  
; FILE REFERENCE: 400/056 (MBHB01-1110)  
; CURRENT APPLICATION NUMBER: US/10/230,006  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: US 60/315,315  
; PRIOR FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 2678  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2220  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-230-006-2220

Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2002 GCTTCTTCAGAGATC 2016  
Db 16 GCTTCTTCAGAGGTC 2

RESULT 3048

US-10-230-006-2223/c  
; Sequence 2223, Application US/102300006  
; Publication No. US20030191077A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Fosnaugh, Kathy  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDI  
; FILE REFERENCE: 400/056 (MBHB01-1110)  
; CURRENT APPLICATION NUMBER: US/10/230,006  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: US 60/315,315  
; PRIOR FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 2678  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2223  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-230-006-2223

Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 828 CTGAGGTCTTCTGCT 842  
Db 16 CGGAGGTCTTCTGCT 2

RESULT 3049

US-10-297-068-1062/c  
; Sequence 1062, Application US/10297068  
; Publication No. US20030228585A1  
; GENERAL INFORMATION:  
; APPLICANT: INOKO, Hidetoshi  
; APPLICANT: KAGIYA, Taeko  
; APPLICANT: ICHIHARA, Tatsuo  
; APPLICANT: Matsumura, Yoshiyuki  
; APPLICANT: MORIYA, Shogo  
; APPLICANT: NISHIDA, Michio  
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES  
; FILE REFERENCE: 1314OP1174  
; CURRENT APPLICATION NUMBER: US/10/297,068  
; CURRENT FILING DATE: 2002-11-27

; PRIOR APPLICATION NUMBER: JP 2000-164798  
; PRIOR FILING DATE: 2000-06-01  
; NUMBER OF SEQ ID NOS: 1298  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1062  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:capture  
US-10-297-068-1062

Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 CCACGCACACGCCCT 633  
Db 17 CCACGCACACGCCCT 3

RESULT 3050

US-10-297-068-1165/c  
; Sequence 1165, Application US/10297068  
; Publication No. US20030228585A1  
; GENERAL INFORMATION:  
; APPLICANT: INOKO, Hidetoshi  
; APPLICANT: KAGIYA, Taeko  
; APPLICANT: ICHIHARA, Tatsuo  
; APPLICANT: Matsumura, Yoshiyuki  
; APPLICANT: MORIYA, Shogo  
; APPLICANT: NISHIDA, Michio  
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES  
; FILE REFERENCE: 1314OP1174  
; CURRENT APPLICATION NUMBER: US/10/297,068  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: JP 2000-164798  
; PRIOR FILING DATE: 2000-06-01  
; NUMBER OF SEQ ID NOS: 1298  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1165  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:capture  
US-10-297-068-1165

Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 619 CCACGCACACGCCCT 633  
Db 17 CCACGCACACGCCCT 3

RESULT 3051

US-10-297-068-1167/c  
; Sequence 1167, Application US/10297068  
; Publication No. US20030228585A1  
; GENERAL INFORMATION:  
; APPLICANT: INOKO, Hidetoshi  
; APPLICANT: KAGIYA, Taeko  
; APPLICANT: ICHIHARA, Tatsuo  
; APPLICANT: Matsumura, Yoshiyuki  
; APPLICANT: MORIYA, Shogo  
; APPLICANT: NISHIDA, Michio  
; TITLE OF INVENTION: KIT AND METHOD FOR DETERMINING HLA TYPES  
; FILE REFERENCE: 1314OP1174  
; CURRENT APPLICATION NUMBER: US/10/297,068  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: JP 2000-164798

; CURRENT FILING DATE: 2003-01-07
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 262
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-338-777-262

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2163 TCCTTTTTCCTTTTTCCTTTT 2177
Db 3 TCATTTTTCCTTTTTCCTTTT 17

RESULT 3043
US-10-230-006-616/c
; Sequence 616, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDIT
; FILE REFERENCE: 400/056 (MBHB01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 616
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-230-006-616

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 454 AGGCAGCCAGCAGCA 468
Db 17 AGGCAGCCAGCACCA 3

RESULT 3044
US-10-230-006-787/c
; Sequence 787, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDIT
; FILE REFERENCE: 400/056 (MBHB01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 787
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-230-006-787

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2002 GCTTCTTCAGAGATC 2016
Db 17 GCTTCTTCAGAGGTC 3

RESULT 3045
US-10-230-006-1313/c
; Sequence 1313, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDIT
; FILE REFERENCE: 400/056 (MBHB01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1313
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-230-006-1313

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 454 AGGCAGCCAGCAGCA 468
Db 15 AGGCAGCCAGCACCA 1

RESULT 3046
US-10-230-006-2137/c
; Sequence 2137, Application US/10230006
; Publication No. US20030191077A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Fosnaugh, Kathy
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: METHOD AND REAGENT FOR THE TREATMENT OF ASTHMA AND ALLERGIC CONDIT
; FILE REFERENCE: 400/056 (MBHB01-1110)
; CURRENT APPLICATION NUMBER: US/10/230,006
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 60/315,315
; PRIOR FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 2678
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2137
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-230-006-2137

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 454 AGGCAGCCAGCAGCA 468
Db 16 AGGCAGCCAGCACCA 2

RESULT 3047
US-10-230-006-2220/c
; Sequence 2220, Application US/10230006
; Publication No. US20030191077A1

US-10-238-700-2758

Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 53 GCGGGGGCGGCGGC 67  
|||||  
Db 17 GCGGGGGCGGCGGC 3  
  
RESULT 3038  
US-10-238-700-2800  
; Sequence 2800, Application US/10238700  
; Publication No. US20030153521A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level  
; FILE REFERENCE: 400/057 (MBHB01-1158-A)  
; CURRENT APPLICATION NUMBER: US/10/238,700  
; CURRENT FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: PCT/US 02/16840  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: US 60/318,471  
; PRIOR FILING DATE: 2001-09-10  
; NUMBER OF SEQ ID NOS: 4666  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2800  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-238-700-2800

Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 51 GCGGGGGCGGCGGC 65  
|||||  
Db 3 GCGGGGGCGGCGGC 17

RESULT 3039  
US-10-238-700-2802  
; Sequence 2802, Application US/10238700  
; Publication No. US20030153521A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Level  
; FILE REFERENCE: 400/057 (MBHB01-1158-A)  
; CURRENT APPLICATION NUMBER: US/10/238,700  
; CURRENT FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: PCT/US 02/16840  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: US 60/318,471  
; PRIOR FILING DATE: 2001-09-10  
; NUMBER OF SEQ ID NOS: 4666  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2802  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-238-700-2802

Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 52 CGGCGGGCGGCGGC 66  
|||||  
Db 1 CGGCGGGCGGCGGC 15

RESULT 3040  
US-10-339-782-472  
; Sequence 472, Application US/10339782  
; Publication No. US20030166026A1  
; GENERAL INFORMATION:  
; APPLICANT: Lynx Therapeutics, Inc.  
; APPLICANT: Goodman, Laurie J  
; APPLICANT: Bowen, Benjamin A  
; TITLE OF INVENTION: Identification of Specific Biomarkers for Breast Cancer Cells  
; FILE REFERENCE: 37-000110US  
; CURRENT APPLICATION NUMBER: US/10/339,782  
; CURRENT FILING DATE: 2003-01-08  
; NUMBER OF SEQ ID NOS: 495  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 472  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-339-782-472

Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2113 TCTGGTTTATAGAAA 2127  
|||||  
Db 3 TCTGGTATTAGAAA 17

RESULT 3041  
US-10-339-793-92  
; Sequence 92, Application US/10339793  
; Publication No. US20030180764A1  
; GENERAL INFORMATION:  
; APPLICANT: Lynx Therapeutics, Inc.  
; APPLICANT: Shang, Jin  
; APPLICANT: Bowen, Benjamin  
; TITLE OF INVENTION: GENES AFFECTED BY CHOLESTEROL TREATMENT AND DURING ADIPOGENESIS  
; FILE REFERENCE: 37-000310US  
; CURRENT APPLICATION NUMBER: US/10/339,793  
; CURRENT FILING DATE: 2003-01-08  
; NUMBER OF SEQ ID NOS: 443  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 92  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-339-793-92

Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1475 GATTCTAACAAAACC 1489  
|||||  
Db 1 GATCCTAACAAAACC 15

RESULT 3042  
US-10-338-777-262  
; Sequence 262, Application US/10338777  
; Publication No. US20030188343A1  
; GENERAL INFORMATION:  
; APPLICANT: Lynx Therapeutics, Inc.  
; APPLICANT: United States Department of Agriculture  
; APPLICANT: Bowen, Benjamin A  
; APPLICANT: Haudenschild, Christian D  
; APPLICANT: Buckler, Edward S  
; TITLE OF INVENTION: Identification of Genes Associated with Growth in Plants  
; FILE REFERENCE: 37-000510US  
; CURRENT APPLICATION NUMBER: US/10/338,777

QY 1425 TGATTGTTCATAGACA 1439  
Db 15 TGATTGTAATAGACA 1  
  
RESULT 3033  
US-10-287-919-1504  
; Sequence 1504, Application US/10287919  
; Publication No. US20030085830A1  
; GENERAL INFORMATION:  
; APPLICANT: Feldmann, Richard J.; Global Determinants, Inc.  
; TITLE OF INVENTION: Methanococcus jannaschii complete genome.  
; FILE REFERENCE: Jim Zegeer Law Offices - 703-684-8333  
; CURRENT APPLICATION NUMBER: US/10/287,919  
; CURRENT FILING DATE: 2002-11-05  
; NUMBER OF SEQ ID NOS: 2706  
; SOFTWARE: Proprietary  
; SEQ ID NO 1504  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Methanococcus jannaschii complete genome.  
; FEATURE:  
; LOCATION: (806407)...(806423)  
; OTHER INFORMATION: Chromosome = 1 Strand = negative ConnectronObjectNumber = 1896  
US-10-287-919-1504  
  
Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2178 TTTTTTTAACTTT 2192  
Db 2 TTTTGTTTAACTTT 16  
  
RESULT 3034  
US-10-163-552-852/c  
; Sequence 852, Application US/10163552  
; Publication No. US20030105051A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Nucleic acid treatment of diseases or conditions related to level  
; TITLE OF INVENTION: HER2  
; FILE REFERENCE: MBHB01-1653-A (400/014)  
; CURRENT APPLICATION NUMBER: US/10/163,552  
; CURRENT FILING DATE: 2002-06-06  
; NUMBER OF SEQ ID NOS: 1997  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 852  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-163-552-852  
  
Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1784 ACCCATTCCTTCCT 1798  
Db 15 ACCCATTCCTTCCT 1  
  
RESULT 3035  
US-10-156-306-3486  
; Sequence 3486, Application US/10156306  
; Publication No. US20030119017A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related  
; TITLE OF INVENTION: Levels of IKK-Gamma and PKR

; FILE REFERENCE: MBHB01-664-A (400/050)  
; CURRENT APPLICATION NUMBER: US/10/156,306  
; CURRENT FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 8013  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3486  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-156-306-3486  
  
Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 51 GCGCGGGGGCGGCG 65  
Db 1 GCGCGGGGGCGGCG 15  
  
RESULT 3036  
US-10-238-700-2710/c  
; Sequence 2710, Application US/10238700  
; Publication No. US20030153521A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Levels  
; FILE REFERENCE: 400/057 (MBHB01-1158-A)  
; CURRENT APPLICATION NUMBER: US/10/238,700  
; CURRENT FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: PCT/US 02/16840  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: US 60/318,471  
; PRIOR FILING DATE: 2001-09-10  
; NUMBER OF SEQ ID NOS: 4666  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2710  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
US-10-238-700-2710  
  
Query Match 0.5%; Score 13.4; DB 1; Length 17;  
Best Local Similarity 93.3%; Pred. No. 2.7e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 288 GCCCGCGCCACCCC 302  
Db 15 GCCCGCGCCACCCC 1  
  
RESULT 3037  
US-10-238-700-2758/c  
; Sequence 2758, Application US/10238700  
; Publication No. US20030153521A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: McSwiggen, James  
; TITLE OF INVENTION: Nucleic Acid Treatment of Diseases or Conditions Related to Levels  
; FILE REFERENCE: 400/057 (MBHB01-1158-A)  
; CURRENT APPLICATION NUMBER: US/10/238,700  
; CURRENT FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: PCT/US 02/16840  
; PRIOR FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: US 60/318,471  
; PRIOR FILING DATE: 2001-09-10  
; NUMBER OF SEQ ID NOS: 4666  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2758  
; LENGTH: 17  
; TYPE: RNA  
; ORGANISM: Homo sapiens



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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 580
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-580

Query Match          0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 193 CAAGTACGAAGAGGA 207
      ||||| ||||| ||||| |||||
Db 1 CAAGGACGAAGAGGA 15

RESULT 3030
US-10-060-756A-1561/c
; Sequence 1561, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1561
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-1561

Query Match          0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1425 TGATTGTCATAGACA 1439
      ||||| ||||| ||||| |||||
Db 17 TGATTGTAATAGACA 3

RESULT 3031
US-10-060-756A-1562/c
; Sequence 1562, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
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; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1562
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-1562

Query Match          0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1425 TGATTGTCATAGACA 1439
      ||||| ||||| ||||| |||||
Db 16 TGATTGTAATAGACA 2

RESULT 3032
US-10-060-756A-1563/c
; Sequence 1563, Application US/10060756A
; Publication No. US20030046717A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jian
; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN
; FILE REFERENCE: PB0177
; CURRENT APPLICATION NUMBER: US/10/060,756A
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/327,898
; PRIOR FILING DATE: 2001-10-09
; NUMBER OF SEQ ID NOS: 4804
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 1563
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-756A-1563

Query Match          0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 451 CACAGGCAGCCAGCA 465  
||||| |||||||

Db 3 CACAGGTAGCCAGCA 17

RESULT 3026

US-10-675-685-657

; Sequence 657, Application US/10675685

; Publication No. US20040063134A1

; GENERAL INFORMATION:

; APPLICANT: Gu, Yizhong

; APPLICANT: Shannon, Mark

; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

; FILE REFERENCE: PB0114

; CURRENT APPLICATION NUMBER: US/10/675,685

; CURRENT FILING DATE: 2003-09-30

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; NUMBER OF SEQ ID NOS: 1881

; SOFTWARE: Aeomica Sequence Listing Engine

; SEQ ID NO 657

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-675-685-657

Query Match 0.5%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 2.7e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 452 ACAGGCAGCCAGCAG 466  
||||| |||||||

Db 1 ACAGGTAGCCAGCAG 15

RESULT 3027

US-10-060-756A-578

; Sequence 578, Application US/10060756A

; Publication No. US20030046717A1

; GENERAL INFORMATION:

; APPLICANT: Zhang, Jian

; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN

; FILE REFERENCE: PB0177

; CURRENT APPLICATION NUMBER: US/10/060,756A

; CURRENT FILING DATE: 2002-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 09/864,761

; PRIOR FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/327,898

; PRIOR FILING DATE: 2001-10-09

; NUMBER OF SEQ ID NOS: 4804

; SOFTWARE: Aeomica Sequence Listing Engine

; SEQ ID NO 578

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-060-756A-578

Query Match 0.5%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 2.7e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 193 CAAGTACGAAGAGGA 207  
||||| |||||||

Db 3 CAAGGACGAAGAGGA 17

RESULT 3028

US-10-060-756A-579

; Sequence 579, Application US/10060756A

; Publication No. US20030046717A1

; GENERAL INFORMATION:

; APPLICANT: Zhang, Jian

; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN

; FILE REFERENCE: PB0177

; CURRENT APPLICATION NUMBER: US/10/060,756A

; CURRENT FILING DATE: 2002-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 09/864,761

; PRIOR FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/327,898

; PRIOR FILING DATE: 2001-10-09

; NUMBER OF SEQ ID NOS: 4804

; SOFTWARE: Aeomica Sequence Listing Engine

; SEQ ID NO 579

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-060-756A-579

Query Match 0.5%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 2.7e+03;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 193 CAAGTACGAAGAGGA 207  
||||| |||||||

Db 2 CAAGGACGAAGAGGA 16

RESULT 3029

US-10-060-756A-580

; Sequence 580, Application US/10060756A

; Publication No. US20030046717A1

; GENERAL INFORMATION:

; APPLICANT: Zhang, Jian

; TITLE OF INVENTION: HUMAN TESTIS EXPRESSED PATCHED LIKE PROTEIN

; FILE REFERENCE: PB0177

; CURRENT APPLICATION NUMBER: US/10/060,756A

; CURRENT FILING DATE: 2002-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

Db17CCGCGGTGTCTCCCC3

RESULT 3022

US-09-817-879-1379/c

Sequence 1379, Application US/09817879

Publication No. US20030171311A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals Inc.

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection

FILE REFERENCE: MBHB00-801-F

CURRENT APPLICATION NUMBER: US/09/817,879

CURRENT FILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 9703

SOFTWARE: PatentIn version 3.0

SEQ ID NO 1379

LENGTH: 17

TYPE: RNA

ORGANISM: artificial sequence

FEATURE:

NAME/KEY: misc\_feature

LOCATION:

OTHER INFORMATION: oligonucleotide substrate

US-09-817-879-1379

Query Match0.5%; Score 13.4; DB 1; Length 17;

Best Local Similarity93.3%; Pred. No. 2.7e+03;

Matches14; Conservative0; Mismatches1; Indels0; Gaps0;

QY220CCACGACGGGAGCAG234

Db15CCACCACGGGAGCAG1

RESULT 3023

US-09-817-879-3735

Sequence 3735, Application US/09817879

Publication No. US20030171311A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals Inc.

TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Hepatitis C Virus Infection

FILE REFERENCE: MBHB00-801-F

CURRENT APPLICATION NUMBER: US/09/817,879

CURRENT FILING DATE: 2001-03-26

NUMBER OF SEQ ID NOS: 9703

SOFTWARE: PatentIn version 3.0

SEQ ID NO 3735

LENGTH: 17

TYPE: RNA

ORGANISM: artificial sequence

FEATURE:

NAME/KEY: misc\_feature

LOCATION:

OTHER INFORMATION: oligonucleotide substrate

US-09-817-879-3735

Query Match0.5%; Score 13.4; DB 1; Length 17;

Best Local Similarity73.3%; Pred. No. 2.7e+03;

Matches11; Conservative3; Mismatches1; Indels0; Gaps0;

QY1385GCCGCGGTGTCTGCC1399

Db3GCCGCGGUGUCUCCC17

RESULT 3024

US-09-982-835A-6/c

Sequence 6, Application US/09982835A

Publication No. US20030235819A1

GENERAL INFORMATION:

APPLICANT: RABIN, Mark B.

TITLE OF INVENTION: MUTATIONS IN THE BRCA1 GENE

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morgan, Lewis & Bockius LLP

STREET: 1111 Pennsylvania Avenue, N.W.

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FastSEQ for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/982,835A

FILING DATE: 30-Sep-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/038,946

FILING DATE: 1998-03-12

APPLICATION NUMBER: US 09/697,149

FILING DATE: 2000-10-27

ATTORNEY/AGENT INFORMATION:

NAME: Michael S. Tuscan, Ph.D.

REGISTRATION NUMBER: 43,210

REFERENCE/DOCKET NUMBER: 44921-5047-02-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-739-3000

TELEFAX: 202-739-3001

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-982-835A-6

Query Match0.5%; Score 13.4; DB 1; Length 17;

Best Local Similarity93.3%; Pred. No. 2.7e+03;

Matches14; Conservative0; Mismatches1; Indels0; Gaps0;

QY1918TACCTTTTTCAG1932

Db15TACCTTTTTCAG1

RESULT 3025

US-10-675-685-654

Sequence 654, Application US/10675685

Publication No. US20040063134A1

GENERAL INFORMATION:

APPLICANT: Gu, Yizhong

APPLICANT: Shannon, Mark

TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

FILE REFERENCE: PB0114

CURRENT APPLICATION NUMBER: US/10/675,685

CURRENT FILING DATE: 2003-09-30

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

NUMBER OF SEQ ID NOS: 1881

SOFTWARE: Aeomica Sequence Listing Engine

SEQ ID NO 654

LENGTH: 17

TYPE: DNA

ORGANISM: Homo sapiens

US-10-675-685-654

Query Match0.5%; Score 13.4; DB 1; Length 17;

Best Local Similarity93.3%; Pred. No. 2.7e+03;

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; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1098
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-1098

Query Match          0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1654 ACTGGTTCTGCATCA 1668
Db 16 ACTGGTTCTGCATGA 2

RESULT 3018
US-09-740-332-819/c
; Sequence 819, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 819
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-819

Query Match          0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1386 CCGCGGTGTCTGCC 1400
Db 17 CCGCGGTGTCTCCCC 3

RESULT 3019
US-09-740-332-1379/c
; Sequence 1379, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1379
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
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; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-1379

Query Match          0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 220 CCACGACGGGAGCAG 234
Db 15 CCACGACGGGAGCAG 1

RESULT 3020
US-09-740-332-3735
; Sequence 3735, Application US/09740332
; Publication No. US20030125270A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: RPI 400/003
; CURRENT APPLICATION NUMBER: US/09/740,332
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9704
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3735
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-740-332-3735

Query Match          0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 73.3%; Pred. No. 2.7e+03;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1385 GCCGCGGTGTCTGCC 1399
Db 3 GCCGCGGUGUCUCCC 17

RESULT 3021
US-09-817-879-819/c
; Sequence 819, Application US/09817879
; Publication No. US20030171311A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Hepatitis C Virus Infection
; FILE REFERENCE: MBHB00-801-F
; CURRENT APPLICATION NUMBER: US/09/817,879
; CURRENT FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 9703
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 819
; LENGTH: 17
; TYPE: RNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: oligonucleotide substrate
US-09-817-879-819

Query Match          0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1386 CCGCGGTGTCTGCC 1400
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; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1192
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-1192

Query Match      0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2479 CTTTAAATGGTGATG 2493
Db 16 CTTCTAATGGTGATG 2

RESULT 3014
US-09-780-533A-2234
; Sequence 2234, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2234
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2234

Query Match      0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 40.0%; Pred. No. 2.7e+03;
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1822 TTTAGAAATCTTTTAA 1836
Db 3 UUUGGAUUCUUUUA 17

RESULT 3015
US-09-780-533A-2337
; Sequence 2337, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)

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; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2337
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-2337

Query Match      0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 55 CGGGGGCGGCGGCAG 69
Db 2 CGGCGGCGGCGGCAG 16

RESULT 3016
US-09-776-474-445/c
; Sequence 445, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Bocher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK1)
; TITLE OF INVENTION: Enzyme
; FILE REFERENCE: MBHB00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 445
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-445

Query Match      0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1654 ACTGGTTCTGCATCA 1668
Db 17 ACTGGTTCTGCATGA 3

RESULT 3017
US-09-776-474-1098/c
; Sequence 1098, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Bocher, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK1)
; TITLE OF INVENTION: Enzyme
; FILE REFERENCE: MBHB00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474

```

; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,674
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: No. US20030054346A1 available
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/021,701
; FILING DATE: 10-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Wendy A.
; REGISTRATION NUMBER: 36,697
; REFERENCE/DOCKET NUMBER: 10971464-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-236-2386
; TELEFAX: 650-852-8063
;
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-09-784-674-112

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 141 GACTGTTTGGGGGA 155
| | | | | | | | | |
Db 1 GTCTGTTTGGGGGA 15

RESULT 3010
US-09-956-857-9/c
; Sequence 9, Application US/09956857
; Publication No. US20030054356A1
; GENERAL INFORMATION:
; APPLICANT: Jacobson, James W.
; APPLICANT: Burroughs, Jennifer L.
; APPLICANT: Oliver, Kerry G.
; TITLE OF INVENTION: Multiple Reporter Read-Out Bioassays
; FILE REFERENCE: 215063.01001
; CURRENT APPLICATION NUMBER: US/09/956,857
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/234,430
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-956-857-9

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1918 TACCTTTTTCAG 1932
| | | | | | | | | |
Db 15 TACCTTTTTCG 1

RESULT 3011
US-09-780-533A-398
; Sequence 398, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 398
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-398

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 40.0%; Pred. No. 2.7e+03;
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1822 TTTAGATCTTTTAA 1836
::: | | | | | | | | | |
Db 1 UUUGGAUUCUUUUA 15

RESULT 3012
US-09-780-533A-929/c
; Sequence 929, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haerberli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 929
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-780-533A-929

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 558 TGGAGGCGGCGCGG 572
| | | | | | | | | |
Db 16 TGGAGGCGGCGCGG 2

RESULT 3013
US-09-780-533A-1192/c
; Sequence 1192, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:









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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2672
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2672
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```
Query Match          0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      47 GCGCGCGCGGGGCG 61
      |||||
Db      2 GGGCGCGCGGGGCG 16
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RESULT 2998
US-09-866-108-2673
; Sequence 2673, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
```

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
; SOFTWARE: Aeomica Sequence Listing Engine
; SEQ ID NO 2673
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108-2673

Query Match          0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      47 GCGCGCGCGGGGCG 61
      |||||
Db      1 GGGCGCGCGGGGCG 15

RESULT 2999
US-09-866-108-10726
; Sequence 10726, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/266,860
; PRIOR FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 15752
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Oligonucleotide structure fo
; OTHER INFORMATION: molecular beacon
US-10-164-915-3

Query Match 0.5%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTGTGTTTGTGTTT 2180
Db 16 TTTTGTGTTTGTGTTT 2

RESULT 2991
US-09-132-231-18
; Sequence 18, Application US/09132231A
; Publication No. US20030198950A1
; GENERAL INFORMATION:
; APPLICANT: HORWITZ, Marshall S.
; APPLICANT: LOEB, Lawrence A.
; TITLE OF INVENTION: METHOD FOR PRODUCING NOVEL DNA SEQUENCES WITH
; FILE REFERENCE: 032425-001
; CURRENT APPLICATION NUMBER: US/09/132,231A
; CURRENT FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: US 08/316,415
; PRIOR FILING DATE: 1994-09-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-132-231-18

Query Match 0.5%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GAGCCGCCGATGCGT 20
Db 2 GAGCCGCCGATACGT 16

RESULT 2992
US-10-138-674-5864/c
; Sequence 5864, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime

; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5864
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-5864

Query Match 0.5%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1561 GACTGCAAAAATCCT 1575
Db 16 GACTGCAAAAAGTCCT 2

RESULT 2993
US-10-287-949A-5864/c
; Sequence 5864, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5864
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-5864

Query Match 0.5%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 2.4e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1561 GACTGCAAAAATCCT 1575
Db 16 GACTGCAAAAAGTCCT 2

RESULT 2994
US-10-156-306-526/c
; Sequence 526, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: McSwiggen, James

; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; FILE REFERENCE: MBHB01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 526
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-156-306-526

Query Match 0.5%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 2.7e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2783 TTGAAAAAATAAAA 2797
Db 15 TTTAAAAAATAAAA 1

RESULT 2995
US-09-866-108-2060/c
; Sequence 2060, Application US/09866108
; Patent No. US20020048800A1
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang



; PRIOR APPLICATION NUMBER: US/09/531,488B
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 08/638,941
; PRIOR FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: UK 8515686
; PRIOR FILING DATE: 1985-06-20
; PRIOR APPLICATION NUMBER: UK 8600754
; PRIOR FILING DATE: 1986-01-14
; PRIOR APPLICATION NUMBER: 08/370,356
; PRIOR FILING DATE: 1995-01-09
; PRIOR APPLICATION NUMBER: 08/073,043
; PRIOR FILING DATE: 1993-06-08
; PRIOR APPLICATION NUMBER: 07/385,952
; PRIOR FILING DATE: 1989-07-28
; PRIOR APPLICATION NUMBER: 06/875,880
; PRIOR FILING DATE: 1986-06-18
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-10-279-061-15

Query Match 0.5%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1264 CAGCCAGACCGGAC 1278
||| |||||
Db 1 CAGCCAGACCGGAC 15

RESULT 2988
US-10-360-275-12
; Sequence 12, Application US/10360275
; Publication No. US2004001464A1
; GENERAL INFORMATION:
; APPLICANT: Active Motif
; APPLICANT: Efimov, Vladimir
; APPLICANT: Fernandez, Joseph
; APPLICANT: Archdeacon, Dorothy
; APPLICANT: Archdeacon, John
; APPLICANT: Choob, Mikhail
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES AND METHODS OF USE FOR MODULATING GENE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: AM102.P.1.1.IUS
; CURRENT APPLICATION NUMBER: US/10/360,275
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/072,975
; PRIOR FILING DATE: 2002-02-09
; PRIOR APPLICATION NUMBER: US 09/805,296
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/189,190
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Sequence
US-10-360-275-12

Query Match 0.5%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTCTTTT 2180
||||| |||||
Db 1 TTTTCTTTT 15

RESULT 2989
US-10-360-275-12/c
; Sequence 12, Application US/10360275
; Publication No. US2004001464A1
; GENERAL INFORMATION:
; APPLICANT: Active Motif
; APPLICANT: Efimov, Vladimir
; APPLICANT: Fernandez, Joseph
; APPLICANT: Archdeacon, Dorothy
; APPLICANT: Archdeacon, John
; APPLICANT: Choob, Mikhail
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES AND METHODS OF USE FOR MODULATING GENE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: AM102.P.1.1.IUS
; CURRENT APPLICATION NUMBER: US/10/360,275
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/072,975
; PRIOR FILING DATE: 2002-02-09
; PRIOR APPLICATION NUMBER: US 09/805,296
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: US 60/189,190
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Sequence
US-10-360-275-12

Query Match 0.5%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800
||||| |||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 2990
US-10-164-915-3/c
; Sequence 3, Application US/10164915
; Publication No. US20030148391A1
; GENERAL INFORMATION:
; APPLICANT: Salafsky, Joshua S.
; TITLE OF INVENTION: Method Using a Surface-Selective No. US20030148391A1linear Optic
; TITLE OF INVENTION: for Detection of Interactions Involving a Conformational Change
; FILE REFERENCE: 11100-035-999
; CURRENT APPLICATION NUMBER: US/10/164,915
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/253,862
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/260,249
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/265,775
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/278,941
; PRIOR FILING DATE: 2001-01-27
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 3
; LENGTH: 16
; TYPE: DNA

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RESULT 2984
US-10-072-975-12/c
; Sequence 12, Application US/10072975
; Publication No. US20030059789A1
; GENERAL INFORMATION:
; APPLICANT: Active Motif
; APPLICANT: Efimov, Vladimir
; APPLICANT: Fernandez, Joseph
; APPLICANT: Archdeacon, Dorothy
; APPLICANT: Archdeacon, John
; APPLICANT: Chakhmakhcheau, Oksana
; APPLICANT: Buryakova, Alla
; APPLICANT: Choob, Mikhail
; APPLICANT: Hondorp, Kyle
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE
; FILE REFERENCE: AM102.P.1.IUS
; CURRENT APPLICATION NUMBER: US/10/072,975
; CURRENT FILING DATE: 2002-02-09
; PRIOR APPLICATION NUMBER: US 60/189,190
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/250,334
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 09/805,296
; PRIOR FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: PCT/US01/0811
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Sequence
US-10-072-975-12
Query Match 0.5%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800
Db 15 AAAAAAAAAAGAAAAA 1

RESULT 2985
US-10-051-436-12
; Sequence 12, Application US/10051436
; Publication No. US20030138045A1
; GENERAL INFORMATION:
; APPLICANT: Active Motif
; APPLICANT: Efimov, Vladimir
; APPLICANT: Fernandez, Joseph
; APPLICANT: Archdeacon, Dorothy
; APPLICANT: Archdeacon, John
; APPLICANT: Chakhmakhcheau, Oksana
; APPLICANT: Buryakova, Alla
; APPLICANT: Choob, Mikhail
; APPLICANT: Hondorp, Kyle
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE
; FILE REFERENCE: AM102.P.1US
; CURRENT APPLICATION NUMBER: US/10/051,436
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/189,190
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/250,334
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Sequence
US-10-072-975-12
Query Match 0.5%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800
Db 15 AAAAAAAAAAGAAAAA 1

RESULT 2986
US-10-051-436-12/c
; Sequence 12, Application US/10051436
; Publication No. US20030138045A1
; GENERAL INFORMATION:
; APPLICANT: Active Motif
; APPLICANT: Efimov, Vladimir
; APPLICANT: Fernandez, Joseph
; APPLICANT: Archdeacon, Dorothy
; APPLICANT: Archdeacon, John
; APPLICANT: Chakhmakhcheau, Oksana
; APPLICANT: Buryakova, Alla
; APPLICANT: Choob, Mikhail
; APPLICANT: Hondorp, Kyle
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE
; FILE REFERENCE: AM102.P.1US
; CURRENT APPLICATION NUMBER: US/10/051,436
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/189,190
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/250,334
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Sequence
US-10-051-436-12
Query Match 0.5%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800
Db 15 AAAAAAAAAAGAAAAA 1

RESULT 2987
US-10-279-061-15
; Sequence 15, Application US/10279061
; Publication No. US20030170811A1
; GENERAL INFORMATION:
; APPLICANT: UEDA, IKUO
; APPLICANT: NIWA, MINEO
; APPLICANT: SAITO, YOSHIMASA
; APPLICANT: YAMADA, HISASHI
; APPLICANT: ISHII, YOSHINORI
; TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF ALPHA-HUMAN ATRIAL NATRIURETIC POLYI
; FILE REFERENCE: 0018-1100-0CONT
; CURRENT APPLICATION NUMBER: US/10/279,061
; CURRENT FILING DATE: 2002-10-24
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; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Sequence
US-10-051-436-12
Query Match 0.5%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTTCCTTTTTCCTTTT 2180
Db 1 TTTTTCCTTTTTCCTTTT 15

RESULT 2986
US-10-051-436-12/c
; Sequence 12, Application US/10051436
; Publication No. US20030138045A1
; GENERAL INFORMATION:
; APPLICANT: Active Motif
; APPLICANT: Efimov, Vladimir
; APPLICANT: Fernandez, Joseph
; APPLICANT: Archdeacon, Dorothy
; APPLICANT: Archdeacon, John
; APPLICANT: Chakhmakhcheau, Oksana
; APPLICANT: Buryakova, Alla
; APPLICANT: Choob, Mikhail
; APPLICANT: Hondorp, Kyle
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE
; FILE REFERENCE: AM102.P.1US
; CURRENT APPLICATION NUMBER: US/10/051,436
; CURRENT FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/189,190
; PRIOR FILING DATE: 2000-03-14
; PRIOR APPLICATION NUMBER: US 60/250,334
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Synthetic Sequence
US-10-051-436-12
Query Match 0.5%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.2e+03;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2786 AAAAAAAAAAAAAA 2800
Db 15 AAAAAAAAAAGAAAAA 1

RESULT 2987
US-10-279-061-15
; Sequence 15, Application US/10279061
; Publication No. US20030170811A1
; GENERAL INFORMATION:
; APPLICANT: UEDA, IKUO
; APPLICANT: NIWA, MINEO
; APPLICANT: SAITO, YOSHIMASA
; APPLICANT: YAMADA, HISASHI
; APPLICANT: ISHII, YOSHINORI
; TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF ALPHA-HUMAN ATRIAL NATRIURETIC POLYI
; FILE REFERENCE: 0018-1100-0CONT
; CURRENT APPLICATION NUMBER: US/10/279,061
; CURRENT FILING DATE: 2002-10-24
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RESULT 2981  
US-09-805-296D-12/c  
; Sequence 12, Application US/09805296D  
; Patent No. US2002015989A1  
; GENERAL INFORMATION:  
; APPLICANT: Active Motif  
; APPLICANT: Efimov, Vladimir  
; APPLICANT: Fernandez, Joseph  
; APPLICANT: Archdeacon, Dorothy  
; APPLICANT: Archdeacon, John  
; APPLICANT: Chakhmakhcheau, Oksana  
; APPLICANT: Buryakova, Alla  
; APPLICANT: Choob, Mikhail  
; APPLICANT: Hondorp, Kyle  
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE  
; FILE REFERENCE: AM102.P.1US  
; CURRENT APPLICATION NUMBER: US/09/805,296D  
; CURRENT FILING DATE: 2001-03-13  
; PRIOR APPLICATION NUMBER: US 60/189,190  
; PRIOR FILING DATE: 2000-03-14  
; PRIOR APPLICATION NUMBER: US 60/250,334  
; PRIOR FILING DATE: 2000-11-30  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Synthetic Sequence  
US-09-805-296D-12  
  
Query Match 0.5%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2.2e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2786 AAAAAAAAAAAAAA 2800  
Db 15 AAAAAAAAAAAAAA 1  
  
RESULT 2982  
US-10-132-002-13  
; Sequence 13, Application US/10132002  
; Publication No. US2003002204A1  
; GENERAL INFORMATION:  
; APPLICANT: Lansdorp, Peter  
; TITLE OF INVENTION: Method for Detecting Multiple Copies of  
; a Repeat Sequence in a Nucleic Acid Molecule  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOWSON & HOWSON  
; STREET: 321 No. US2003002204A1ristown Road  
; CITY: Spring House  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19477  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/132,002  
; FILING DATE: 25-Apr-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/730,635  
; FILING DATE: 11-OCT-1996

ATTORNEY/AGENT INFORMATION:  
; NAME: Bak, Mary E.  
; REGISTRATION NUMBER: 31,215  
; REFERENCE/DOCKET NUMBER: B&P7USA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (215) 540-9200  
; TELEFAX: (215) 540-5818  
; TELEX: N/A  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-10-132-002-13  
  
Query Match 0.5%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2.2e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 53 GGCGGGGGCGCGGC 67  
Db 1 GGCGGGGGCGCGGC 15  
  
RESULT 2983  
US-10-072-975-12  
; Sequence 12, Application US/10072975  
; Publication No. US20030059789A1  
; GENERAL INFORMATION:  
; APPLICANT: Active Motif  
; APPLICANT: Efimov, Vladimir  
; APPLICANT: Fernandez, Joseph  
; APPLICANT: Archdeacon, Dorothy  
; APPLICANT: Archdeacon, John  
; APPLICANT: Chakhmakhcheau, Oksana  
; APPLICANT: Buryakova, Alla  
; APPLICANT: Choob, Mikhail  
; APPLICANT: Hondorp, Kyle  
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE  
; FILE REFERENCE: AM102.P.1.1US  
; CURRENT APPLICATION NUMBER: US/10/072,975  
; CURRENT FILING DATE: 2002-02-09  
; PRIOR APPLICATION NUMBER: US 60/189,190  
; PRIOR FILING DATE: 2000-03-14  
; PRIOR APPLICATION NUMBER: US 60/250,334  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: 09/805,296  
; PRIOR FILING DATE: 2001-03-13  
; PRIOR APPLICATION NUMBER: PCT/US01/0811  
; PRIOR FILING DATE: 2001-03-13  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Synthetic Sequence  
US-10-072-975-12  
  
Query Match 0.5%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2.2e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2166 TTTTTCCTTTT 2180  
Db 1 TTTTTCCTTTT 15

; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (5)..(6)  
; OTHER INFORMATION: The residue between C at position 5 and T at position 6 is acridi  
; OTHER INFORMATION: ne  
US-10-239-595-6

Query Match 0.5%; Score 13.6; DB 1; Length 22;  
Best Local Similarity 80.0%; Pred. No. 3.4e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2785 GAAAAA..... 2804  
||| ||||| ||||| |||  
Db 21 GAAGAAAAAGAGAAAGAAA 2

RESULT 2978  
US-09-504-231A-824/c  
; Sequence 824, Application US/09504231A  
; Patent No. US20020013458A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth  
; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATE  
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION  
; FILE REFERENCE: IPI 247/282  
; CURRENT APPLICATION NUMBER: US/09/504,231A  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR APPLICATION NUMBER: 09/274,553  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3242  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 824  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-504-231A-824

Query Match 0.5%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2.2e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2204 CTTCAAATGGGAGAC 2218  
||||||| |||||  
Db 15 CTTCAAATAGGAGAC 1

RESULT 2979  
US-09-274-553D-824/c  
; Sequence 824, Application US/09274553D  
; Patent No. US20020082225A1  
; GENERAL INFORMATION:  
; APPLICANT: Blatt, Lawrence  
; APPLICANT: McSwiggen, James  
; APPLICANT: Roberts, Beth

; APPLICANT: Pavco, Pamela  
; APPLICANT: Macejak, Dennis  
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELATEI  
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION  
; FILE REFERENCE: IPI 247/282  
; CURRENT APPLICATION NUMBER: US/09/274,553D  
; CURRENT FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 09/257,608  
; PRIOR FILING DATE: 1999-02-24  
; PRIOR APPLICATION NUMBER: 60/100,842  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: 60/083,217  
; PRIOR FILING DATE: 1998-04-27  
; NUMBER OF SEQ ID NOS: 3148  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 824  
; LENGTH: 15  
; TYPE: RNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target  
US-09-274-553D-824

Query Match 0.5%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2.2e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2204 CTTCAAATGGGAGAC 2218  
||||||| |||||  
Db 15 CTTCAAATAGGAGAC 1

RESULT 2980  
US-09-805-296D-12  
; Sequence 12, Application US/09805296D  
; Patent No. US20020155989A1  
; GENERAL INFORMATION:  
; APPLICANT: Active Motif  
; APPLICANT: Efimov, Vladimir  
; APPLICANT: Fernandez, Joseph  
; APPLICANT: Archdeacon, Dorothy  
; APPLICANT: Archdeacon, John  
; APPLICANT: Chakhmakcheau, Oksana  
; APPLICANT: Buryakova, Alla  
; APPLICANT: Choob, Mikhail  
; APPLICANT: Hondorp, Kyle  
; TITLE OF INVENTION: OLIGONUCLEOTIDE ANALOGUES, METHODS OF SYNTHESIS AND METHODS OF USE  
; FILE REFERENCE: AM102.P.1US  
; CURRENT APPLICATION NUMBER: US/09/805,296D  
; CURRENT FILING DATE: 2001-03-13  
; PRIOR APPLICATION NUMBER: US 60/189,190  
; PRIOR FILING DATE: 2000-03-14  
; PRIOR APPLICATION NUMBER: US 60/250,334  
; PRIOR FILING DATE: 2000-11-30  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 15  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Construct  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Synthetic Sequence  
US-09-805-296D-12

Query Match 0.5%; Score 13.4; DB 1; Length 15;  
Best Local Similarity 93.3%; Pred. No. 2.2e+03;  
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2166 TTTTTCCTTTTTCCTTTT 2180  
||||||| |||||  
Db 1 TTTTTCCTTTTTCCTTTT 15





; OTHER INFORMATION: human GFAT antisense  
US-10-688-706-2110

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2782 ATTGAAAAAATAAAAAAAAAA 2801  
| | | | | | | | | | | | | | | | | | | |  
Db 1 ATTTAAAAACAAAAACAGAAA 20

RESULT 2969  
US-10-688-706-2110/c  
; Sequence 2110, Application US/10688706  
; Publication No. US20040102412A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corp.  
; APPLICANT: Broschat, Kay  
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION  
; FILE REFERENCE: 01393/1  
; CURRENT APPLICATION NUMBER: US/10/688,706  
; CURRENT FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: 60/419,268  
; PRIOR FILING DATE: 2002-10-17  
; NUMBER OF SEQ ID NOS: 3071  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2110  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: human GFAT antisense  
US-10-688-706-2110

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2171 TTTTTTTTTTTTTTTAACT 2190  
| | | | | | | | | | | | | | | | | | | |  
Db 20 TTCTGTTTGTGTTTAAAT 1

RESULT 2970  
US-10-688-706-2269/c  
; Sequence 2269, Application US/10688706  
; Publication No. US20040102412A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corp.  
; APPLICANT: Broschat, Kay  
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION  
; FILE REFERENCE: 01393/1  
; CURRENT APPLICATION NUMBER: US/10/688,706  
; CURRENT FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: 60/419,268  
; PRIOR FILING DATE: 2002-10-17  
; NUMBER OF SEQ ID NOS: 3071  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2269  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: human GFAT antisense  
US-10-688-706-2269

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2169 TTTTTTTTTTTTTTTAA 2188  
| | | | | | | | | | | | | | | | | | | |

Db 20 TGTTTCTGTTTGTGTTTAA 1

RESULT 2971  
US-10-688-706-2404/c  
; Sequence 2404, Application US/10688706  
; Publication No. US20040102412A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corp.  
; APPLICANT: Broschat, Kay  
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION  
; FILE REFERENCE: 01393/1  
; CURRENT APPLICATION NUMBER: US/10/688,706  
; CURRENT FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: 60/419,268  
; PRIOR FILING DATE: 2002-10-17  
; NUMBER OF SEQ ID NOS: 3071  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2404  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: human GFAT antisense  
US-10-688-706-2404

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2255 TTTATTGCAATATTTATTC 2274  
| | | | | | | | | | | | | | | | | | | |  
Db 20 TTTATTGAAATTTGTTTC 1

RESULT 2972  
US-10-688-706-2457/c  
; Sequence 2457, Application US/10688706  
; Publication No. US20040102412A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corp.  
; APPLICANT: Broschat, Kay  
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION  
; FILE REFERENCE: 01393/1  
; CURRENT APPLICATION NUMBER: US/10/688,706  
; CURRENT FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: 60/419,268  
; PRIOR FILING DATE: 2002-10-17  
; NUMBER OF SEQ ID NOS: 3071  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2457  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: artificial  
; FEATURE:  
; OTHER INFORMATION: human GFAT antisense  
US-10-688-706-2457

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1176 CTCATCTTGGAGCAGAAAT 1195  
| | | | | | | | | | | | | | | | | | | |  
Db 20 CTGAGCATGGATGACGAAAT 1

RESULT 2973  
US-10-688-706-2467/c  
; Sequence 2467, Application US/10688706  
; Publication No. US20040102412A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacia Corp.

```
Db      20 CTCCTTAGCTGAACCTCTCT 1
RESULT 2964
US-10-304-124-43/c
; Sequence 43, Application US/10304124
; Publication No. US20040102404A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lawrence Panasci
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF KU86 EXPRESSION
; FILE REFERENCE: HTS-0015
; CURRENT APPLICATION NUMBER: US/10/304,124
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-124-43
Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1238 CTGTGTAAGAATTCACAGA 1257
        ||||| || ||||| |||||
Db      20 CTGTGGAATGAATACACACA 1

RESULT 2965
US-10-304-124-77
; Sequence 77, Application US/10304124
; Publication No. US20040102404A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lawrence Panasci
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF KU86 EXPRESSION
; FILE REFERENCE: HTS-0015
; CURRENT APPLICATION NUMBER: US/10/304,124
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 77
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-304-124-77
Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1238 CTGTGTAAGAATTCACAGA 1257
        ||||| || ||||| |||||
Db      1 CTGTGGAATGAATACACACA 20

RESULT 2966
US-10-688-706-385
; Sequence 385, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2110
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; CURRENT FILING DATE: 2003-10-17
```

```
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 385
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-385
Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2592 TTTAATTGAAACTCTCTGTT 2611
        ||||| || ||||| |||||
Db      1 TTTAATAGCAGCTCTGTGTT 20

RESULT 2967
US-10-688-706-394
; Sequence 394, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 394
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: human GFAT antisense
US-10-688-706-394
Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2591 ATTTAATTGAAACTCTCTGT 2610
        ||||| || ||||| |||||
Db      1 ATTTAATAGCAGCTCTGTGT 20

RESULT 2968
US-10-688-706-2110
; Sequence 2110, Application US/10688706
; Publication No. US20040102412A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corp.
; APPLICANT: Broschat, Kay
; TITLE OF INVENTION: ANTISENSE MODULATION OF GFAT EXPRESSION
; FILE REFERENCE: 01393/1
; CURRENT APPLICATION NUMBER: US/10/688,706
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: 60/419,268
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 3071
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2110
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
```

```
QY      2643 GGGCTGAACCCCTAAGGTGAG 2662
      |||||
Db      20 GGGCTGAACCCCAAGCAGAG 1
      |||||

RESULT 2959
US-10-302-027-17
; Sequence 17, Application US/10302027
; Publication No. US20040102391A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF GANKYRIN EXPRESSION
; FILE REFERENCE: PTS-0068
; CURRENT APPLICATION NUMBER: US/10/302,027
; CURRENT FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 135
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-302-027-17

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1919 ACCTTTTTCAGTGTAA 1938
      |||||
Db      1 ACATTTTTCAGAGTAAA 20
      |||||

RESULT 2960
US-10-303-420-27
; Sequence 27, Application US/10303420
; Publication No. US20040102398A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF B7H EXPRESSION
; FILE REFERENCE: RTS-0417
; CURRENT APPLICATION NUMBER: US/10/303,420
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 271
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-303-420-27

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      587 GATGCCTACCGCGCTCCGA 606
      |||||
Db      1 GCTGCCTACCATCGCTCTGA 20
      |||||

RESULT 2961
US-10-303-420-183/c
; Sequence 183, Application US/10303420
; Publication No. US20040102398A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF B7H EXPRESSION
; FILE REFERENCE: RTS-0417
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```
; CURRENT APPLICATION NUMBER: US/10/303,420
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 271
; SEQ ID NO 183
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-303-420-183

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      587 GATGCCTACCGCGCTCCGA 606
      |||||
Db      20 GCTGCCTACCATCGCTCTGA 1
      |||||

RESULT 2962
US-10-304-113-49
; Sequence 49, Application US/10304113
; Publication No. US20040102623A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF PAK1 EXPRESSION
; FILE REFERENCE: RTS-0415
; CURRENT APPLICATION NUMBER: US/10/304,113
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 167
; SEQ ID NO 49
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-113-49

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2589 CTATTTAATTGAACTCTCT 2608
      |||||
Db      1 CTCTTAGCTGAACCTCTCT 20
      |||||

RESULT 2963
US-10-304-113-127/c
; Sequence 127, Application US/10304113
; Publication No. US20040102623A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF PAK1 EXPRESSION
; FILE REFERENCE: RTS-0415
; CURRENT APPLICATION NUMBER: US/10/304,113
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 167
; SEQ ID NO 127
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-304-113-127

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2589 CTATTTAATTGAACTCTCT 2608
      |||||
Db      1 CTCTTAGCTGAACCTCTCT 20
      |||||

RESULT 2964
US-10-304-113-127/c
; Sequence 127, Application US/10304113
; Publication No. US20040102623A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF PAK1 EXPRESSION
; FILE REFERENCE: RTS-0415
; CURRENT APPLICATION NUMBER: US/10/304,113
; CURRENT FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 167
; SEQ ID NO 127
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-304-113-127

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY      458 AGCCAGCAGCAGGCGCTGGCC 477
      ||||| | | | | | | | |
Db      1 AGCCAGTATCTGGCCTGCC 20

RESULT 2954
US-10-637-009-43
; Sequence 43, Application US/10637009
; Publication No. US20040091920A1
; GENERAL INFORMATION:
; APPLICANT: TSUJI, Toru
; APPLICANT: YANAGAWA, Hiroshi
; TITLE OF INVENTION: Method of Constructing DNA Library and Utilization Thereof
; FILE REFERENCE: P24048
; CURRENT APPLICATION NUMBER: US/10/637,009
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: PCT 2000-293692
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 10/396334
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: PCT 2001-29138
; PRIOR FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Primer
US-10-637-009-43

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      596 CGCCGCTCCGACCTGCTGCT 615
      ||||| | | | | | | | |
Db      1 CCCCTCTATGACCTGCTGCT 20

RESULT 2955
US-10-298-404-21/c
; Sequence 21, Application US/10298404
; Publication No. US20040097443A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF JERKY-LIKE 1 EXPRESSION
; FILE REFERENCE: HTS-0011
; CURRENT APPLICATION NUMBER: US/10/298,404
; CURRENT FILING DATE: 2002-11-16
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-298-404-21

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1720 TTGGACCTATTATCAGAAG 1739
      ||||| | | | | | | | |
Db      20 TTGTACAGATAATCAGAAG 1

RESULT 2956
US-10-298-404-56
; Sequence 56, Application US/10298404
```

```
; Publication No. US20040097443A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF JERKY-LIKE 1 EXPRESSION
; FILE REFERENCE: HTS-0011
; CURRENT APPLICATION NUMBER: US/10/298,404
; CURRENT FILING DATE: 2002-11-16
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 56
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-298-404-56

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1720 TTGGACCTATTATCAGAAG 1739
      ||||| | | | | | | | |
Db      1 TTGTACAGATAATCAGAAG 20

RESULT 2957
US-10-299-089-76
; Sequence 76, Application US/10299089
; Publication No. US20040097447A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF INTERLEUKIN 22 RECEPTOR EXPRESSION
; FILE REFERENCE: RTS-0440
; CURRENT APPLICATION NUMBER: US/10/299,089
; CURRENT FILING DATE: 2002-11-16
; NUMBER OF SEQ ID NOS: 144
; SEQ ID NO 76
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-299-089-76

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2643 GGGCTGAACCCCTAAGGTGAG 2662
      ||||| | | | | | | | |
Db      1 GGGCTGAACCCCAAGGCAGAG 20

RESULT 2958
US-10-299-089-136/c
; Sequence 136, Application US/10299089
; Publication No. US20040097447A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF INTERLEUKIN 22 RECEPTOR EXPRESSION
; FILE REFERENCE: RTS-0440
; CURRENT APPLICATION NUMBER: US/10/299,089
; CURRENT FILING DATE: 2002-11-16
; NUMBER OF SEQ ID NOS: 144
; SEQ ID NO 136
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-299-089-136

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

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RESULT 2949
US-10-280-183A-421
; Sequence 421, Application US/10280183A
; Publication No. US20040081964A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Bachmanov, Alexander A
; APPLICANT: Beauchamp, Gary K.
; APPLICANT: Chatterjee, Aurobindo
; APPLICANT: De Jong, Pieter J.
; APPLICANT: Li, Shanru
; APPLICANT: Li, Xia
; APPLICANT: Ohmen, Jeffrey D
; APPLICANT: Reed, Danielle R.
; APPLICANT: Ross, David
; APPLICANT: Tordoff, Michael G.
; TITLE OF INVENTION: GENE AND SEQUENCE VARIATION ASSOCIATED WITH SENSING
; FILE REFERENCE: PC18306A
; CURRENT APPLICATION NUMBER: US/10/280,183A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/200,794
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 421
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Mouse
US-10-280-183A-421

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1562 ACTGCAAAATCCTTCTCCA 1581
      ||||| ||| |||||
Db       1 ACTGCAATGTCCAACCTCCA 20

RESULT 2950
US-10-292-849-60/c
; Sequence 60, Application US/10292849
; Publication No. US20040092463A1
; GENERAL INFORMATION:
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: MODULATION OF PIM-1 EXPRESSION
; FILE REFERENCE: RTS-0170
; CURRENT APPLICATION NUMBER: US/10/292,849
; CURRENT FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 138
; SEQ ID NO 60
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-292-849-60

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1260 TTCTCAGCCCAAGACCGGACA 1279
      ||| ||||| ||| |||
Db       20 TTCAAAGCCCAAGACCTCACA 1

RESULT 2951
US-10-292-849-118
; Sequence 118, Application US/10292849
```

```
; Publication No. US20040092463A1
; GENERAL INFORMATION:
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: MODULATION OF PIM-1 EXPRESSION
; FILE REFERENCE: RTS-0170
; CURRENT APPLICATION NUMBER: US/10/292,849
; CURRENT FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 138
; SEQ ID NO 118
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-292-849-118

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1260 TTCTCAGCCCAAGACCGGACA 1279
      ||| ||||| ||| |||
Db       1 TTCAAAGCCCAAGACCTCACA 20

RESULT 2952
US-10-293-864-36/c
; Sequence 36, Application US/10293864
; Publication No. US20040092465A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF HUNTINGTIN INTERACTING PROTEIN 1 EXPRESSION
; FILE REFERENCE: RTS-0432
; CURRENT APPLICATION NUMBER: US/10/293,864
; CURRENT FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 36
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-293-864-36

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      458 AGCCAGCAGCAGCGCTGGCC 477
      ||||| ||| ||||| |||
Db       20 AGCCAGTATCTGGCCTGCC 1

RESULT 2953
US-10-293-864-113
; Sequence 113, Application US/10293864
; Publication No. US20040092465A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF HUNTINGTIN INTERACTING PROTEIN 1 EXPRESSION
; FILE REFERENCE: RTS-0432
; CURRENT APPLICATION NUMBER: US/10/293,864
; CURRENT FILING DATE: 2002-11-11
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 113
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-293-864-113

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
; Sequence 169, Application US/10309290
; Publication No. US20040023241A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chillakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphey, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glenda
; APPLICANT: Starling, Gary
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Haihong
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 169
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-10-309-290-169

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1650 CTTCACTGGTTCTGCATCAC 1669
Db      1 CTTCCCTGGTTGAGCACCCAC 20
      ||||| ||||| ||||| |||||
      ||||| ||||| ||||| |||||
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RESULT 2947
US-10-703-864-64
; Sequence 64, Application US/10703864
; Publication No. US20040077580A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: Susan Murray
; APPLICANT: Madeline M. Butler
; APPLICANT: Nicholas M. Dean
; TITLE OF INVENTION: ANTISENSE MODULATION OF PI3K P85 EXPRESSION
; FILE REFERENCE: ISIS0057-102 (ISPH-0519)
; CURRENT APPLICATION NUMBER: US/10/703,864
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: US/09/715,983
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-703-864-64

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2110 CCTTCTGGTTTGTAGAACT 2129
Db      1 CCTGCTGGTATTGGACACT 20
      ||| ||||| ||||| |||||
      ||| ||||| ||||| |||||

RESULT 2948
US-10-280-183A-236/c
; Sequence 236, Application US/10280183A
; Publication No. US20040081964A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc.
; APPLICANT: Bachmanov, Alexander A
; APPLICANT: Beauchamp, Gary K.
; APPLICANT: Chatterjee, Aurobindo
; APPLICANT: De Jong, Pieter J.
; APPLICANT: Li, Shanru
; APPLICANT: Li, Xia
; APPLICANT: Ohmen, Jeffrey D
; APPLICANT: Reed, Danielle R.
; APPLICANT: Ross, David
; APPLICANT: Tordoff, Michael G.
; TITLE OF INVENTION: GENE AND SEQUENCE VARIATION ASSOCIATED WITH SENSING
; FILE REFERENCE: PC18306A
; CURRENT APPLICATION NUMBER: US/10/280,183A
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/200,794
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 236
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Mouse
; OTHER INFORMATION:
US-10-280-183A-236

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1331 TGCTTGCTCTCATTTCAGCCT 1350
Db      20 TCCTTGCTCTGCTTTCTGCCT 1
      ||||| ||||| ||||| |||||
      ||||| ||||| ||||| |||||
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; PRIOR APPLICATION NUMBER: 60/288,395
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 60/308,901
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/313,388
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/324,757
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/288,900
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 203
; SEQ ID NO 171
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-138-588-171

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2396 TTATCGGTAATTTAATGGG 2415
Db      1 TTATGCTTGTTCATGGG 20

RESULT 2942
US-10-210-556-34/c
; Sequence 34, Application US/10210556
; Publication No. US20040023904A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTPRA EXPRESSION
; FILE REFERENCE: PTS-0015
; CURRENT APPLICATION NUMBER: US/10/210,556
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 227
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-210-556-34

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1370 AGCCAGGCCATCTGTGCCGC 1389
Db      20 ATCCAGGCCACCTGTGAGGC 1

RESULT 2943
US-10-210-556-157
; Sequence 157, Application US/10210556
; Publication No. US20040023904A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTPRA EXPRESSION
; FILE REFERENCE: PTS-0015
; CURRENT APPLICATION NUMBER: US/10/210,556
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 227
; SEQ ID NO 157
; LENGTH: 20
```

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; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-210-556-157

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1370 AGCCAGGCCATCTGTGCCGC 1389
Db      1 ATCCAGGCCACCTGTGAGGC 20

RESULT 2944
US-10-211-179-27
; Sequence 27, Application US/10211179
; Publication No. US20040023906A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOTYROSYL PHOSPHATASE ACTIVATOR EXPRI
; FILE REFERENCE: PTS-0011
; CURRENT APPLICATION NUMBER: US/10/211,179
; CURRENT FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 119
; SEQ ID NO 27
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-211-179-27

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2203 TCTTCAAATGGGAGACTCTT 2222
Db      1 TCTGCAAATGGGCCAGTCTT 20

RESULT 2945
US-10-211-179-94/c
; Sequence 94, Application US/10211179
; Publication No. US20040023906A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOTYROSYL PHOSPHATASE ACTIVATOR EXPRI
; FILE REFERENCE: PTS-0011
; CURRENT APPLICATION NUMBER: US/10/211,179
; CURRENT FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 119
; SEQ ID NO 94
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-211-179-94

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2203 TCTTCAAATGGGAGACTCTT 2222
Db      20 TCTGCAAATGGGCCAGTCTT 1

RESULT 2946
US-10-309-290-169
```



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; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1578
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-1578

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 903 AAGTACAGAGCGGCGACTGTCC 922
Db 1 AAGAACGGAGGCGGATTATCC 20

RESULT 2937
US-10-289-762-2361/c
; Sequence 2361, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2361
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-2361

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1114 CTTGCCTATGCTCTGTGAAG 1133
Db 20 CTTGCCTATAGGGGTGAAG 1

RESULT 2938
US-10-289-762-4000/c
; Sequence 4000, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4000
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-4000

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1310 TTGGAGACGAACATACAGAA 1329
Db 20 TTGCTGCCGAACCTACAGAA 1
```

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RESULT 2939
US-10-289-762-4383/c
; Sequence 4383, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 4383
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-4383

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1114 CTTGCCTATGCTCTGTGAAG 1133
Db 20 CTTCCCTATGTATGGGAG 1

RESULT 2940
US-10-455-229-12
; Sequence 12, Application US/10455229
; Publication No. US20040016030A1
; GENERAL INFORMATION:
; APPLICANT: LOWE, BRENDA A.
; APPLICANT: CHOMET, PAUL
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PRODUCTION OF MAIZE LINES
; TITLE OF INVENTION: WITH INCREASED TRANSFORMABILITY
; FILE REFERENCE: DEKM:195US
; CURRENT APPLICATION NUMBER: US/10/455,229
; CURRENT FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: 60/386,522
; PRIOR FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-455-229-12

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1084 AGAAGGTGAAGCTGTTCAAT 1103
Db 1 AGAACGTGAAGCTGAGCGTT 20

RESULT 2941
US-10-138-588-171
; Sequence 171, Application US/10138588
; Publication No. US20040018594A1
; GENERAL INFORMATION:
; APPLICANT: Alsbrook et al.
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES, NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-347A
; CURRENT APPLICATION NUMBER: US/10/138,588
; CURRENT FILING DATE: 2002-05-01
```

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 289 CCCGCGCCACCCCTCTCC 308  
||||| ||||| ||||| |||||

Db 20 CCCGCGCCCGCCCGCCCCC 1

RESULT 2932  
US-10-407-449-9/c  
; Sequence 9, Application US/10407449  
; Publication No. US20040005601A1  
; GENERAL INFORMATION:  
; APPLICANT: Siddiqui-Jain, Adam  
; APPLICANT: Hurley, Laurence  
; APPLICANT: Farrell, Thomas  
; APPLICANT: Grand, Cory  
; APPLICANT: Bearss, David  
; TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLIX DNA  
; FILE REFERENCE: 53223-20004.00  
; CURRENT APPLICATION NUMBER: US/10/407,449  
; PRIOR APPLICATION NUMBER: 2003-04-04  
; PRIOR FILING DATE: 2002-08-04  
; PRIOR APPLICATION NUMBER: US 60/370,358  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: Unknown  
; PRIOR FILING DATE: 2003-03-20  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-407-449-9

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 289 CCCGCGCCACCCCTCTCC 308  
||||| ||||| ||||| |||||

Db 20 CCCGCGCCCGCCCGCCCCC 1

RESULT 2933  
US-10-188-470-13/c  
; Sequence 13, Application US/10188470  
; Publication No. US20040005707A1  
; GENERAL INFORMATION:  
; APPLICANT: Scott Cooper  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF INTEGRIN BETA 5 EXPRESSION  
; FILE REFERENCE: PTS-0024  
; CURRENT APPLICATION NUMBER: US/10/188,470  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 130  
; SEQ ID NO 13  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-188-470-13

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2364 AAGAAACAGTGCCTTGAGTG 2383  
||||| ||||| ||||| |||||

Db 20 AAGAGAGATTGCGTCGAGTG 1

RESULT 2934  
US-10-189-267-136  
; Sequence 136, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 136  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-189-267-136

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 768 CCAAGAACCCCTCTGAACCTC 787  
||||| ||||| ||||| |||||

Db 1 CCAAGATCCCTCTTAAATC 20

RESULT 2935  
US-10-189-267-258/c  
; Sequence 258, Application US/10189267  
; Publication No. US20040006030A1  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Susan M. Freier  
; APPLICANT: Kenneth W. Dobie  
; TITLE OF INVENTION: ANTISENSE MODULATION OF TGF-BETA 2 EXPRESSION  
; FILE REFERENCE: PTS-0038  
; CURRENT APPLICATION NUMBER: US/10/189,267  
; CURRENT FILING DATE: 2002-07-02  
; NUMBER OF SEQ ID NOS: 284  
; SEQ ID NO 258  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: M. musculus  
; FEATURE:  
US-10-189-267-258

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 768 CCAAGAACCCCTCTGAACCTC 787  
||||| ||||| ||||| |||||

Db 20 CCAAGATCCCTCTTAAATC 1

RESULT 2936  
US-10-289-762-1578  
; Sequence 1578, Application US/10289762  
; Publication No. US20040006218A1  
; GENERAL INFORMATION:  
; APPLICANT: Grifais, R.  
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
; TITLE OF INVENTION: and treatment of infection  
; FILE REFERENCE: 9710-003-999  
; CURRENT APPLICATION NUMBER: US/10/289,762

US-10-349-143-8908  
; Sequence 8908, Application US/10349143  
; Publication No. US20040005584A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET.020CPI  
; CURRENT APPLICATION NUMBER: US/10/349,143  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US/09/422,978  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 8908  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: 1..20  
; OTHER INFORMATION: downstream amplification primer 99-1997 for SEQ 1043, in complete  
US-10-349-143-8908  
  
Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 970 AGCCAAATCGAAAAATGGAG 989  
Db 1 AGCCAAATGAACAAATAGAG 20  
  
RESULT 2929  
US-10-349-143-9924  
; Sequence 9924, Application US/10349143  
; Publication No. US20040005584A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET.020CPI  
; CURRENT APPLICATION NUMBER: US/10/349,143  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US/09/422,978  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 9924  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: 1..20  
; OTHER INFORMATION: downstream amplification primer 99-8289 for SEQ 2059, in complete  
US-10-349-143-9924  
  
Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1493 GACAAAAATGGAGAAACACAG 1512  
Db 1 GATATAAGGAGATACACAG 20  
  
RESULT 2930  
US-10-349-143-10846/c  
; Sequence 10846, Application US/10349143  
; Publication No. US20040005584A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Daniel  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Chumakov, Ilya  
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...  
; FILE REFERENCE: GENSET.020CPI  
; CURRENT APPLICATION NUMBER: US/10/349,143  
; CURRENT FILING DATE: 2003-01-21  
; PRIOR APPLICATION NUMBER: US/09/422,978  
; PRIOR FILING DATE: 1999-10-20  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850  
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23  
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614  
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21  
; NUMBER OF SEQ ID NOS: 11796  
; SEQ ID NO 10846  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: primer\_bind  
; LOCATION: 1..20  
; OTHER INFORMATION: downstream amplification primer 99-21377 for SEQ 2981, in complete  
US-10-349-143-10846

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2124 GAAACTTGTAGAAACGAAGC 2143  
Db 20 GAAACCACTATAAACGAAGC 1  
  
RESULT 2931  
US-10-407-449-5/c  
; Sequence 5, Application US/10407449  
; Publication No. US20040005601A1  
; GENERAL INFORMATION:  
; APPLICANT: Siddiqui-Jain, Adam  
; APPLICANT: Hurley, Laurence  
; APPLICANT: Farrell, Thomas  
; APPLICANT: Grand, Cory  
; APPLICANT: Bearss, David  
; TITLE OF INVENTION: METHODS FOR TARGETING QUADRUPLIX DNA  
; FILE REFERENCE: 53223-20004.00  
; CURRENT APPLICATION NUMBER: US/10/407,449  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US 60/404,966  
; PRIOR FILING DATE: 2002-08-04  
; PRIOR APPLICATION NUMBER: US 60/370,358  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: Unknown  
; PRIOR FILING DATE: 2003-03-20  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-407-449-5

```

; SEQ ID NO 68
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-188-646-68

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 33 GGACAGCAAGCCCGCGCGC 52
    ||||| ||||| |||||
Db 1 GGACAGGAAGGTGCGCACGC 20

RESULT 2924
US-10-188-646-137/c
; Sequence 137, Application US/10188646
; Publication No. US20040005565A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
; FILE REFERENCE: RTS-0373
; CURRENT APPLICATION NUMBER: US/10/188,646
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 137
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-188-646-137

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 33 GGACAGCAAGCCCGCGCGC 52
    ||||| ||||| |||||
Db 20 GGACAGGAAGGTGCGCACGC 1

RESULT 2925
US-10-188-779A-64/c
; Sequence 64, Application US/10188779A
; Publication No. US20040005567A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF CYCLIN-DEPENDENT KINASE 4 EXPRESSION
; FILE REFERENCE: PTS-0042
; CURRENT APPLICATION NUMBER: US/10/188,779A
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 282
; SEQ ID NO 64
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-188-779A-64

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1593 GGAACCCCTCCTGGCTGG 1612
    ||||| ||||| |||||
Db 20 GAGAACCCATCCTGGCTGG 1
```

```

RESULT 2926
US-10-188-779A-127
; Sequence 127, Application US/10188779A
; Publication No. US20040005567A1
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF CYCLIN-DEPENDENT KINASE 4 EXPRESSION
; FILE REFERENCE: PTS-0042
; CURRENT APPLICATION NUMBER: US/10/188,779A
; CURRENT FILING DATE: 2002-07-02
; NUMBER OF SEQ ID NOS: 282
; SEQ ID NO 127
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-188-779A-127

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2339 AGTCCCGGTGGAGGTTCTGT 2358
    ||||| ||||| |||||
Db 1 AGGCCCGGTGGAGGTTCTTT 20

RESULT 2927
US-10-349-143-5752
; Sequence 5752, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5752
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: upstream amplification primer 99-6613 for SEQ 1818,
US-10-349-143-5752

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1535 AGGTTAGGAGTAGGGAAG 1554
    ||||| ||||| |||||
Db 1 AGATGAGGAGTGGAGGAAG 20

RESULT 2928
```





```
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 23
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-360-510-23

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 903 AAGTACAGAGCGACTGTCC 922
Db 20 AGGTACAGAGACGTGTC 1

RESULT 2916
US-10-360-510-183/c
; Sequence 183, Application US/10360510
; Publication No. US20030220282A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/10/360,510
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US/09/854,883
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 183
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-360-510-183

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1590 ACTGGGAACCCCTCCTGGCC 1609
Db 20 ACTGGGAAGCCCTTCTGTGC 1

RESULT 2917
US-10-360-510-301
; Sequence 301, Application US/10360510
; Publication No. US20030220282A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/10/360,510
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US/09/854,883
```

```
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; PRIOR FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 389
; SEQ ID NO 301
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-360-510-301

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 350 CCTCCCTACCAGCAGCTGGC 369
Db 1 CCTCCTTACCAGCAAGAGGC 20

RESULT 2918
US-10-159-834-58
; Sequence 58, Application US/10159834
; Publication No. US20030228688A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF ISOPRENYLCYSTEINE CARBOXYL METHYLTRANSFERASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0299
; CURRENT APPLICATION NUMBER: US/10/159,834
; CURRENT FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 58
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-159-834-58

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2212 GGGAGACTCTTTGAAATGAC 2231
Db 1 GGAAACACAGTTTGAAATGAC 20

RESULT 2919
US-10-159-834-117/c
; Sequence 117, Application US/10159834
; Publication No. US20030228688A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF ISOPRENYLCYSTEINE CARBOXYL METHYLTRANSFERASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0299
; CURRENT APPLICATION NUMBER: US/10/159,834
; CURRENT FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 130
; SEQ ID NO 117
; LENGTH: 20
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-159-834-117

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
```

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; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Designed
; OTHER INFORMATION: oligonucleotide probe for Southern hybridization
US-10-148-835-118

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      365 CTGGCCTACTCCAGTCGCGC 384
Db      1 CTGGCCTTGTCCTGACGCGC 20

RESULT 2912
US-10-148-835-119
; Sequence 119, Application US/10148835
; Publication No. US20030207380A1
; GENERAL INFORMATION:
; APPLICANT: SAITO et al.
; TITLE OF INVENTION: MUTANT ER alpha AND TEST SYSTEMS FOR TRANSACTIVATION
; FILE REFERENCE: 2185-0648P
; CURRENT APPLICATION NUMBER: US/10/148,835
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Designed
; OTHER INFORMATION: oligonucleotide probe for Southern hybridization
US-10-148-835-119

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      369 CCTACTCCAGTCGCGCGC 388
Db      1 CCTGTCCCTGACGCGCGC 20

RESULT 2913
US-10-151-612-16
; Sequence 16, Application US/10151612
; Publication No. US20030215872A1
; GENERAL INFORMATION:
; APPLICANT: Kohn, Leonard D
; APPLICANT: Suzuki, Koichi
; APPLICANT: Mori-Aoki, Atsumi
; APPLICANT: Iishi, Ken
; APPLICANT: Klinman, Dennis M
; APPLICANT: Rice, John M
; TITLE OF INVENTION: IMMUNE ACTIVATION BY DOUBLE-STRANDED POLYNUCLEOTIDES
; FILE REFERENCE: 0079661/0502168
; CURRENT APPLICATION NUMBER: US/10/151,612
; CURRENT FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA

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; ORGANISM: Rattus sp.
US-10-151-612-16

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      829 TGAGGTCTTCTGCTCAGTCC 848
Db      1 TGAAGACTTCTGCTCGGACC 20

RESULT 2914
US-10-310-677-34/c
; Sequence 34, Application US/10310677
; Publication No. US20030219772A1
; GENERAL INFORMATION:
; APPLICANT: Kuyl v.d., Antoinette C.
; APPLICANT: Cornelissen, Marion
; TITLE OF INVENTION: Means and methods for treatment evaluation
; FILE REFERENCE: P55190US10
; CURRENT APPLICATION NUMBER: US/10/310,677
; CURRENT FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: EP 01200228.3
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: EP 01203703.2
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/325,722
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TAG004
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(5)
; OTHER INFORMATION: /note="A stands for inosine"
US-10-310-677-34

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2343 CCGTGGAGGTTCTGTATT 2362
Db      20 CCAGTGGAGTCACTGTTTT 1

RESULT 2915
US-10-360-510-23/c
; Sequence 23, Application US/10360510
; Publication No. US20030220282A1
; GENERAL INFORMATION:
; APPLICANT: Lex M. Cowser
; APPLICANT: Jacqueline Wyatt
; APPLICANT: Susan M. Freier
; APPLICANT: Brett P. Monia
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; TITLE OF INVENTION: ANTISENSE MODULATION OF PTP1B EXPRESSION
; FILE REFERENCE: ISPH-0576
; CURRENT APPLICATION NUMBER: US/10/360,510
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US/09/854,883
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/629,644
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/487,368
; PRIOR FILING DATE: 2000-01-18

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; TITLE OF INVENTION: METHOD FOR ASSESSMENT OF GENE EXPRESSION IN SMALL BIOLOGICAL SAM
; FILE REFERENCE: 01154/2001-203
; CURRENT APPLICATION NUMBER: US/10/109,349A
; CURRENT FILING DATE: 2002-06-12
; NUMBER OF SEQ ID NOS: 282
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-109-349A-167

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      633 TGGATGCGCGGGCCTGGCC 652
Db      20 TGGATGCTGCTGGTGGCC 1

RESULT 2905
US-10-356-625-116/c
; Sequence 116, Application US/10356625
; Publication No. US20030186290A1
; GENERAL INFORMATION:
; APPLICANT: Tournier-Lasserre, Elisabeth
; APPLICANT: Joutel, Anne
; APPLICANT: Bousser, Marie-Germaine
; APPLICANT: Bach, Jean-Francois
; TITLE OF INVENTION: GENE INVOLVED IN CADASIL, METHOD OF DIAGNOSIS AND
; TITLE OF INVENTION: THERAPEUTIC APPLICATION
; FILE REFERENCE: 03715.0048-00000
; CURRENT APPLICATION NUMBER: US/10/356,625
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/230,652
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: FR 96 09733
; PRIOR FILING DATE: 1996-08-01
; PRIOR APPLICATION NUMBER: FR 97 04680
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: PCT/FR97/01433
; PRIOR FILING DATE: 1997-07-31
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 116
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-10-356-625-116

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1540 AGGAGAGTAGGGAAGGAACA 1559
Db      20 AGGAGAGTGGCACAGGAACA 1

RESULT 2906
US-10-352-615-66/c
; Sequence 66, Application US/10352615
; Publication No. US20030190285A1
; GENERAL INFORMATION:
; APPLICANT: VAN DEN VEN, W.J.M.
; APPLICANT: SCHOENMAKERS, H.F.P.M.
; TITLE OF INVENTION: MULTIPLE-TUMOR ABERRENT GROWTH
; GENES
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: The Webb Law Firm
; STREET: 700 Koppers Building, 436 Seventh Avenue
; CITY: Pittsburgh
; STATE: PA
; COUNTRY: USA
; ZIP: 15219-1818
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/352,615
; FILING DATE: 28-Jan-2003
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,454
; FILING DATE: 15-AUG-1997
; APPLICATION NUMBER: PCT/EP/00716
; FILING DATE: 19-FEB-1996
; APPLICATION NUMBER: 95200390.3
; FILING DATE: 17-FEB-1995
; APPLICATION NUMBER: 95201951.1
; FILING DATE: 14-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Johnson, Barbara E
; REGISTRATION NUMBER: 31,198
; REFERENCE/DOCKET NUMBER: 702-971100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 412-471-8815
; TELEFAX: 412-471-4094
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-352-615-66

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2672 CAGTGTGTGTGGTGAATG 2691
Db      20 CATGTGTGTGCCTGAGATG 1

RESULT 2907
US-10-080-979-47/c
; Sequence 47, Application US/10080979
; Publication No. US20030191075A1
; GENERAL INFORMATION:
; APPLICANT: Cook, Philip Dan
; APPLICANT: Manoharan, Muthiah
; APPLICANT: Bennett, Frank C.
; TITLE OF INVENTION: Oligonucleotide Conjugates For Hepatic Delivery
; FILE REFERENCE: Isis-5028
; CURRENT APPLICATION NUMBER: US/10/080,979
; CURRENT FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-080-979-47

Query Match          0.5%; Score 13.6; DB 1; Length 20;

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```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02024
US-10-367-470-17

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2155 TTTTCTCTCTTTT 2174
Db      20 TTTTGTAGAAATTTT 1

RESULT 2901
US-10-173-805-1
; Sequence 1, Application US/10173805
; Publication No. US20030170240A1
; GENERAL INFORMATION:
; APPLICANT: SAKANO, Katsuichi
; APPLICANT: HIGASHIHASHI, No. US20030170240Aluyuki
; APPLICANT: HASHIMOTO, Ryuji
; TITLE OF INVENTION: Method for Elevating the Concentration of Free
; TITLE OF INVENTION: Insulin-Like Growth Factor
; FILE REFERENCE: Q54313
; CURRENT APPLICATION NUMBER: US/10/173,805
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/331,851
; PRIOR FILING DATE: 1999-06-28
; PRIOR APPLICATION NUMBER: JP P1996-349968
; PRIOR FILING DATE: 1996-12-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: STS
; LOCATION: (1)..(20)
; OTHER INFORMATION: One of PCR primers for cloning of the 5' end of
; OTHER INFORMATION: IGFBP-3 gene from rat pancreas cDNA library
; OTHER INFORMATION: The Sequence is described at page 38, line 19
; OTHER INFORMATION: of the specification.
; PUBLICATION INFORMATION:
; AUTHORS: Shimasaki, S.
; JOURNAL: Biochem. Biophys. Res. Commun.
; VOLUME: 165
; PAGES: 907-
; DATE: 1989
US-10-173-805-1

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      628 CGCCTGGATGCCGCGGCC 647
Db      1 CGCATGCATCCCGCGGCC 20

RESULT 2902
US-10-055-728-34/c
; Sequence 34, Application US/10055728
; Publication No. US2003017020A1
; GENERAL INFORMATION:
; APPLICANT: van der Kuyl, Antoinette C.
; APPLICANT: Cornelissen, Marion
; TITLE OF INVENTION: MEANS AND METHODS FOR TREATMENT EVALUATION
; FILE REFERENCE: 5244US (REN/P55190US00)
; CURRENT APPLICATION NUMBER: US/10/055,728
```

```
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/325,722
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: EP 0120373.2
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: EP 01200228.3
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)..(5)
; OTHER INFORMATION: a stands for inosine
US-10-055-728-34

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2343 CCCGTGGAGTTCTGTATT 2362
Db      20 CCAGTGGAGTTCATGTTTT 1

RESULT 2903
US-10-053-645A-26
; Sequence 26, Application US/10053645A
; Publication No. US20030176376A1
; GENERAL INFORMATION:
; APPLICANT: Robert E. Klem
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A
; TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2
; TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF
; FILE REFERENCE: 10412-022-999
; CURRENT APPLICATION NUMBER: US/10/053,645A
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/263,244
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Synthetic Antisense
; OTHER INFORMATION: Oligonucleotide
US-10-053-645A-26

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      49 GCGCGCGGGCGCGCGGCA 68
Db      1 GCGCGCGGGCGGGCGGGCA 20

RESULT 2904
US-10-109-349A-167/c
; Sequence 167, Application US/10109349A
; Publication No. US20030186246A1
; GENERAL INFORMATION:
; APPLICANT: Medical College of Ohio
; APPLICANT: Willey, James C.
; APPLICANT: Crawford, Erin L.
; TITLE OF INVENTION: MULTIPLEX STANDARDIZED REVERSE TRANSCRIPTASE-POLYMERASE CHAIN REAC
```

```
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide AGT02013
US-10-367-470-10

Query Match          0.5%;   Score 13.6;   DB 1;   Length 20;
Best Local Similarity 80.0%;   Pred.No. 3.1e+03;
Matches 16;   Conservative 0;   Mismatches 4;   Indels 0;   Gaps 0;

QY      2155 TTTTCTCCTTTT 2174
          |||||
Db       1 TTTTAAATTTT 20

RESULT 2897
US-10-367-470-11
; Sequence 11, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide AGT02014
US-10-367-470-11

Query Match          0.5%;   Score 13.6;   DB 1;   Length 20;
Best Local Similarity 80.0%;   Pred.No. 3.1e+03;
Matches 16;   Conservative 0;   Mismatches 4;   Indels 0;   Gaps 0;

QY      2155 TTTTCTCCTTTT 2174
          |||||
Db       1 TTTTAAATTTT 20

RESULT 2898
US-10-367-470-12/c
; Sequence 12, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
```

```
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Complement DNA oligo AGT02009
US-10-367-470-12

Query Match          0.5%;   Score 13.6;   DB 1;   Length 20;
Best Local Similarity 80.0%;   Pred.No. 3.1e+03;
Matches 16;   Conservative 0;   Mismatches 4;   Indels 0;   Gaps 0;

QY      2155 TTTTCTCCTTTT 2174
          |||||
Db       20 TTTTAAATTTT 1

RESULT 2899
US-10-367-470-14/c
; Sequence 14, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligo AGT02021
US-10-367-470-14

Query Match          0.5%;   Score 13.6;   DB 1;   Length 20;
Best Local Similarity 80.0%;   Pred.No. 3.1e+03;
Matches 16;   Conservative 0;   Mismatches 4;   Indels 0;   Gaps 0;

QY      2155 TTTTCTCCTTTT 2174
          |||||
Db       20 TTTTACAATTTT 1

RESULT 2900
US-10-367-470-17/c
; Sequence 17, Application US/10367470
; Publication No. US20030165963A1
; GENERAL INFORMATION:
; APPLICANT: Applied Gene Technologies, Inc.
; APPLICANT: Dattagupta, Nanibhushan
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES
; FILE REFERENCE: 47541-20004.20
; CURRENT APPLICATION NUMBER: US/10/367,470
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/823,647B
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US 09/616,761
; PRIOR FILING DATE: 2000-07-14
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
```

; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: US 08/624,447  
; PRIOR FILING DATE: 1996-08-19  
; PRIOR APPLICATION NUMBER: PCT/US94/11279  
; PRIOR FILING DATE: 1994-10-06  
; PRIOR APPLICATION NUMBER: US 08/133,963  
; PRIOR FILING DATE: 1993-10-07  
; NUMBER OF SEQ ID NOS: 145  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 89  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Amycolatopsis mediterranei  
US-10-267-255-89

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 507 TGCCCTCGCACCACGGGCGC 526  
||| | ||| | ||| | |||  
Db 20 TGGCGGCGCAGCAGCGGACGC 1

RESULT 2893  
US-10-267-255-90  
; Sequence 90, Application US/10267255  
; Publication No. US20030124689A1  
; GENERAL INFORMATION:  
; APPLICANT: Sherman, D  
; APPLICANT: Mao, Y  
; APPLICANT: Varoglu, M  
; APPLICANT: He, M  
; APPLICANT: Sheldon, P  
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster  
; FILE REFERENCE: 600.456US1  
; CURRENT APPLICATION NUMBER: US/10/267,255  
; CURRENT FILING DATE: 2002-10-09  
; PRIOR APPLICATION NUMBER: US 09/266,965  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: US 08/624,447  
; PRIOR FILING DATE: 1996-08-19  
; PRIOR APPLICATION NUMBER: PCT/US94/11279  
; PRIOR FILING DATE: 1994-10-06  
; PRIOR APPLICATION NUMBER: US 08/133,963  
; PRIOR FILING DATE: 1993-10-07  
; NUMBER OF SEQ ID NOS: 145  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 90  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Amycolatopsis mediterranei  
US-10-267-255-90

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 507 TGCCCTCGCACCACGGGCGC 526  
||| | ||| | ||| | |||  
Db 1 TGGCGGCGCAGCAGCGGACGC 20

RESULT 2894  
US-10-367-470-8  
; Sequence 8, Application US/10367470  
; Publication No. US20030165963A1  
; GENERAL INFORMATION:  
; APPLICANT: Applied Gene Technologies, Inc.  
; APPLICANT: Dattagupta, Nanibhushan  
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 47541-20004.20

; CURRENT APPLICATION NUMBER: US/10/367,470  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US/09/823,647B  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: US 09/616,761  
; PRIOR FILING DATE: 2000-07-14  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide AGT02008  
US-10-367-470-8

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2155 TTTTCTCTCTCTCTCTCTCT 2174  
||||| ||||| ||||| |||||  
Db 1 TTTTATAAAATTTTCTCTCT 20

RESULT 2895  
US-10-367-470-9  
; Sequence 9, Application US/10367470  
; Publication No. US20030165963A1  
; GENERAL INFORMATION:  
; APPLICANT: Applied Gene Technologies, Inc.  
; APPLICANT: Dattagupta, Nanibhushan  
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 47541-20004.20  
; CURRENT APPLICATION NUMBER: US/10/367,470  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US/09/823,647B  
; PRIOR FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: US 09/616,761  
; PRIOR FILING DATE: 2000-07-14  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide AGT02012  
US-10-367-470-9

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2155 TTTTCTCTCTCTCTCTCTCT 2174  
||||| ||||| ||||| |||||  
Db 1 TTTTATAAAATTTTCTCTCT 20

RESULT 2896  
US-10-367-470-10  
; Sequence 10, Application US/10367470  
; Publication No. US20030165963A1  
; GENERAL INFORMATION:  
; APPLICANT: Applied Gene Technologies, Inc.  
; APPLICANT: Dattagupta, Nanibhushan  
; TITLE OF INVENTION: NUCLEIC ACID HAIRPIN PROBES AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: 47541-20004.20  
; CURRENT APPLICATION NUMBER: US/10/367,470  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US/09/823,647B



; TITLE OF INVENTION: Proteins
; FILE REFERENCE: 2543-1-028
; CURRENT APPLICATION NUMBER: US/10/227,616
; CURRENT FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: GB 0004576.5
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: GB 0031341.1
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY:
; OTHER INFORMATION: Primer
US-10-227-616-88

Query Match 0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 849 CTGGAAGATTGTCGCTCCTC 868
||| ||| ||| ||| ||| ||| |||
Db 1 CTGGAGGATTGTCATACTC 20

RESULT 2889
US-10-161-229-99
; Sequence 99, Application US/10161229
; Publication No. US20030100527A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Hartmann, Gunther
; TITLE OF INVENTION: Immunostimulatory Nucleic Acid Molecules for
; TITLE OF INVENTION: Activating Dendritic Cells
; FILE REFERENCE: C01039/70061
; CURRENT APPLICATION NUMBER: US/10/161,229
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 09/191,170
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: US 08/960,774
; PRIOR FILING DATE: 1997-10-30
; PRIOR APPLICATION NUMBER: US 08/738,652
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: US 08/386,063
; PRIOR FILING DATE: 1995-02-07
; PRIOR APPLICATION NUMBER: US 08/276,358
; PRIOR FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-161-229-99

Query Match 0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1966 AATATTACCTTGAAAAAA 1985
||| ||| ||| ||| ||| ||| |||
Db 1 AAAATCAACGTTGAAAAAA 20

RESULT 2890
US-10-003-354-67/c
; Sequence 67, Application US/10003354
; Publication No. US20030114400A1

; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0348
; CURRENT APPLICATION NUMBER: US/10/003,354
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 67
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-003-354-67

Query Match 0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2620 AATAACTTTGTCCTCCTCCT 2639
||| ||| ||| ||| ||| ||| |||
Db 20 AAGAACCTTCTCTCCTCCTCCT 1

RESULT 2891
US-10-279-186-70/c
; Sequence 70, Application US/10279186
; Publication No. US20030114407A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR
; TITLE OF INVENTION: ETBR-LP-2 EXPRESSION
; FILE REFERENCE: RTS-0346
; CURRENT APPLICATION NUMBER: US/10/279,186
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US/10/003,126
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 70
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-279-186-70

Query Match 0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 250 GGTCCCCCACCTCTCCTCCG 269
||| ||| ||| ||| ||| ||| |||
Db 20 GGTGGCCTACCTCTCCACCG 1

RESULT 2892
US-10-267-255-89/c
; Sequence 89, Application US/10267255
; Publication No. US20030124689A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456US1
; CURRENT APPLICATION NUMBER: US/10/267,255
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 09/266,965

RESULT 2884  
US-10-017-995-855/c  
; Sequence 855, Application US/10017995  
; Publication No. US20030055014A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids  
; FILE REFERENCE: C1037/7025 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/017,995  
; CURRENT FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: US 60/255,534  
; PRIOR FILING DATE: 2000-12-14  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 855  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-017-995-855

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1776 TTTTGAACCCCATTCCTTT 1795  
|||||  
Db 20 TTTTGAACGTCATGTTTT 1

RESULT 2885  
US-10-173-539-19  
; Sequence 19, Application US/10173539  
; Publication No. US20030059812A1  
; GENERAL INFORMATION:  
; APPLICANT: Richon, Victoria  
; APPLICANT: Zhou, Xianbo  
; APPLICANT: Rifkind, Richard A.  
; APPLICANT: Marks, Paul A.  
; TITLE OF INVENTION: HDAC9 Polypeptides and Polynucleotides  
; TITLE OF INVENTION: and Uses Thereof  
; FILE REFERENCE: 3254.1000-003  
; CURRENT APPLICATION NUMBER: US/10/173,539  
; CURRENT FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: 60/298,173  
; PRIOR FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: 60/311,686  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: 60/316,995  
; PRIOR FILING DATE: 2001-09-04  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer used to amplify human DNA  
US-10-173-539-19

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2548 AATTAAGAGGATGCTGGGT 2567  
|||  
Db 1 AATGTACAGGATGCTGGGT 20

RESULT 2886

US-10-181-107-164  
; Sequence 164, Application US/10181107  
; Publication No. US20030083295A1  
; GENERAL INFORMATION:  
; APPLICANT: Hong Zhang  
; APPLICANT: Lex M. Cowser  
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 3 EXPRESSION  
; FILE REFERENCE: RTSP-0325  
; CURRENT APPLICATION NUMBER: US/10/181,107  
; CURRENT FILING DATE: 2002-07-11  
; PRIOR APPLICATION NUMBER: PCT/US01/00888  
; PRIOR FILING DATE: 2001-01-11  
; PRIOR APPLICATION NUMBER: 09/484,617  
; PRIOR FILING DATE: 2000-01-18  
; NUMBER OF SEQ ID NOS: 176  
; SEQ ID NO 164  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-181-107-164

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1742 GACAAGTACTGGCTCTTTAT 1761  
|||||  
Db 1 GACAGTTACTTGCTCCTTAT 20

RESULT 2887  
US-10-181-846-109/c  
; Sequence 109, Application US/10181846  
; Publication No. US20030083297A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas M. Dean  
; APPLICANT: Lex M. Cowser  
; TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION  
; FILE REFERENCE: RTSP-0363  
; CURRENT APPLICATION NUMBER: US/10/181,846  
; CURRENT FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: PCT/US01/01416  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 09/490,692  
; PRIOR FILING DATE: 2000-01-24  
; NUMBER OF SEQ ID NOS: 176  
; SEQ ID NO 109  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-181-846-109

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1992 TGTGTATCTAGCTTCTTCAG 2011  
|||||  
Db 20 TGTGTTCTGGCCTCTGCAG 1

RESULT 2888  
US-10-227-616-88  
; Sequence 88, Application US/10227616  
; Publication No. US20030099662A1  
; GENERAL INFORMATION:  
; APPLICANT: Boyd, Robert Simon  
; APPLICANT: Stamps, Alasdair Craig  
; APPLICANT: Terrett, Jonathan Alexander

```
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 749
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-749

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1966 AATATTACCTTGAAAAAA 1985
Db 1 AAAATCAACGTTGAAAAAA 20

RESULT 2880
US-10-112-653-826/c
; Sequence 826, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Beig, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 826
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-826

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1776 TTTTGAACCCCATTCCTT 1795
Db 20 TTTTGAACGTCATGTTTT 1

RESULT 2881
US-10-017-995-353/c
; Sequence 353, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 353
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-353

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1543 AGACTAGGGAAGGAACAGGA 1562
Db 20 AGACTGAGGAAGGAAGTGGGA 1

RESULT 2882
US-10-017-995-525/c
; Sequence 525, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 525
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-525

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1776 TTTTGAACCCCATTCCTT 1795
Db 20 TTTTGAACGTCATGTTTT 1

RESULT 2883
US-10-017-995-776
; Sequence 776, Application US/10017995
; Publication No. US20030055014A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids
; FILE REFERENCE: C1037/7025 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/017,995
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/255,534
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 776
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-017-995-776

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1966 AATATTACCTTGAAAAAA 1985
Db 1 AAAATCAACGTTGAAAAAA 20
```

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RESULT 2875
US-10-060-301-120/c
; Sequence 120, Application US/10060301
; Publication No. US20020182622A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, Yusuke et al.
; TITLE OF INVENTION: A METHOD FOR SNP (SINGLE NUCLEOTIDE POLYMORPHISM) TYPING
; FILE REFERENCE: 1254-0195p
; CURRENT APPLICATION NUMBER: US/10/060,301
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: JP 2001-25700
; PRIOR FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Reverse Primer for SNP ID 60
US-10-060-301-120
Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2094 CGTGTTCAAACGGGGCCTT 2113
Db 20 CGTCTCAAACACTGTGGCCTT 1

RESULT 2876
US-10-125-181-17
; Sequence 17, Application US/10125181
; Publication No. US20020187954A1
; GENERAL INFORMATION:
; APPLICANT: WRIGHT, Jim A.
; APPLICANT: YOUNG, Aiping H.
; APPLICANT: LEE, Yoon S.
; TITLE OF INVENTION: INSULIN-LIKE GROWTH FACTOR II ANTISENSE
; TITLE OF INVENTION: OLIGONUCLEOTIDE
; TITLE OF INVENTION: SEQUENCES AND METHODS OF USING SAME TO MODULATE CELL
; TITLE OF INVENTION: GROWTH
; FILE REFERENCE: 032396-046
; CURRENT APPLICATION NUMBER: US/10/125,181
; CURRENT FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/295,593
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,791
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Human
US-10-125-181-17
Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 251 GTCCCCCACCCTCTCCTCCGC 270
Db 1 GTCCACCACGCTCCCCGCCGC 20

RESULT 2877
US-10-112-653-342/c
; Sequence 342, Application US/10112653
; Publication No. US20030050268A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-342
Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1543 AGAGTAGGGAAGGAACAGCA 1562
Db 20 AGACTGAGGAAGGAACCTGGA 1

RESULT 2878
US-10-112-653-502/c
; Sequence 502, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/279,642
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 1040
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 502
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-112-653-502
Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1776 TTTTGTGAACCCCATTTCTTT 1795
Db 20 TTTTGTGAACGTCATGTTTT 1

RESULT 2879
US-10-112-653-749
; Sequence 749, Application US/10112653
; Publication No. US20030050268A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Berg, Daniel J.
; TITLE OF INVENTION: IMMUNOSTIMULATORY NUCLEIC ACID FOR
; TITLE OF INVENTION: TREATMENT OF NON-ALLERGIC INFLAMMATORY DISEASES
; FILE REFERENCE: C01039/70060(AWS)
; CURRENT APPLICATION NUMBER: US/10/112,653
```



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US-10-314-578-855/c
; Sequence 855, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 855
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-855

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1776 TTTTGAACCCCATCTTT 1795
Db 20 TTTTGAACGTCATGTTTT 1

RESULT 2872
US-10-287-971-307
; Sequence 307, Application US/10287971
; Publication No. US20040067882A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-480A
; CURRENT APPLICATION NUMBER: US/10/287,971
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 09/997,425
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 10/035,568
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/338,626
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/401,479
; PRIOR FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/333,072
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/348,283
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/393,262
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/406,181
; PRIOR FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 397
; SOFTWARE: CuraSeqIst version 0.1
; SEQ ID NO 307
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-10-287-971-307

Query Match      0.5%; Score 13.6; DB 1; Length 20;
```

```
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1459 AGACCAGAGTCCAGCTGATT 1478
Db 1 AGACCAAGCTCCAGCTGTTT 20

RESULT 2873
US-10-403-902A-80/c
; Sequence 80, Application US/10403902A
; Publication No. US20030224418A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bansal, Aruna
; APPLICANT: Kleyn, Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
; FILE REFERENCE: 24736-2048B
; CURRENT APPLICATION NUMBER: US/10/403,902A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/802,640
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-10-403-902A-80

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 642 CGGGCCTGGCCGAGAACCTG 661
Db 20 CAGCACTGGCCGAGATCCTG 1

RESULT 2874
US-10-060-301-94
; Sequence 94, Application US/10060301
; Publication No. US20020182622A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, Yusuke et al.
; TITLE OF INVENTION: A METHOD FOR SNP (SINGLE NUCLEOTIDE POLYMORPHISM) TYPING
; FILE REFERENCE: 1254-0195P
; CURRENT APPLICATION NUMBER: US/10/060,301
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: JP 2001-25700
; PRIOR FILING DATE: 2001-02-01
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Reverse Primer for SNP ID 47
US-10-060-301-94

Query Match      0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1197 AGATGGCAGCTAGGAAGAAC 1216
Db 1 AGAACGCAGCAAGGAGCAC 20
```

QY 1051 AGCGCTCATGTGACTCTCC 1070  
Db 20 ACCACTCATGAGACTCTCC 1

RESULT 2867  
US-10-144-140-14  
; Sequence 14, Application US/10144140  
; Publication No. US20030211606A1  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Susan M. Freier  
; TITLE OF INVENTION: ANTISENSE MODULATION OF DYRK4 EXPRESSION  
; FILE REFERENCE: RTS-0362  
; CURRENT APPLICATION NUMBER: US/10/144,140  
; CURRENT FILING DATE: 2002-05-10  
; NUMBER OF SEQ ID NOS: 87  
; SEQ ID NO 14  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-10-144-140-14

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 530 GCCGGCCTACTGCCCCACCT 549  
Db 1 GCAGGCCAGCTGCTCCACCT 20

RESULT 2868  
US-10-314-578-353/c  
; Sequence 353, Application US/10314578  
; Publication No. US20030212026A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Schetter, Christian  
; APPLICANT: Vollmer, Jorg  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids  
; FILE REFERENCE: C1039/7035 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/314,578  
; CURRENT FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US 60/156,113  
; PRIOR FILING DATE: 1999-09-25  
; PRIOR APPLICATION NUMBER: US 60/156,135  
; PRIOR FILING DATE: 1999-09-27  
; PRIOR APPLICATION NUMBER: US 60/227,436  
; NUMBER OF SEQ ID NOS: 1145  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 353  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-314-578-353

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1543 AGAGTAGGGAAGGAACAGGA 1562  
Db 20 AGACTGAGGAAGGAAGTGA 1

RESULT 2869  
US-10-314-578-525/c

; Sequence 525, Application US/10314578  
; Publication No. US20030212026A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Schetter, Christian  
; APPLICANT: Vollmer, Jorg  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids  
; FILE REFERENCE: C1039/7035 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/314,578  
; CURRENT FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US 60/156,113  
; PRIOR FILING DATE: 1999-09-25  
; PRIOR APPLICATION NUMBER: US 60/156,135  
; PRIOR FILING DATE: 1999-09-27  
; PRIOR APPLICATION NUMBER: US 60/227,436  
; NUMBER OF SEQ ID NOS: 1145  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 525  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-314-578-525

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1776 TTTTGTGAACCCCATTTCTTT 1795  
Db 20 TTTTGTGAACGTCATGTTTT 1

RESULT 2870  
US-10-314-578-776  
; Sequence 776, Application US/10314578  
; Publication No. US20030212026A1  
; GENERAL INFORMATION:  
; APPLICANT: Krieg, Arthur M.  
; APPLICANT: Schetter, Christian  
; APPLICANT: Vollmer, Jorg  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids  
; FILE REFERENCE: C1039/7035 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/10/314,578  
; CURRENT FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US 60/156,113  
; PRIOR FILING DATE: 1999-09-25  
; PRIOR APPLICATION NUMBER: US 60/156,135  
; PRIOR FILING DATE: 1999-09-27  
; PRIOR APPLICATION NUMBER: US 60/227,436  
; NUMBER OF SEQ ID NOS: 1145  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 776  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-10-314-578-776

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1966 AATATTACCTTGAAAAAAA 1985  
Db 1 AAAATCAACGTTGAAAAAAA 20

RESULT 2871  
US-10-314-578-525/c

Db 1 CTGAGGATTGTCAATACTC 20

RESULT 2862

US-09-771-355-5

; Sequence 5, Application US/09771355

; Publication No. US20020086840A1

; GENERAL INFORMATION:

; APPLICANT: Reddy, Gurucharan

; APPLICANT: Zarling, David A.

; TITLE OF INVENTION: USE OF RAD51 INHIBITORS FOR p53 GENE THERAPY

; FILE REFERENCE: A-68872-1/RFT/RMS/BTC

; CURRENT APPLICATION NUMBER: US/09/771,355

; CURRENT FILING DATE: 2001-01-26

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Antisense

US-09-771-355-5

Query Match 0.5%; Score 13.6; DB 1; Length 20;

Best Local Similarity 80.0%; Pred. No. 3.1e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 563 GCGGGCGGTGACGCCCG 582

|||||

Db 1 GCGGGCGGTGACGCCCG 20

RESULT 2863

US-10-144-488-57

; Sequence 57, Application US/10144488

; Publication No. US20030212017A1

; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia

; APPLICANT: Susan M. Preier

; TITLE OF INVENTION: ANTISENSE MODULATION OF FARNESYL TRANSFERASE BETA SUBUNIT EXPRESSION

; FILE REFERENCE: RTS-0363

; CURRENT APPLICATION NUMBER: US/10/144,488

; CURRENT FILING DATE: 2002-05-10

; NUMBER OF SEQ ID NOS: 80

; SEQ ID NO 57

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-10-144-488-57

Query Match 0.5%; Score 13.6; DB 1; Length 20;

Best Local Similarity 80.0%; Pred. No. 3.1e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 782 AACCTCCCTGTCAAGGA 801

|||||

Db 1 AGCCCGCCTGCCAGAAGGA 20

RESULT 2864

US-10-163-272-13

; Sequence 13, Application US/10163272

; Publication No. US20030224517A1

; GENERAL INFORMATION:

; APPLICANT: Kenneth W. Dobie

; TITLE OF INVENTION: ANTISENSE MODULATION OF BETA-SITE APP-CLEAVING ENZYME 2 EXPRESSION

; FILE REFERENCE: RTS-0378

; CURRENT APPLICATION NUMBER: US/10/163,272

; CURRENT FILING DATE: 2002-06-04

; NUMBER OF SEQ ID NOS: 158

; SEQ ID NO 13

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-10-163-272-13

Query Match 0.5%; Score 13.6; DB 1; Length 20;

Best Local Similarity 80.0%; Pred. No. 3.1e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2340 GTCCCCGTGGAGTTCTGTA 2359

|||||

Db 1 GTCCCCCTGCAGGTGTCTA 20

RESULT 2865

US-10-163-272-90/c

; Sequence 90, Application US/10163272

; Publication No. US20030224517A1

; GENERAL INFORMATION:

; APPLICANT: Kenneth W. Dobie

; TITLE OF INVENTION: ANTISENSE MODULATION OF BETA-SITE APP-CLEAVING ENZYME 2 EXPRESSION

; FILE REFERENCE: RTS-0378

; CURRENT APPLICATION NUMBER: US/10/163,272

; CURRENT FILING DATE: 2002-06-04

; NUMBER OF SEQ ID NOS: 158

; SEQ ID NO 90

; LENGTH: 20

; TYPE: DNA

; ORGANISM: H. sapiens

; FEATURE:

US-10-163-272-90

Query Match 0.5%; Score 13.6; DB 1; Length 20;

Best Local Similarity 80.0%; Pred. No. 3.1e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2340 GTCCCCGTGGAGTTCTGTA 2359

|||||

Db 20 GTCCCCCTGCAGGTGTCTA 1

RESULT 2866

US-10-181-873A-19/c

; Sequence 19, Application US/10181873A

; Publication No. US20030212019A1

; GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett

; APPLICANT: Jacqueline Wyatt

; TITLE OF INVENTION: ANTISENSE MODULATION OF COT ONCOGENE EXPRESSION

; FILE REFERENCE: RTSP-0346

; CURRENT APPLICATION NUMBER: US/10/181,873A

; CURRENT FILING DATE: 2002-12-13

; PRIOR APPLICATION NUMBER: PCT/US01/01417

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: 09/489,868

; PRIOR FILING DATE: 2000-01-20

; NUMBER OF SEQ ID NOS: 89

; SEQ ID NO 19

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Antisense Oligonucleotide

US-10-181-873A-19

Query Match 0.5%; Score 13.6; DB 1; Length 20;

Best Local Similarity 80.0%; Pred. No. 3.1e+03;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

APPLICANT: Marcusson, Eric G.  
APPLICANT: Wyatt, Jacqueline  
APPLICANT: Zhang, Hong  
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling  
FILE REFERENCE: ISPH-545  
CURRENT APPLICATION NUMBER: US/10/619,220  
CURRENT FILING DATE: 2003-07-14  
PRIOR APPLICATION NUMBER: 09/802,669  
PRIOR FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: US 09/665,615  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 09/290,640  
PRIOR FILING DATE: 1999-04-12  
NUMBER OF SEQ ID NOS: 180  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 67  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Sequence  
US-10-619-220-67

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 231 GCAGCAATGGGAATCCGCGG 250  
||||| ||| ||| |||  
Db 1 GCAGCAAGGGAACAGCGG 20

RESULT 2859

US-09-984-637-7  
Sequence 7; Application US/09984637  
Publication No. US20040048246A1  
GENERAL INFORMATION:

APPLICANT: Tosoh Corporation  
TITLE OF INVENTION: OLIGONUCLEOTIDE FOR DETECTION OF HIV-1 AND DETECTION METHOD  
FILE REFERENCE: PA211-0315  
CURRENT APPLICATION NUMBER: US/09/984,637  
CURRENT FILING DATE: 2001-10-30  
NUMBER OF SEQ ID NOS: 30  
SEQ ID NO 7  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Oligonucleotide hybridizable with a specific site of HIV-1 RNA  
US-09-984-637-7

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2155 TTTTTCCTCTTTT 2174  
||||| ||| ||| |||  
Db 1 TTTTCTTACTTTGTTT 20

RESULT 2860

US-09-923-517-67  
Sequence 67; Application US/09923517  
Publication No. US20020039741A1  
GENERAL INFORMATION:

APPLICANT: Nicholas M. Dean; Robert A. McKay; Loren J. Miraglia; Brenda F. Baker  
TITLE OF INVENTION: Antisense Oligonucleotide Compositions and Methods for the Modulation of Activating Protein 1  
NUMBER OF SEQUENCES: 139  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Jane Massey Licata

STREET: 66 East Main Street  
CITY: Marlton  
STATE: NJ  
COUNTRY: USA  
ZIP: 08053  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: WINDOWS 95  
SOFTWARE: WORDPERFECT 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/923,517  
FILING DATE: 07-Aug-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/364,416  
FILING DATE: 1999-07-30  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISPH-0209  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 810-1515  
TELEFAX: (609) 810-1454  
INFORMATION FOR SEQ ID NO: 67:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: Nucleic Acid  
STRANDEDNESS: Single  
TOPOLOGY: Linear  
ANTI-SENSE: Yes  
SEQUENCE DESCRIPTION: SEQ ID NO: 67:  
US-09-923-517-67

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 632 CTGGATGCCGGCGCTGC 651  
||||| ||| ||| |||  
Db 1 CTGGATGCCGGCTGCTGC 20

RESULT 2861

US-09-792-440B-9  
Sequence 9; Application US/09792440B  
Publication No. US20030017456A1  
GENERAL INFORMATION:

APPLICANT: Boyd, Robert Simon  
APPLICANT: Stamps, Alasdair Craig  
APPLICANT: Terrett, Jonathan Alexander  
APPLICANT: Tyson, Kerry Louise  
TITLE OF INVENTION: Diagnosis and Treatment and Related  
TITLE OF INVENTION: Preparations  
FILE REFERENCE: 2543-1-006N  
CURRENT APPLICATION NUMBER: US/09/792,440B  
CURRENT FILING DATE: 2002-05-21  
PRIOR APPLICATION NUMBER: GB 0004576.5  
PRIOR FILING DATE: 2000-02-25  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 20  
TYPE: DNA  
ORGANISM: human  
US-09-792-440B-9

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 849 CTGGAAGATTGCTCCTC 868  
||||| ||| ||| |||



RESULT 2856

US-10-188-248-184/c  
; Sequence 184, Application US/10188248  
; Publication No. US20040029790A1  
; GENERAL INFORMATION:

; APPLICANT: Patturajan, Meera  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Anderson, David W.  
; APPLICANT: Taupier Jr., Raymond J.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Guo, Xiaojia Sasha  
; APPLICANT: Casman, Stacie J.  
; APPLICANT: Hfalt, Tord  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Shimkets, Richard A.  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Zhong, Mei  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Li, Li  
; APPLICANT: Shenoy, Suresh G.  
; APPLICANT: Gorman, Linda  
; APPLICANT: Edinger, Shlomit R.

; TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS  
; FILE OF INVENTION: THE SAME

; FILE REFERENCE: 21402-297D  
; CURRENT APPLICATION NUMBER: US/10/188,248  
; CURRENT FILING DATE: 2002-07-02  
; PRIOR APPLICATION NUMBER: 60/303,046  
; PRIOR FILING DATE: 2001-07-05  
; PRIOR APPLICATION NUMBER: 60/303,828  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: 60/358,932  
; PRIOR FILING DATE: 2002-02-22  
; PRIOR APPLICATION NUMBER: 60/304,502  
; PRIOR FILING DATE: 2001-07-11  
; PRIOR APPLICATION NUMBER: 60/305,011  
; PRIOR FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: 60/305,262  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 60/307,536  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/306,085  
; PRIOR FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: 60/308,228  
; PRIOR FILING DATE: 2001-07-27  
; PRIOR APPLICATION NUMBER: 60/323,449  
; PRIOR FILING DATE: 2001-09-19

; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 234

; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 184

; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe  
US-10-188-248-184

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1082 GTAGAAGGTGAAGCTGTTCA 1101  
| | | | | | | | | | | | | | | | | |  
Db 20 GGACAAGGTGAATCTGCTCA 1

RESULT 2857

US-10-072-012-1014  
; Sequence 1014, Application US/10072012  
; Publication No. US20040033493A1  
; GENERAL INFORMATION:

; APPLICANT: Tchernev, Velizar  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Li, Li  
; APPLICANT: Gangolli, Esha  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Anderson, David W.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Taupier Jr., Raymond J.  
; APPLICANT: Gusev, Vladimir Y.  
; APPLICANT: Colman, Steven D.  
; APPLICANT: Wolenc, Adam R.  
; APPLICANT: Pena, Carol E. A  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Grosse, William M.  
; APPLICANT: Alsobrook II, John P.  
; APPLICANT: Lepley, Denise M.  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Burgess, Catherine E.

; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-258

; CURRENT APPLICATION NUMBER: US/10/072,012  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: 60/265,102  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 60/265,514  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/265,517  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/265,412  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/265,395  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/266,406  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 60/266,767  
; PRIOR FILING DATE: 2001-02-05  
; PRIOR APPLICATION NUMBER: 60/267,057  
; PRIOR FILING DATE: 2001-02-07  
; PRIOR APPLICATION NUMBER: 60/266,975  
; PRIOR FILING DATE: 2001-02-07  
; PRIOR APPLICATION NUMBER: 60/267,459  
; PRIOR FILING DATE: 2001-02-08

; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1391

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1014

; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Ag2956 Reverse  
US-10-072-012-1014

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1069 CCTGACATCCTTAGTAGAAG 1088  
| | | | | | | | | | | | | | | | | |  
Db 1 CCAGAGATCCTTGGCAGAAG 20

RESULT 2858

US-10-619-220-67  
; Sequence 67, Application US/10619220  
; Publication No. US20040033979A1  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Nicholas M.



```
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 776
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-776
```

```
Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1966 AATATTACCTTGAAAAAAA 1985
      ||||| ||||| ||||| |||||
Db 1 AAAATCAACGTTGAAAAAAA 20
```

```
RESULT 2849
US-09-776-479-855/c
; Sequence 855, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 855
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-855
```

```
Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1776 TTTTGAACCCCATCTTT 1795
      ||||| ||||| ||||| |||||
Db 20 TTTTGAACGTCATGTTT 1
```

```
RESULT 2850
US-09-776-479-855/c
; Sequence 855, Application US/09776479
; Publication No. US20040067902A9
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
```

```
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 855
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-855
```

```
Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1776 TTTTGAACCCCATCTTT 1795
      ||||| ||||| ||||| |||||
Db 20 TTTTGAACGTCATGTTT 1
```

```
RESULT 2851
US-09-993-731-85/c
; Sequence 85, Application US/09993731
; Publication No. US20030105040A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B-R EXPRESSION
; FILE REFERENCE: RTS-0302
; CURRENT APPLICATION NUMBER: US/09/993,731
; CURRENT FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 85
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-993-731-85
```

```
Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1081 AGTAGAGGTGAAGCTGTT 1100
      ||||| ||||| ||||| |||||
Db 20 AGCAGTGGGTGAAGCTGTAC 1
```

```
RESULT 2852
US-09-953-348-89/c
; Sequence 89, Application US/09953348
; Publication No. US20030134398A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, David. H
; APPLICANT: Mao, Yingqing
; APPLICANT: Varoglu, Mustafa
; APPLICANT: He, Min
; APPLICANT: Sheldon, Paul
; TITLE OF INVENTION: MITOMYCIN BIOSYNTHETIC GENE CLUSTER
; FILE REFERENCE: 600.530US1
; CURRENT APPLICATION NUMBER: US/09/953,348
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: PCT/US00/06394
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/266965
; PRIOR FILING DATE: 1999-03-12
```

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1543 AGAGTAGGGAAGGAACAGGA 1562  
||| | ||||| |||  
Db 20 AGACTGAGGAAGGAAGTGGGA 1

RESULT 2844  
US-09-776-479-353/c  
; Sequence 353, Application US/09776479  
; Publication No. US20040067902A9  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 353  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-353

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1543 AGAGTAGGGAAGGAACAGGA 1562  
||| | ||||| |||  
Db 20 AGACTGAGGAAGGAAGTGGGA 1

RESULT 2845  
US-09-776-479-525/c  
; Sequence 525, Application US/09776479  
; Publication No. US20030087848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 525  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-525

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1776 TTTTGTGAACCCCATCTTT 1795  
||||| ||| |||  
Db 20 TTTTGTGAACGTCATGTTT 1

RESULT 2846  
US-09-776-479-525/c  
; Sequence 525, Application US/09776479  
; Publication No. US20040067902A9  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 525  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-525

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1776 TTTTGTGAACCCCATCTTT 1795  
||||| ||| |||  
Db 20 TTTTGTGAACGTCATGTTT 1

RESULT 2847  
US-09-776-479-776  
; Sequence 776, Application US/09776479  
; Publication No. US20030087848A1  
; GENERAL INFORMATION:  
; APPLICANT: Bratzler, Robert L.  
; APPLICANT: Petersen, Deanna M.  
; APPLICANT: Fouron, Yves  
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
; TITLE OF INVENTION: Treatment of Asthma and Allergy  
; FILE REFERENCE: C1037/7013 (HCL/MAT)  
; CURRENT APPLICATION NUMBER: US/09/776,479  
; CURRENT FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: US 60/179,991  
; PRIOR FILING DATE: 2000-02-03  
; NUMBER OF SEQ ID NOS: 1093  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 776  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Sequence  
US-09-776-479-776

Query Match 0.5%; Score 13.6; DB 1; Length 20;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1966 AATATTACCTGAAAAAA 1985  
||| | ||||| |||  
Db 1 AAAATCAACGTCGAAAAAA 20

RESULT 2848  
US-09-776-479-776  
; Sequence 776, Application US/09776479



```
RESULT 2840
US-09-784-674-776/c
; Sequence 776, Application US/09784674
; Publication No. US20030054346A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Karen W.
; Wolber, Paul K.
; Delenstarr, Glenda C.
; Webb, Peter G.
; Kincaid, Robert H.
; TITLE OF INVENTION: Methods for evaluating oligonucleotide
; probe sequences
; NUMBER OF SEQUENCES: 1165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Records Manager, Legal Department, Hewlett-Packard
; STREET: 3000 Hanover Street
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/784,674
; FILING DATE: 15-Feb-2001
; CLASSIFICATION: No. US20030054346A1 available
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/021,701
; FILING DATE: 10-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Choi, Wendy A.
; REGISTRATION NUMBER: 36,697
; REFERENCE/DOCKET NUMBER: 10971464-1
; TELEPHONE: 650-236-2386
; TELEFAX: 650-852-8063
; INFORMATION FOR SEQ ID NO: 776:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 776:
US-09-784-674-776

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2782 ATTGAAAAAATAAATAA 2801
Db 20 ATTGACAGAGAAAAATAA 1

RESULT 2841
US-09-915-485-34/c
; Sequence 34, Application US/09915485
; Publication No. US20030083281A1
; GENERAL INFORMATION:
; APPLICANT: Mark J. Graham
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF SERUM AMYLOID A4 EXPRESSION
; FILE REFERENCE: RTS-0251
; CURRENT APPLICATION NUMBER: US/09/915,485
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 89
```

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; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-915-485-34

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1390 GGTGTCTGCCCTGCAGAACT 1409
Db 20 GGTGTCTGGCTGCTAAACT 1

RESULT 2842
US-09-918-187-62
; Sequence 62, Application US/09918187
; Publication No. US20030083282A1
; GENERAL INFORMATION:
; APPLICANT: Rosanne M. Crooke
; APPLICANT: Mark J. Graham
; TITLE OF INVENTION: ANTISENSE MODULATION OF STEAROYL-COA DESATURASE EXPRESSION
; FILE REFERENCE: ISPH-0590
; CURRENT APPLICATION NUMBER: US/09/918,187
; CURRENT FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 80
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-918-187-62

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 484 CCAGAGCCAGGAGGAGCGG 503
Db 1 CCCGAGCCAGGAGAGAAAGG 20

RESULT 2843
US-09-776-479-353/c
; Sequence 353, Application US/09776479
; Publication No. US20030087848A1
; GENERAL INFORMATION:
; APPLICANT: Bratzler, Robert L.
; APPLICANT: Petersen, Deanna M.
; APPLICANT: Fouron, Yves
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the
; FILE REFERENCE: C1037/7013 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/09/776,479
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,991
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 353
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-776-479-353

Query Match          0.5%; Score 13.6; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.1e+03;
```



